Efficiency of Clonal Selection on Improving Some Economical Characters of Sweet Potato (*Ipomoea batatas* L.)

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ABSTRACT

Two field experiments were conducted in order to study the effect of one cycle of clonal selection on some economical characters of sweet potato and to estimate the magnitude of variability and heritability, as well as calculate phenotypic correlation coefficients among all possible pairs of the studied characters. In this respect, this work was carried out at the Experimental Station Farm (at Abies), the Faculty of Agriculture, Alex. Univ., during two summer seasons of 2014 and 2015. The obtained results illustrated, generally, that the estimated coefficients of variability and ranges for the all studied characters of "Abies" cultivar reflected high and enough variability, which suggested high possibilities of conducting successful and efficient selection to produce improved cultivar with better performance than its original population. Also, the recorded results demonstrated, in general, that one cycle of clonal selection population; exhibited high efficiency for improving all studied characters, but with different rates, comparing with the original population. The estimated values of the broad sense heritability (h^2_{bs}) for the various studied characters were found to be in the range from 71.09% for roots number plant^{-1}, up to 99.17% for root dry matter. Correlation estimate revealed many significant associations among the various pairs of the studied characters; which appeared to be desirable for achievement the objectives of the selection in the present study. Accordingly, improving roots yield and its components of sweet potato can be achieved through purification of "Abies" cultivar to produce improved clones through clonal selection program.

Key words: sweet potato, clonal selection, heritability, correlation, genetic variability.

INTRODUCTION

Sweet potato (*Ipomoea batatas* (L.) Lam) is a member of the Convolvulaceae and considered the most important popular root and food crop in Egypt as well as many other tropic and sub-tropic countries. It belong to the genus *Ipomoea*, which has four ploidy levels; the cultivated sweet potato; a hexaploid [2n = 6x = 90] (Austin, 1988).

Because of its, relatively, low yield productivity of sweet potato and great variability which noticed among individual plants of commercially grown population; it is vital to start a breeding program for improving sweet potato. In asexual propagated crops, the clonal selection method considered more suitable for this purpose, since it is well known that sweet potato is one of the most important crop belong to asexual group. Many investigators studied the effects of clonal selection method to improve asexual propagated vegetable crops, such as garlic (Lammerink and Wallace, 1987; Sakr, 1996), artichoke (Habib, 2001), potato (Souza, 2005) and sweet potato (GunjanJha, 2012). Whereas, their results indicated that using clonal selection program was an effective method in improving the studied characters of these crops. The magnitude of variability among sweet potato genotypes; which estimated by Anshebo *et al*. (2004); Engida *et al*.

(2006 and 2007); GunjanJha (2008 and 2012) recorded considerable variability among the genotypes for the characters under consideration.

It is known that the effectiveness of plant breeding programs, particularly, in selection depends on the relative importance of genetic and non-genetic factors in the expression of phenotypic differences among genptypes in a population, referred to heritability. Heritability is a measure of genetic relationship between parent and progeny and has been widely used in determining the degree to which a character may be transmitted from parents to offspring. Heritability estimates for some important characters of sweet potato carried out by several researchers (Evoor *et al*., 2008; GunjanJha 2012; Wera *et al*., 2014; Sandhu *et al*., 2015).

Selection for storage root yield, which is a polygenic trait, often leads to changes in other characters. Therefore, knowledge of the relationship that exists between storage root yield and other characters and interrelationships among various characters is necessary in order to design appropriate selection criteria in sweet potato breeding programs. In this respect, phenotypic correlation coefficients between various of pairs of sweet potato characters were estimated by many investigators (Teshome *et al*., 2004; Devi *et al*.,

2008; Gedamu *et al.*, 2010; Afuape *et al.*, 201; GunjanJha, 2012).

Accordingly, the present investigation was established to select some clones of local sweet potato "Abies" cultivar in addition to determine interrelationships among the various studied agronomic traits, using the estimation of phenotypic correlation coefficients, in order to the heritability percentages in broad sense were estimated for their importance in evaluative purposes in breeding programs.

MATERIALS AND METHODS
Experimental site
During both summer seasons of 2014 and 2015, two field trials were carried out at the Experimental Station Farm, in Abies region, the Faculty of Agriculture, Alexandria University, Alexandria Governorate, Egypt.

Original genetic material (First season)
The clonal selection breeding program started with commercial population consisting of about 3000 stem cuttings of sweet potato "Abies" cultivar, which considered the widely cultivar grown in Alexandria and other Governorates in Egypt. Both top and middle portions of vine cuttings of mature plants with 3 – 4 nodes and about 20 – 30cm long were clipped off and planted on one side of the row on April 20th of 2014. The experimental area included 190 rows, 4.0 m long and 0.7 m wide, and the spacing between plants was 0.25m. All agricultural practices such as fertilization, irrigation and pests control were performed as recommended for commercial sweet potato production.

Data recorded and estimates of variability
The recorded data were measured on the basis of individual plants at three periods. The first period was about 90 days from transplanting i.e., when the plants were totally grown, where two vegetative growth characters; i.e., vine length(cm) and branches number plant[-1] were determined. At the harvesting stage, the second period, after about 135 days from transplanting, storage roots were dug up of each hill , then the following characters were recorded; root length (cm), root diameter (cm), root weight (g), roots number plant[-1], total roots yield plant[-1], marketable roots yield plant[-1], root dry matter (%), and the carotene content (mg/100g fresh weight) was assayed according to Davies procedure (1976).

The mentioned characters were manipulated to calculate the statistical parameters; mean (X), rang (R), and coefficient of variation (C.V.%) for each character.

Selection the first clones generation
The best 125 plants from the original population, at the beginning roots formation, were primarily selected on the basis of the two vegetative growth characters, as reported earlier. At harvesting stage, a second selection according to the above-reported traits of the roots yield and its components, was conducted to came out 50 plants. The stem cuttings of each selected plants as well as samples of original population were cut separately and transplanted in the nursery on September 10th of 2014 , for the next season. A third and more severe selection; on the basis of root dry matter and carotene content was conducted within the second selected plants to obtain, finally, on six plants (clones).

Evaluation of the derived clones with the original population (second season)
Stem cuttings of each clone of the best six selected clones and representative samples of the original population of "Abies" cultivar, were prepared and transplanted to evaluate in summer season on April 20, 2015, using a randomized complete blocks design (RCBD) with three replicates. Each plot consisted of three rows, 4m long and 0.70 m wide. The planting was done on the rows at 0.25m spacing and all recommended cultural practices for commercial sweet potato production were followed.

Data of the various interested characters; as the first season; were recorded to be used for genetic evaluation and estimation some of the most important biometrical parameters; such as phenotypic correlation coefficients between different pairs of studied characters which estimated, as described by Mather and Jinks (1971). Heritability in broad sense (h^2_{bs}%) were also calculated as suggested by Allard (1960) as follows:

$$H^2_{bs}\% = (\delta^2_g / \delta^2_p) \times 100$$

$\delta^2_p = \delta^2_g + \delta^2_e$

$\delta^2_g = MS_g - (MS_e)/r$

Where

δ^2_p = phenotypic variance

δ^2_g = genotypic variance

δ^2_e = environmental variance (error mean square)

Statistical analysis
All collected data of the previously mentioned characters were recorded, statically analyzed according to the used design and as illustrated by Al-Rawi and Khalf-Allah (1980), using Co-Stat Software (2004). The differences among the various means were tested using Duncan's multiple range test (L.S.R.).

RESULTS AND DISCUSSION
The results of the estimated values for the statistical parameters; means (x), ranges (R) and coefficients of variation (C.V.%) for all the studied traits of the original population of sweet potato "Abies" cultivar are given in Table(1). The recorded result indicated that the original population expressed high variability for most studied characters as appeared from the estimated values of coefficients of variation which ranged from 20.24% for root diameter to 54.98% for marketable roots yield plant[-1].

Table 1: Means ($\overline{\text{X}}$), ranges and coefficients of variation (C.V. %) for all studied characters of the original population of "Abies" cultivar of sweet potato in 2014 season.

Parameters / Character	Rang (R)	Mean X	Coefficient of variation (C.V.%)
Vine length (cm)	50 – 230	117.47	30.73
Branches No. plant[-1]	2 – 7	4.33	31.76
Root length (cm)	8 – 24	14.50	22.77
Root diameter (cm)	4 – 11	7.61	20.24
Root weight (g)	0.70 – 600.0	255.00	49.28
Roots number plant[-1]	2 – 10	4.09	40.99
Total roots yield plant[-1] (kg)	0.200 – 2.00	1.01	51.56
Marketable yield plant[-1] (kg)	0.15 – 1.800	0.81	54.98
Root dry matter (%)	20 – 43	32.59	22.40
Carotene contents	2 – 7	4.59	28.24

Also, all studied characters had wide range between the lowest and highest value for each character. Such results may be taken place due to that "Abies" cultivar has been commercially grown without any purification for a long time. Therefore, this supported the high possibilities of conducting successful and efficient selection to introduce clones, with better performances than their original population. These results were in confirmatory with the findings of other workers as Engida *et al.* (2007) and GunjanJha (2008) for number of roots plant[-1]; Teshome *et al.* (2004); Engide *et al.* (2007); Evoor *et al.* (2008); GunjanJha (2008) for root length. Teshome *et al.* (2004); Engida *et al.* (2007); GunjanJha (2008) for roots yield plant[-1].

Concerning the comparisons among the means values of the studied characters of the seven different populations; i.e., populations derived from the clonal selection cycle (clone1 to clone6), and the original population (O.P.) are listed in Table (2). The obtained results indicated, clearly, that all selected clones showed different degrees of superiority over the original population. These results seemed to be in accordance with the results obtained by several investigators as Wanas (2002) for number of roots plant[-1] and roots yield plant[-1] characters, and Omran *et al.* (2002b) for root dry matter; when they compared some sweet potato genotypes for these characters. The highest mean values in this respect appeared to be in the clone number 3 (clone3), followed by the clone4 and clone6. These three clones reflected, significantly, the highest mean values in the most studied characters. The relative increments of these three clones (clone3, clone4 and clone-6) on their total roots yield plant[-1], marketable roots yield plant[-1], root weight, root dry matter and carotene content, were estimated by 72.72%, 94.44%, 21.53%, 31.52% and 19.05%, respectively in the case of clone3; 59.09%, 88.89%, 21.53%, 35.81% and19.05%, respectively, in the case of clone4 and 63.64%, 92.22%, -0.06%, 1.85% and 19.05%,

consecutively, in the case of clone6. These results illustrated, generally, that the one cycle of clonal selection reflected high efficiency for improving all studied characters with different rats. Evaluation studies of the developed new sweet potato clones and/or cultivars were realized by several workers as Omran *et al.*(2002a); Wanas (2002); Anshebo *et al.* (2004). These evaluation work recorded significant differences among the selected clones or genotypes of sweet potato in their studied characters.

The estimates of phenotypic and genotypic variances as well as heritability (in broad sense) percentages for all studied characters of the studied genotypes of sweet potato are shown in Table (3). The results revealed considerable phenotypic and genotypic variances among the genotypes for all the studied traits. In all traits a large portion of the phenotypic variance was accounted by the genetic components. Generally, the obtained results indicated that the most of the observable variability were gave rise due to the genetic variations, since the contributions of genetic variance to phenotypic variance ranged from 0.71% for roots number plant[-1] to 0.99% for root dry matter. This is indication for the existence of immense inherent variability that remains unchanged by environmental conditions among the genotypes which in turn is more useful for exploitation in selection program. The obtained results are in the parallel with the findings obtained by Engida *et al.* (2007) who had obtained similar trends concerning the estimates of gentypic and phenotypic variances for several sweet potato characters.

The estimated values of the broad sense heritability (H^2_{bs}%) are presented in Table (3). The registered results illustrated, generally, that the estimated percentages of H^2_{bs}, for the various studied characters were found to be in the range from 71.09% for roots number plant[-1], up to 99.71% for root dry matter.

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Table 3: Estimates of phenotypic variance (δ^2_p), genotypic variance (δ^2_g) and broad sense heritability ($H^2_{b.s.}$%) for the ten studied characters of the evaluated genotypes of sweet potato

Parameters / Characters	σ^2_g	σ^2_p	$H^2_{b.s.}$%
Vin length (cm)	1930.91	2048.66	94.25
Branches No. plant[-1]	3.474	4.269	81.38
Root length (cm)	25.768	29.481	87.41
Root diameter (cm)	11.896	12.809	92.87
Root weight (g)	4557.194	4815.45	94.64
Roots number plant[-1]	1.931	2.716	71.09
Total roots yield plant[-1] (kg)	0.078	0.091	85.71
Marketable roots yield plant[-1] (kg)	0.151	0.163	92.64
Root dry matter (%)	88.139	88.874	99.17
Carotene contents	0.415	0.553	75.05

The estimates of heritability percentages in broad sense for both roots number plant[-1] and carotene content characters showed, relatively, high value of 71.09% and 75.05%, each in turn. This result demonstrated that genetic variance seemed to contribute with relatively high portion of the total variance. Engida *et al*. (2007) found that the estimated heritability (in broad sense) value of number of storage roots was found to be 73.00%. These results indicated that additive genetic variance constituted much more to the total variance than non-additive effects in the inheritance of such characters

In turns of the remaining eight characters; vine length, branches number plant[-1], root length, root diameter, root weight, total roots yield plant[-1], marketable roots yield plant[-1] and root dry matter; the estimated values of H^2_{bs}% were found to be high (more than 80%). The results of the most previously mentioned characters are, in general, in compatible with the findings of Anshebo *et al*. (2004) for number of branches plant[-1] and root weight; Engida *et al*. (2007); Evoor *et al*., (2008); GunjaniJha (2008) for vine length and Engida *et al*. (2007), Evoor *et al*. (2008); GunjanJha (2008) for tuber roots yield per plot. These authors reported that the estimated values of heritability in broad sense for all mentioned characters of sweet potato were found to be high. Their results indicated, generally, that the presence of additive components of genetic variance was more important than that of non-additive component in the inheritance of these characters. Hence, satisfactory progress can be achieved by individual selection on these characters.

With regard to the estimated values of phenotypic correlation coefficients among all possible pairs of the studied characters, the gained results of Table (4) illustrated, generally, that 12 out of the possible 45 relationships appeared to be desirable for the improvement of sweet potato using clonal selection method, and highly correlated, since their estimated correlation coefficients were found to be either significant or highly significant. On the

other hand, the other phenotypic correlation coefficients (33 relationships) were found too small to be significant.

Desirable association were detected between total roots yield plant[1] with each of root weight (with a positive trend), and roots number plant[-1] (with negative trend). In the same line, desirable correlation coefficients were observed between marketable roots yield plant[-1] with each of total root yield plant[-1] and root weight with positive associations. Gedamu *et al*. (2010) found that total yield reflected positive effect with each of marketable and root weight. The existence of significant association between total roots yield and average roots weight was confirmed by Islam *et al*. (2002) and Engida *et al*. (2006).The results indicated also that the character of root length reflected negative and significant correlation with roots number plant[-1], and with the character of root weight with positive and highly significant correlation. Among significant phenotypic associations exhibited between pairs of the studied characters, highly significant positive correlations were observed between carotene content with each of vine length, branches number, root diameter and root dry matter with significant positive correlation. On the other side, negative correlations were showed between root dry matter and root diameter (with significant level), and vine length with branches number (with highly significant level). These results indicated that increasing any of these characters would associated with a reducing effect on the other, suggesting that attention should be given in breeding programs for these characters.

Various workers studied the relationships between different traits in sweet potato such as Islam *et al*. (2002); Engida *et al*. (2006). Islam *et al*. (2002) showed that the characters vine length, number of roots and root diameter recorded positive and significant correlation with roots yield character. While, Alcoy (2007) reported a significant association between total roots yield and marketable roots yield.

CONCLUSION

All selected clones after one cycle of clonal selection breeding program reflected improvement and superiority over the original population, for all studied characters with different degrees. The results of variance components and heritability estimates indicated that most of the variability were due to genetic variation, and the contribution of additive gene action was much more to the total variance than the non-additive gene action in the inheritance of such characters. Accordingly, improving roots yield and its components of sweet potato can be achieved through purification of "Abies" cultivar and introducing improved clones through clonal selection program.

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الملخص العربى

كفاءة انتخاب السلالة الخضرية علي تحسين بعض الصفات الاقتصادية في البطاطا

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نفذت تجربتان حقليتان وذلك بهدف دراسة تأثير دورة من انتخاب السلالة الخضرية علي بعض الصفات الهامة في البطاطا صنف أبيس بالإضافة إلي تقدير حجم الاختلافات وذلك من خلال تقدير معامل الاختلاف والمدي، كفاءة التوريث بالمعنى الواسع وكذلك معامل الارتباط المظهري بين أزواج الصفات المختلفة، أجريت هذه الدراسة بمحطة البحوث الزراعية بأبيس التابعة لكلية الزراعة – جامعة الإسكندرية– خلال الموسم الصيفى لعامى ٢٠١٤ و ٢٠١٥.

أظهرت النتائج بصفة عامة وجود اختلافات وراثية واضحة وبدرجات متفاوته بين النباتات للصفات المختلفة وذلك في العشيرة الأصلية للبطاطا، والتي عكست أهمية البدء بأحد برامج التربية لتحسين البطاطا والتي منها انتخاب السلالة الخضرية. أوضحت النتائج أيضا أن استخدام برنامج انتخاب السلالة الخضرية أدي إلي تحسين ملحوظ ومعنوي في كل الصفات موضع الدراسة بعد دورة من الانتخاب مقارنة بالعشيرة الأصلية وذلك من خلال تقدير المتوسطات للصفات المختلفة ومقارنتها إحصائيا. تقدير كفاءة التوريث بالمعنى الواسع للصفات المدروسة تراوحت بين ٧١.٠٩%– ٩٩.١٧% لصفتى عدد الجذور للنبات والمادة الجافة للجذور على الترتيب. وعكست دراسة معامل الارتباط المظهري وجود العديد من علاقات الارتباط المرغوبة بين أزواج الصفات المختلفة، مما يعكس أهمية أخذها في الاعتبار عند إجراء الانتخاب كأحد الوسائل(الأدوات) الهامة التي يمكن أن يستفيد بها مربي النباتات في برامج الانتخاب.