HERITABILITY AND PHENOTYPIC CORRELATION COEFFICIENT ESTIMATES FOR SOME IMPORTANT CHARACTERS OF SWEET POTATO (Ipomoea batatas (L), Lam)

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ABSTRACT

Sixteen clones and the original population of sweet potato "Abies" cultivar were used in this study. The experimental work was conducted during two successive summer seasons of 2005 and 2006. The study aims to calculate the phenotypic correlation coefficients among all possible pairs of the agronomic studied traits; i.e., vine length, number of branches plant^{-1}, number of roots plant^{-1}, root fresh weight, roots weight plant^{-1}, root dimensions (root length and root diameter) as well as some chemical compositions of roots viz. total sugars, starch, carbohydrates and carotene. In addition, heritability percentages, in broad sense, were estimated using the analysis of variance components for sixteen sweet potato clones.

The results, generally, indicated that most of the observable variabilities were due to the studied genetic variations, since, the contributions of genetic variance to phenotypic variance for the traits ranged from 30.95% for number of roots plant^{-1} to 96.24% for vine length. This gave an indication for the existence of enormous inherent variability that remains unaltered by environmental conditions among the clones, which in turn is more useful for exploitation in selection programs. The results of the estimated values of heritability percentage in broad sense (H^2_{bs}) appeared to be low (30.95% for vine length), intermediate (51.57% for root diameter), relatively high (69.27% and 70.29% for number of branches plant^{-1} and weight of roots plant^{-1}, respectively), and high for the remaining eight characters, which were found to be more than 87%. Moreover, the estimated phenotypic correlation coefficients, values, generally, illustrated that 19 out of all possible 66 relationships appeared to be desirable for the improvement of sweet potato study by using clonal selection technique, since, their estimated correlation coefficients were found to be either significant or highly significant. On the other hand, the other phenotypic correlation coefficients (47 relationships) were found too small to be significant. So, understanding the association between root yield plant^{-1} and other agronomic traits indicated that the interrelationships among various agronomic traits are necessary for the intelligent choice for evaluative purposes and breeding methods which would make possible selection for simultaneous improvement of desirable traits in any crop under consideration.

Key words: Agronomic traits, correlation coefficients, heritability, sweet potato

INTRODUCTION

Sweet potato [(Ipomoea batatas (L), Lam, 2n= 6x= 90); Ozias-Akins and Jarret, 1994] is considered the most important popular root and food crop in Egypt as well as many other tropic and sub-tropic countries. As a world crop, it ranks the second most important root and tuber crops after potato (Woolfe, 1992 and FAO, 1997), since, tuberous or storage roots are a good source of carbohydrates, proteins, vitamins C and A, carotene and some minerals (Woolfe, 1992; Morrison et al., 1993; Onwveme and Charles, 1994).

Heritability (H) is one of the most important parameters that should be considered in breeding studies for metric characters. The effectiveness of plant breeding programs, particularly, in selection for traits improvement depends on the relative importance of genetic and non-genetic factors in the expression of phenotypic differences among genotypes in a population, referred to heritability. It is estimated as the ratio of the observable variation due to genotypic differences (Vg) to the total phenotypic variation (Vp); i.e. Vg/Vp. The structure of Vg depends on the degree of relationship between individuals within entries; Vg equals the total generic variance if the entries are clones and is an estimate of H. In theory, both H^2_{bs} in (broad sense) and h^2_{ns} in (narrow sense) heritability estimates can vary from 0 to 1.0 and they usually are multiplied by 100 and referred to as heritability percentage. Heritability estimates for some important characters of sweet potato were carried out by several researchers, such as Jones (1969, 1970, 1977 and 1986); Kamalam et al. (1977); Thamburaj and Muthukrishnan (1978); Naskar et al. (1986); Chen et al. (1989); Mok et al. (1997); Anshebo et al. (2004). Their results illustrated, generally, that the estimated percentages of heritability in both broad and narrow senses ranged from low to moderately high values. Also, the differences in the estimated values could be actually related to the particular genetic population in which it was estimated under what particular conditions and the used method of estimation. In addition, most of authors stated that the visual selection for the studied characters of sweet potato would be reasonably effective.

Correlation coefficient is as an important tool for the breeder to help in selecting a difficult measured character through the selection of another easier in measuring, when they are significantly correlated. Therefore, knowledge of the relationship among various characters is necessary to design appropriate selection criteria in sweet potato breeding programs. According to Grafuis (1959), increasing total yield would be made easier by selecting for components because the components are more simply inherited than the total yield itself, which is a polygenic trait. Thus, studies on correlation enable the breeder to know the mutual relationship between characters on which selection can be used for genetic improvement.

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In this respect, phenotypic correlation coefficients between various pairs of sweet potato characters were estimated by many investigators (e.g. Jones 1969 and 1977; Lowe and Wilson 1974 and 1975; Kamalam *et al.* 1977; Thamburaj and Muthukrishnan 1978; Li 1982; Naskar *et al.* 1986; Li *et al.* 1990; Hossain *et al.* 2000; Omran *et al.* 2002; Anshebo *et al.* 2004 and Tsegaye *et al.* 2006). The results of these authors concerning the relationships between various pairs of sweet potato characters suggested, generally, that improvement aimed at any of the studied character would automatically lead to improvement of the other.

Accordingly, the present investigation was established to determine interrelationships among the various studied agronomic traits to assist sweet potato's breeders in their selection program, using the estimation of phenotypic correlation coefficients. Moreover, the heritability percentages in broad sense were estimated for their importance in evaluative purposes in breeding programs.

MATERIALS AND METHODS

This investigation was performed at the Experimental Station Farm, at Abies region, Faculty of Agriculture, Alexandria University, Alexandria, Egypt, during two successive summer seasons of 2005 and 2006.

The used genetic material of this study started with original population of sweet potato "Abies" cultivar. The stem cuttings, 25-35 cm long, were taken, prepared and transplanted on one side of the row on April 17th, 2005. Then, the best sixteen clones from the original population were selected. Clonal selection technique was conducted on the sweet potato to improve some vegetative growth, yield and its components as well as some chemical components of roots.

The stem cuttings of the sixteen clones as well as samples of the original sweet potato population of "Abies" cultivar were, separately, transplanted in the nursery on September 10, 2005, for further investigation.

The good and healthy stem cuttings of each clone and original population were transplanted to the field on April 14th, 2006. In this experiment, a randomized complete blocks design (R.C.B.D) with three replicates was used. Each replicate included 17 experimental units. Each plot consisted of four rows, 4 m long and 70 cm wide with spacing of 25 cm between the growing plants. All cultural practices were, also, applied as usually recommended for sweet potato's commercial production whenever they appeared necessary.

Measurements from the different genetic population; the tested sixteen selected clones and its original population; for sweet potato characters under consideration were taken on an individual plant basis. The studied characters were: vine length (cm), number of branches plant^{-1}, number of roots plant^{-1}, root fresh weight (g), root dry matter content (%), roots weight plant^{-1} (kg), root length (cm), root diameter (cm), and the chemical compositions of roots as total sugars (mg.g^{-1}d.w.), starch (mg.g^{-1}d.w.), carbohydrates (mg.g^{-1}d.w.), and carotene (mg.g^{-1}d.w.).

The data of the various studied characters were recorded, as previously mentioned, to be used for the estimation of the important parameters, phenotypic correlation coefficients and heritability percentages in broad sense. Data of the studied characters were arranged and statistically analyzed, using the standard method of the randomized complete blocks design, following the procedures described by Gomez and Gomez (1984), using Co-Stat Software (2004), computer program for statistics. The analysis of variance presented in Table 1

Table 1: Analysis of variance for the estimation of means squares for the replicates, genotypes and error components.

Source of variation (S. O. V.)	Degree of freedom (D. F.)	Sum of squares (S.S.)	Mean squares (M.S.)	Expected mean square (E.M.S)
Replicats.	r-1	SSr	MSr	$\sigma^2_e + g\,\sigma^2_r$
Genotypes	g-1	SSg	MSg	$\sigma^2_e + r\sigma^2_g$
Error	(r-1)(g-1)	SSe	MSe	σ^2_e

The phenotypic correlation coefficients, between the different pairs of the studied characters were estimated as illustrated by Mather and Jinks (1971), using the formula:

Phenotypic correlation =

$$\frac{co-\mathrm{var}\,iance"\,xy"}{\sqrt{\mathrm{var}\,ianceX\,\,\mathrm{var}\,ianceY}}$$

where:

X and Y were the characters (X) and (Y)

Heritability (H^2_{bs} %) in broad sense was also calculated according to Allard (1960), following this formula:

$$H^2_{bs}\% = \frac{\sigma_2 g}{\sigma_2 p} \times 100$$

70

where:

$$\sigma_g^2 = MSg - MSe/r$$

$$\sigma_p^2 = \sigma^2 g + \sigma^2 e$$

$\sigma_p^2 =$ Phenotypic variance

$\sigma_g^2 =$ Genotypic variance

$\sigma_e^2 =$ Environmental variance (error mean square)

RESULTS AND DISCUSSION

The obtained results for the estimated values of the various components of means square; i.e.,

replications, genotypes and errors; as well as degree of freedom of the studied characters are presented in Table 2. The results showed generally that there were highly significant (P< 0.01) differences among the genotypes for all the studied characters. These results may be attributed to the existence of large amount of variability among the selected sixteen clones (genotypes) of sweet potato. This finding is in general accordance with that obtained by Anshebo et al. (2004), who found that the analysis of variance revealed significant differences among the sweet potato genotypes for all traits under the study.

Table 2: Means squares of replicates, genotypes and errors for the different studied characters of the sixteen evaluated clones of sweet potato.

Parameters / Characters	MSr (2)^x	MSg (15)^y	MSe (30)^z
Vine length	84.7378	921.8257**	11.8576
No. of branches plant^{-1}	0.4262	9.3002**	1.1976
No. of roots plant^{-1}	0.0074	4.0926**	1.7496
Weight of roots plant^{-1}	20.8522	307608.94**	37980.7730
Root fresh weight	22.7196	1164.3237**	38.1056
Root dry matter	0.2709	14.6949**	0.65812
Root length	2.5207	4.6522**	0.2191
Root diameter	0.3353	0.7417**	0.1769
Total sugars	15.5416	744.5829**	30.6054
Starch	10.5472	704.0085**	13.9382
Carbohydrates	4.8232	1459.8517**	39.1355
Carotene	4.3444	0.0062**	0.00022

MS_g = Mean square due to genotypes MSe = Error mean square MSr = Replication mean square
x, y and z = Figures in parenthesis indicate the degree of freedom for MSr, MS_g and MSe

The estimates of phenotypic and genotypic variances as well as heritability (in broad sense) percentages for all studied characters of the sixteen clones of sweet potato are shown in Table 3. The results revealed considerable phenotypic and genotypic variances among the genotypes (clones) for all the parameters under consideration. In all traits a large portion of the phenotypic variance was accounted by the genetic component, with the exception of number of roots plant^{-1} and root diameter, in which the contributions of genetic variance to phenotypic variance were only 30.95% and 51.57%, respectively. Generally, the results reflected that most of the observable variabilities were due to the genetic variations, since, the contributions of genetic variance to phenotypic variance ranged from 69.27% for number of branches plant^{-1} to 96.24% for vine length. This is indication for the existence of immense inherent variability that remains unaltered by environmental conditions among the genotypes, which in turn is more useful for exploitation in selection program. These results are in general accordance with the findings of Jones et al. (1969), who investigated considerable phenotypic variance among ten storage root traits in sweet potato, and in every case a large part of this variance was accounted for the genotypic variance. Also, the present results are in the parallel

with the findings obtained by Tsegaye et al. (2007), who had obtained similar trends concerning the estimates of genotypic 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 results illustrated generally that the estimated percentages of H^2_{bs}, for the various studied characters, were found to be in the range from 30.95% for number of roots plant^{-1}, up to 96.24% for vine length. The estimated percentage of H^2_{bs} showed low value for number of roots plant^{-1} (30.95%). However, the estimated value of this character, in the present study, showed lower value than those obtained by Jones (1969) and Tsegaye et al. (2007), who found that the estimated heritability (in broad sense) values of number of storage roots were found to be 73.00% and 71.92%, respectively. Similarly, Thamburaj and Muthukrishnan (1978) and Mok et al. (1997) reported high heritability estimates for number of storage roots per plant. This result indicates that non-additive genetic variance constituted much more to the total variance than additive effects in the inheritance of such a character. Also, the low heritability value for the number of roots plant^{-1} character may suggest that this trait was greatly influenced by environmental factors.

Table 3: Estimates of phenotypic, genotypic and error variance components, and heritability percentages (in broad sense) for the studied characters of sweet potato.

Parameters / Characters	σ^2_g	σ^2_e	σ^2_p	H^2_{bs} %
Vine length	303.323	11.8576	315.181	96.24
No. of branches plant^{-1}	2.701	1.1976	3.899	69.27
No. of roots plant^{-1}	0.7843	1.7496	2.5339	30.95
Weight of roots plant^{-1}	89876.056	37980.7730	127856.82	70.29
Root fresh weight	375.406	38.1056	413.512	90.78
Root dry matter	4.679	0.65812	5.337	87.67
Root length	1.478	0.2191	1.697	87.09
Root diameter	0.1883	0.1769	0.3651	51.57
Total sugars	237.992	30.6054	268.597	88.60
Starch	230.023	13.9382	243.961	94.29
Carbohydrates	473.572	39.1355	512.707	92.37
Carotene	0.002	0.00022	0.0022	90.91

σ^2_g = Genotypic variance

σ^2_e = Error variance

σ^2_p = Phenotypic variance

H^2_{bs} % = Heritability percentage in broad sense

As for the character root diameter, the estimated value of H^2_{bs} was found to be intermediate (51.57%). This result seemed to be equal with that obtained by Tsegaye et al. (2007) for storage root diameter (H^2_{bs} = 50.84%). The estimates of heritability percentages in broad sense for both number of branches plant^{-1} and weight of roots plant^{-1} characters showed, relatively, high values, 69.27% and 70.29%, respectively. This result illustrates that genetic variance seemed to contribute with relatively high portion to the total variance.

Concerning the remaining eight characters; root length, root dry matter, total sugars, root fresh weight, carotene, carbohydrates, starch and vine length; the estimated values of H^2_{bs} % were found to be high (more than 87%). The results of the most previously mentioned characters, in the current study, are in general agreement with the findings of Jones (1969) for vine length; Jones (1970) for root weight plant^{-1}; Jones (1971) for root weight; Kamalam et al. (1977) for storage root weight and vine length; Mok et al. (1997) for storage roots weight plant^{-1} and storage root dry matter content and Anshebo et al. (2004) for number of branches plant^{-1} and weight of single tuber (root) and tuber length. 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 component 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.

Concerning the estimated values of phenotypic correlation coefficients among all possible pairs of the studied characters, the results of Table 4 illustrated, generally, that 19 out of the possible 66 relationships appeared to be desirable for the improvement of sweet potato study by 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 (47 relationships) were found too small to be significant.

The results indicated that the character of vine length reflected desirable positive correlations with each of number of roots plant^{-1} and weight of roots plant^{-1}. This result indicated that selection for long vines (a desirable form) would lead, spontaneously, for the improvement of the characters more number of roots plant^{-1} and weighted roots plant^{-1}. However, Jones (1970) reported that phenotypic correlation between vine length and root weight was found small to show significant.

Desirable associations were detected between number of branches plant^{-1} with each of weight of roots plant^{-1} (with a positive trend), and root length (with a negative trend). In contrast, Thamburaj and Muthukrishnan (1978) observed high degree of positive association between number of branches plant^{-1} and length of root. In the same line, desirable correlation coefficients were observed between number of roots plant^{-1} with each of root length and root diameter (with negative associations), and roots weight plant^{-1} and total sugars content (with positive association). These results are in accordance with the findings of Jones (1970), for the correlation between

Table 4: Phenotypic correlation coefficients among the studied characters of sweet potato "Abies" cultivar.

Characters	No. of branches plant⁻¹	No. of roots plant⁻¹	Weight of roots plant⁻¹	Root fresh weight	Root dry matter	Root length	Root diameter	Total sugars	Starch	Carbohy-drates	Carotene
Vine length (cm)	0.080	0.297*	0.331*	0.046	0.169	0.168	-0.093	-0.216	-0.052	0.043	0.182
No. of branches plant⁻¹		-0.241	0.298*	-0.233	-0.256	-0.335*	-0.144	-0.154	-0.242	0.011	-0.047
No. of roots plant⁻¹			0.337*	-0.038	-0.097	-0.362**	-0.371*	0.330*	-0.115	-0.143	-0.199
Weight of roots plant⁻¹ (kg)				0.319*	0.295*	-0.006	0.365**	-0.221	0.114	-0.027	0.489**
Root fresh weight (g)					0.199	0.041	0.236	-0.179	-0.129	-0.144	0.084
Root dry matter (%)						-0.132	0.233	-0.198	0.151	0.082	0.178
Root length (cm)							-0.369	-0.187	0.005	-0.302*	-0.229
Root diameter (cm)								-0.198	0.151	0.072	0.253
Total sugars (mg.g⁻¹d.w)									0.024	0.423**	0.095
Starch (mg.g⁻¹ d.w)										0.524**	0.438**
Carbohydrates (mg.g⁻¹ d.w)											0.638**

* = Significant at 0.05 of probability level.
** = Highly significant at 0.01 of probability level.

roots weight and number of roots plant^{-1}; and Omran et al. (2002) for the relationship between tuber roots yield plant^{-1} and number of tuber roots plant^{-1}. Since, they found significant positive correlations between each pair of these characters.

The results of the present study indicated that the character of weight of roots plant^{-1} was significantly, correlated with each of root fresh weight and root dry matter content (with positive and desirable trends). This result is in agreement with the finding of Omran et al. (2002), who found positive correlation between tuber roots yield plant^{-1} and dry weight of tuber roots. On the contrary, Li (1982) revealed a negative direct effect between root dry matter content and storage root yield plant^{-1}. Tsegaye et al. (2006) pointed out that storage root yield plant^{-1} had positive and significant correlation with individual storage root weight. Moreover, the results of the present study are in consistent with those obtained by Kamalam et al. (1977); Thamburaj and Muthukrishnan (1978); Li (1982); Hossain et al. (2000) and Anshebo et al. (2004), who reported high positive phenotypic correlations between individual storage root weight with storage roots yield plant^{-1}.

Among significant phenotypic associations exhibited between pairs of the studied characters, highly significant positive correlations were observed between weight of roots plant^{-1} with each of root diameter and carotene content. Positive correlation was, also, observed between root fresh weight and root diameter. This information was in agreement with the finding of Tsegaye et al. (2006), who revealed that highly significant positive correlation was observed between storage root girth and individual storage root weight. This suggested that improvement aimed at any of the studied character would automatically lead to improvement in the other. The work of Lowe and Wilson (1974 and 1975) also linked an increase in storage root girth with an increase in individual storage root weight, and change in storage root shape, which is undesirable trait. On the other hand, negative correlations, in the current study, were showed between root length with each of root diameter (with highly significant level) and carbohydrates content (with significant level). These results reflected 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.

Desirable and highly significant correlations were detected between pairs of the chemical components characters; viz. total sugars and carbohydrates; starch with each of carbohydrates and carotene; carbohydrates and carotene. These associations appeared to have positive trends between each pair of characters. These relationships suggested, clearly, that selection for any of these traits would subsequently result in increasing the other one.

A part from information on the association between root yield plant^{-1} and other agronomic characters indicated that an understanding of the interrelationships among various agronomic traits is necessary for the intelligent choice of breeding procedures and evaluative purposes which would make possible selection for simultaneous improvement of desirable traits. In the current investigation many of the characters were positively and negatively correlated with each other.

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الملخص العربي

تقدير كفاءة التوريث ومعامل الارتباط المظهري لبعض الصفات الهامة في البطاطا

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[1و2] قسم الخضر – كلية الزراعة – جامعة الإسكندرية

نفذت هذه الدراسة في الموسمين الصيفيين لعامين متتاليين هما ٢٠٠٥ و ٢٠٠٦ بمحطة البحوث الزراعيــة بــأبيس والتابعــة لكليــة الزراعة جامعة الإسكندرية ، وذلك بهدف تقدير كفاءة التوريث بمعناها الواسع عن طريق تقدير القيم النسبية لكل من التباين الــوراثي والتبــاين البيئي لستة عشر سلالة خضرية والناتجة من برنامج انتخاب للسلالة الخضرية في البطاطا صنف أبيس . كذلك تقدير معامل الارتباط المظهري بين أزواج الصفات موضع الدراسة وذلك للعشائر المنتخبة بالإضافة الى العشيرة الأصلية ، حيث أن الأرتباط المظهري يتيح الفرصة للمربى للاستفادة منها في برامج التربية بالإنتخاب وذلك للأستعانه في الأنتخاب بصفة معقدة أو صعبة القياس بأخرى سهلة القيــاس ومرتبطــة معهــا بصورة مرغوبة.

تم زراعة العشيرة الأصلية لنباتات البطاطا وأنتخب منها ستة عشر سلالة خضرية وذلك خلال الموسم الصيفى لعام ٢٠٠٥، ثم تم تنفيذ تجربة لتقيم العشائر الورائية المختلفة بإستخدام تصميم القطاعات العشوائية الكاملة مع استخدام ثلاث مكررات فــي الموســم الــصيفي ٢٠٠٦. وكانت الصفات المدروسة هى طول العرش وعدد الأفرع / نبات ، عدد الجذور/ نبات ، وزن الجذور / نبات ، وزن الجذر الطــازج ، النــسبة المئوية للمادة الجافة في الجذور ، طول الجذر ، قطر الجذر ، كذلك بعض التقديرات الكيميائية للجذور من حيث محتواها من السكريات الكليــة، النشا ، الكربوهيدرات و الكاروتين.

عكست تقديرات مكونات التباين وجود تأثيرات عالية المعنوية لتباينات للتراكيب الورائية لجميع الصفات المدروسة ، كما ظهر وجــود قيم عالية للتباين الورائي بالنسبة للتباين الكلي (المظهري) لجميع الصفات فيما عدا صفة عدد الجذور / نبات وصفة قطر الساق ، حيث انعكــس ذلك على قيم كفاءة التوريث بمعناها الواسع والتي قدرت بنسبة ٣٠٫٩٥% و ٥١٫٥٧% للصفتين على التوالي. بينما تراوحت القــيم المحــسوبة لكفاءة التوريث في باقي الصفات المدروسة ما بين ٦٩٫٢٧% لصفة عدد الأفرع / نبات إلى ٩٦٫٢٤% لصفة طول العرش.

وبالنسبة لتقديرات قيم معاملات الأرتباط المظهرى بين أزواج الصفات الممكنة بين الصفات المدروسة وعددها ستة وستون معــاملا والتي تظهر مدى ونوع العلاقات بينها ، تبين أن هناك عدد من العلاقات بين أزواج الصفات قد قدرت بقيم إمــا معنويــة أو عاليــة المعنويــة وعددها تسعة عشر علاقة ومنها مجموعة من العلاقات جاءت موجبة أو سالبة ولكنها مرغوبة لدراسة تحسين الصفات فــي البطاطــا أو علــى العكس من ذلك في باقي الصفات فقد قدرت العلاقات المظهرية بين صفات أخرى ولكنها غير معنوية.

ونستخلص من ذلك بصفة علمة أهمية تقديرات كل من كفاءة التوريث ومعاملات الارتباط المظهري للصفات في محصول البطاطا لمــا لهما من أهمية في الأغراض التقييمية و برامج التربية بهدف التحسين.