

HERITABILITY ESTIMATES OF SOME QUANTITATIVE TRAITS IN POTATOES

Gulsum OZTURK*, Zihin YILDIRIM

Ege University, Faculty of Agriculture, Department of Field Crops, Bornova-Izmir, TURKEY

*Corresponding author: gulsum.ozturk@ege.edu.tr

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ABSTRACT

Broad-sense heritability (H) values of some quantitative traits in a potato population comprising 21 genotypes grown at Bornova, Izmir, Turkey during the 2013 and 2014 growing seasons were estimated by using the variance components analysis method. Based on the combined analysis of variance performed over two years, the following moderate to high level H values were found for plant height (0.77), leaf width (0.69), leaf length (0.71), single tuber weight (0.74), plant yield (0.60) and starch content (0.87). The expected genetic advance based on the selection of 25 % upper part was 8.2 cm for plant height; 0.5 for tuber number; 18.5 g for single tuber weight; 150.8 g for plant yield; 2.2 kg for plot yield and 1.9 % for starch content.

Keywords: Variance components, genotypic variance, genetic coefficient of variation, genetic advance

INTRODUCTION

In plant breeding, selection is applied to the populations having genetic variability for the desired characters. The genetic variability is generated by crossing different individuals or mutating genes of interest by induced mutagenesis. Main purpose of a selection program is to increase the mean of the selected portion of the population and thus to select individuals with high genotypic value. Selection in practice depends on the phenotypes of the individuals and in the absence of genotypic portion of the variance the genetic advance from selection cannot be estimated.

Phenotypic variance includes genotypic variance and environmental variance as well as the interactions of genotype x environment. Also genotypic variance may be divided in to additive, dominance and epistatic components. The ratio of genotypic variance to total phenotypic variance describes broad-sense heritability while the ratio of pure additive component of genotypic variance to total phenotypic variance is referred to as narrow-sense heritability. Thus, these heritability estimates may be helpful to calculate expected genetic gain from selection or response to selection being applied.

Potatoes produced worldwide are tetraploid so their genetic structures are much more complicated as compared to diploid crops. The gamete formation and the ratio of gametes in the segregation of the AAaa duplex parent are more complex and mixed up with high number of ratios of the individuals. The genotype frequencies at equilibrium are estimated as $(p+q)^4$ in autotetraploids (Li, 1955) in comparison to the Hardy-Weinberg equation $(p+q)^2$, of the diploid (Falconer, 1960). Therefore, most

of the genetic studies in potatoes have been conducted at the diploid level.

As described above, heritability in broad-sense has been defined as the ratio of genotypic variance (σ^2_g) to the phenotypic variance (σ^2_{ph}) and denoted by H. The narrow sense heritability (h^2) was defined as the ratio of additive variance to the phenotypic variance (σ^2_{ph}). Although narrow sense heritability is more precise, it presents difficulties in its estimation. The simple and widely used technique in the genetic analyses of crops is the variance components analysis developed by Comstock and Moll (1963). This technic has been used widely in potatoes since the clones maintained the genetic variance.

Yildirim and Caliskan (1985) estimated broad-sense heritabilities in potatoes based on the variance component analysis for plant height (0.63), leaf area (0.78), tuber number (0.73), tuber weight (0.90), yield (0.87) and starch content (0.76).

Eraslan and Yildirim (1997) reported high values for plant height (0.92), leaf area index (0.82), tuber weight (0.86), and starch content (0.81) at Menemen, Izmir location. Desai and Jaimini (1997) reported moderate H values in a potato population. Similar broad-sense heritability estimates reported by Regassa and Basavaraj (2005), which are for plant height (0.42), stem number (0.49), leaf area (0.83), tuber number (0.73), plant yield (0.72) and dry matter content (0.71). Most recent heritability estimates obtained based on 38 genotypes grown at one location for two years for plant height, leaf area, stem number, tuber yield having high H values (Mishra et al., 2006).

However, there is no recent study of heritabilities in potato in the Aegean region. Therefore, the purpose of this study was to update the estimation of variance components and heritability values for certain physiological and agronomical traits of the potato population grown at Bornova, Izmir, Turkey for two years.

MATERIALS AND METHODS

Genetic Material

A total of 21 potato genotypes with various origins were selected to grow at Bornova-Izmir, Turkey. The information pertinent to these genotypes is shown in Table 1 (Anonymous, 2014a; Anonymous, 2014b; Anonymous, 2014c).

Table 1. The origin of potato genotypes and their pedigrees

Genotypes	Origin	Pedigree
Juwell	Germany	-
Shelford	United States	FL-1625 x Hermes
Bettina	Germany	-
Soprano	Netherlands	-
Agria	Germany	Quarta x Semlo
Pentland Dell	UK	Roslin Chania x Roslin Sasumua
Lady Olimpia	Netherlands	Agria x KW78-34-470
Musica	USA	FL1625 x Hermes
Royal	United Kingdom	Midas x 92-BUY-1
Lady Claire	United Kingdom/Netherlands	Agria x KW 78-34-470
Melody	United Kingdom	VF74-45 x W72-22-496
Agata	Netherlands	BM 52.72 x Sirco
Folva	Denmark	Mirada x Maris Piper
Brooke	USA	FL1867 x Hermes
Atlantic	Canada	Wauseon x Lenape
Granola	Germany	3333 60 x 267 04
Hermes	Netherlands	DDR5158 x SW163/55
Marabel	Netherlands	Nena x MA75364
Nif	Ege Univ.Fac. of Agri.	Cosima x R.143
Clone 122	Ege Univ.Fac. of Agri.	Cosima x R.143
Resy	Netherlands	SVP502017 x MPI 19268

Climate and soil characteristics of the Experimental area

The field trial was set up at the experimental field of Agricultural Faculty, Ege University located in Bornova, Izmir, Turkey. The native root zone of the soil in the experimental field was composed of 80.2 % sand, 18.1 % silt and 1.7 % clay. The soil was loamy sand with pH of 8.1. The long term average temperature was 17.1 °C, and the precipitation was 596.3 mm. A typical Mediterranean type climate conditions with hot and dry summers and rainy winters prevail in the region (Kavut et al., 2014).

Experimental Design

The field trial was arranged in a Randomized Complete Blocks Design with 3 replications. One plot consisted of 2 rows, 3 m long and 70 cm apart. The spacing between the plants on the rows was 30 cm, having 20 plants.

The field trial was run during the 2013 and 2014 growing seasons. The seed tubers were planted on 6 March 2013 and on 13 February 2014 by hand and the required standard agronomical practices were applied. The yield trial was harvested on July 8, 2013 and June 16-17, 2014.

Plant and tuber characteristics were measured during the growing season and at the harvest. The following morphological and yield characteristics were measured on randomly selected 3 plants in each plot: plant height (cm), stem number, leaf number, leaf width and length, tuber number, single tuber weight (g), plant yield (g). At the harvest, plot yield (kg), tuber width (cm) and length (cm) and starch content (%) were measured as described by Yildirim and Caliskan, (1985).

Statistical Analyses

The analysis of variance suitable for the experimental design was run on the data combined over two years. The means of traits studied were compared by using the Standard LSD test as described by Steel et al. (1997).

Estimations of variance components and genetic advance

The random model was accepted in order to construct the expected mean squares for the genotype, genotype x year and environmental variances. The expected mean squares given by Comstock and Moll (1963) are shown in Table 2.

Table 2. Expected mean squares for the source of variation

Source of variation	Degrees of freedom	Mean square	Expected mean squares
Genotype	n-1	MS ₁	$\sigma^2_e + r\sigma^2_{gy} + ry\sigma^2_g$
Genotype x year	(n-1) (y-1)	MS ₂	$\sigma^2_e + r\sigma^2_{gy}$
Error	y (n-1) (r-1)	MS ₃	σ^2_e

y= year: 2
r= replication: 3
n=21

The genotypic and the phenotypic variances were estimated by using the mean squares given in table 2:

$$\text{Genotypic variance } (\sigma^2_g) = MS_1 - MS_2 / ry$$

$$\text{Genotype x year interaction } (\sigma^2_{gy}) = MS_2 - MS_3 / r$$

$$\text{Environmental variance } (\sigma^2_e) = \sigma^2_e = MS_3$$

$$\text{Phenotypic variance } (\sigma^2_{ph}) = \sigma^2_g + \sigma^2_{gy} / y + \sigma^2_e / ry$$

The broad sense heritability was estimated by using the genotypic and phenotypic variances as following:

$$H (\text{broad-sense}) = \sigma^2_g / \sigma^2_{ph}$$

Where σ^2_g = genotypic variance

σ^2_{ph} = phenotypic variance

Genotypic coefficient of variation (GCV) was estimated by using genetic standard deviation: $\frac{\sigma_g}{x} \cdot 100$

Genetic advance was calculated by using the formula: $i \cdot S_{ph} \cdot H$

RESULTS AND DISCUSSION

The F values pertinent to genotypes, and genotype x year interaction sources of variation given in table 3 indicated significant variations for genotypes and genotype x year interaction for all the traits studied at the

Table 4. The means of physiological traits of the potato genotypes grown at Bornova-Izmir, Turkey during the 2013 and 2014 growing seasons.

Genotypes	Plant height (cm)	Number of stems	Number of leaves	Leaf width (cm)	Leaf length (cm)
Juwel	43.8	4.0	55.2	2.5	4.1
Shelford	34.8	2.5	55.0	2.1	3.3
Bettina	46.6	4.0	85.6	1.9	3.4
Soprano	36.1	2.6	46.0	2.0	3.4
Agria	54.6	4.3	93.9	2.1	3.3
Pentland Dell	39.4	2.8	53.8	1.6	2.6
Lady Olimpia	43.4	3.8	79.7	2.1	3.5
Musica	36.7	3.8	55.1	2.0	3.2
Royal	34.1	3.8	48.1	2.1	3.5
Lady Claire	36.2	4.1	75.6	2.2	3.6
Melody	36.3	3.5	56.1	2.4	3.8
Agata	29.1	4.6	53.9	2.0	3.4
Folva	45.2	4.7	89.6	1.9	3.4
Brooke	32.6	2.9	55.9	1.9	3.3
Atlantic	30.7	2.2	43.0	1.9	3.0
Granola	22.2	3.4	30.4	2.2	3.3
Hermes	25.4	3.7	44.4	1.9	3.1
Marabel	27.1	3.2	40.7	2.0	3.0
Nif	28.9	2.7	56.4	1.8	3.1
Clone 122	25.3	2.8	40.7	1.7	2.7
Resy	24.2	2.4	37.8	1.8	2.8
LSD (0.05)	1.06	0.22	1.21	0.09	0.11

$p \leq 0.01$ levels. Therefore, means of genotypes could be compared and the genotypic variability and the heritabilities could be estimated.

Table 3. The F values of the genotype and genotype x year interaction component of variation for quantitative traits of potato population grown at Bornova-Izmir, Turkey during the 2013 and 2014 growing seasons.

Traits	Genotype	Genotype xYear
Plant height (cm)	505.789**	118.013**
Number of stems	94.110**	84.727**
Number of leaves	1695.252**	1221.133**
Leaf width (cm)	39.595**	10.447**
Leaf length (cm)	84.212**	29.894**
Tuber number	38.849**	28.686**
Single tuber weight (g)	36.832**	9.661**
Plant yield (g)	67.400**	26.864**
Plot yield (kg)	273.092**	148.718**
Tuber width (cm)	73.941**	28.891**
Tuber length (cm)	174.581**	64.303**
Starch content (%)	25.887**	3.304**

** : denotes significance at the $p \leq 0.01$ level

Comparison of genotype means

Means of the physiological traits are shown in table 4. The genotype Agria had the highest means for plant height (54.6 cm) and number of leaves (93.9). Folva had the highest mean for number of stem (4.7). Juwel had the highest means for leaf width (2.5 cm) and length (4.1 cm).

Means of the agronomical trait studied are shown in table 5. It could be seen in table 5 that Agria had the highest means for single tuber weight (140.2 g), plot yield (15.8 kg) and tuber width (5.6 cm). Musica had the

highest means for tuber number (10.2), plant yield (991.6 g) and tuber length (8.3 cm). Brooke had the highest starch content (18.4 %).

Table 5. The means of the agronomical traits of the potato genotypes grown at Bornova-Izmir, Turkey during the 2013 and 2014 growing seasons.

Genotypes	Tuber number	Single tuber weight (g)	Plant yield (g)	Plot yield (kg)	Tuber width (cm)	Tuber length (cm)	Starch content (%)
Juwell	9.4	86.4	809.8	13.6	5.1	6.9	13.3
Shelford	7.4	82.3	622.8	8.8	4.7	6.2	17.5
Bettina	9.6	91.4	867.3	15.8	5.2	7.0	15.4
Soprano	5.7	73.3	404.8	5.5	4.4	7.1	13.2
Agria	6.5	140.2	854.9	15.8	5.6	7.9	13.6
Pentland Dell	5.2	71.9	379.8	5.7	4.1	6.7	14.2
Lady Olimpia	7.7	110.8	847.7	13.2	4.9	7.5	14.8
Musica	10.2	100.1	991.6	15.2	4.6	8.3	12.8
Royal	6.9	86.9	606.4	6.9	5.0	6.1	14.2
Lady Claire	8.2	81.3	675.6	11.1	4.8	5.9	16.3
Melody	10.1	84.9	830.7	13.0	4.8	6.5	13.9
Agata	8.9	82.9	697.1	11.3	4.7	6.4	11.5
Folva	9.0	76.3	666.6	10.5	4.6	6.6	12.8
Brooke	9.3	84.5	734.5	8.9	4.7	5.9	18.4
Atlantic	5.9	105.2	636.3	9.2	4.9	6.1	17.4
Granola	6.6	46.1	265.8	4.1	3.9	5.1	13.2
Hermes	7.5	65.7	459.6	6.3	4.5	5.6	15.4
Marabel	7.1	69.9	478.5	6.6	4.5	6.2	13.3
Nif	9.5	77.9	715.7	8.7	4.7	5.9	13.8
Clone 122	6.7	60.8	407.7	5.1	4.6	5.6	14.4
Resy	6.2	66.9	405.8	6.1	4.4	6.5	13.8
LSD _(0.05)	0.69	9.17	67.81	0.64	0.12	0.17	0.96

Genetic variability

Estimates of the variance components, heritability and genetic coefficient of variation are shown in table 6. Genotypic variance, genotype x year interaction variance and phenotypic variance were significant at the $p \leq 0.01$ level. Genetic coefficient of variation was high for plot yield (26.2 %), plant height (21.2 %) and single tuber weight (20.4 %). The heritabilities in board sense (H) were high for starch content (0.87), plant height (0.77), single tuber weight (0.74), leaf length (0.71), leaf width (0.69); moderate for tuber length (0.61), plant yield (0.60) and plot yield (0.46), respectively. The heritability estimates for leaf number (0.28), tuber number (0.26) and stem number (0.10) had low values. Low heritability estimates could be the result of the genotype x environment interactions.

Genetic advance

Selection differential and the genetic advance obtained are shown in table 7. Estimates of the expected genetic advance are the result of the tentative selection applied in the population based on the heritability estimates. Plant yield (150.8 g), single tuber weight (18.5 g), plant height (8.2 cm), leaf number (6.3) and plot yield (2.2 kg) had comparatively high genetic advances than that of the other traits.

Heritability estimates presented in this study were in close agreement with the estimates reported previously (Yildirim and Caliskan, 1985; Eraslan and Yildirim, 1997; Regassa and Basavaraj, 2005; Mishra et al., 2006). In general estimates of heritabilities over 0.7 have been accepted as usable in plant breeding programs (Yildirim and Dere, 2005). Heritability estimates reported mostly are based on the variance component analysis. The accuracy of this kind of estimate depends on the certain assumptions about the application of the variance component analysis method. First, the validity of the expected mean square depends on the randomness. Unfortunately, in practice it is difficult to select genotypes, locations and years at random. In practice, only the replication is accepted as random. Therefore, the expected mean squares are assumed to be in agreement with the random model.

Comstock and Moll (1963) have given the expected mean square estimates for variance components in the analysis of variance table. The variance components method applied in different studies are based on the calculation of variance components by using the expected mean squares in a random model, which is in fact a mixed model theoretically.

Table 6. Estimates of variance components and heritabilities for physiological and agronomical traits of the potato population grown at Bornova-Izmir, Turkey during the 2013 and 2014 growing seasons.

Traits	Mean	S ² g	S ² gy	S ² e	S ² ph	HBroad Sense	GCV (%)
Plant height (cm)	34.9	54.55**	32.92**	0.85	71.2	0.77	21.2
Number of stems	3.41	0.06**	0.01**	0.04	0.56	0.10	6.7
Number of leaves	56.9	88.0**	453.2**	1.11	314.8	0.28	16.5
Leaf width (cm)	2.0	0.03**	0.02**	0.01	0.04	0.69	8.5
Leaf length (cm)	3.3	0.08**	0.08**	0.01	0.12	0.71	8.4
Tuber number	7.8	0.62**	3.38**	0.37	2.37	0.26	10.1
Single tuber weight (g)	83.1	288**	183.7**	63.6	390.4	0.74	20.4
Plant yield (g)	636.1	23496.5**	29984.4**	3477.9	390.68	0.60	24.1
Plot yield (kg)	9.6	6.32**	15.0**	0.31	13.87	0.46	26.2
Tuber width (cm)	4.7	0.08**	0.09**	0.11	0.14	0.56	5.9
Tuber length (cm)	6.5	0.39**	0.46**	0.02	0.63	0.63	9.7
Starch content (%)	14.4	2.67**	0.55**	0.71	3.06	0.87	11.32

** : denotes significance at the $p \leq 0.01$ level

S²g, S²gy, S²e, S²ph: estimates of genotypic, genotype x year interaction, environmental and phenotypic variances respectively

H: estimate of heritability in broad sense

GCV (%): estimate of genotypic coefficient of variation

Table 7. Results of the individual selection applied for the physiological and agronomical traits of the potato population grown at Bornova, Izmir, Turkey during the 2013 and 2014 growing seasons.

Traits	Range	Mean of selected genotypes	Selection differential	Genetic advance
Plant height (cm)	22.2-54.6	46.7	11.8	8.2
Number of stems	2.2-4.7	4.4	1.0	0.1
Number of leaves	30.4-93.9	84.9	28.0	6.3
Leaf width (cm)	1.6-2.5	2.3	0.3	0.2
Leaf length (cm)	2.6-4.1	3.7	0.4	0.3
Tuber number	5.2-10.2	9.7	1.9	0.5
Single tuber weight (g)	46.1-140.2	109.5	26.4	18.5
Plant yield (g)	265.8-991.6	878.4	242.3	150.8
Plot yield (kg)	4.1-15.8	14.7	5.1	2.2
Tuber width (cm)	4.1-5.6	5.2	0.5	0.3
Tuber length (cm)	5.1-8.3	7.6	1.1	0.6
Starch content (%)	11.5-18.4	17.0	2.6	1.9

i: Selection intensity approximately 1.27 for the 25 % of the upper part of population

Besides, the estimation of heritability by the variance component methods reported by several workers had certain limitations due to the selection of genotypes, locations and years. Most of the reports have been based on the growing selected genotypes at one location for 2 or more years or at two or more location in one year. In these estimations the magnitude of heritabilities could be inflated due to second order interaction of the genotype x location x year.

Yildirim and Caliskan (1985) reported heritability estimates based on growing genotypes at 3 locations for 2 years in the target area. These estimates could be accepted as more accurate in comparison to the several heritabilities reported. The heritability estimates found in this study were also in close agreement with the reported values by these researchers.

The values regarding the selection applied for the genotypes with high mean were given in tables 6 and 7, which resulted in selection differential ranged from 0.3 (leaf width) to 242.3 g (plant yield). Based on the selection differential estimates, we should expect increase

of 11.8 cm for plant height, 28 for number of leaves, 26.4 g for tuber weight, 243.3 g for plant yield, 5.1 kg for plot yield, and 26 % starch content.

Based on the estimation of genetic advances, the realized expected genetic gains for plant height, number of leaf, single tuber weight, plant yield, plot yield and starch contents would be 8.2 cm, 6.3, 18.5 g, 150.8 g, 2.2 kg and 1.9 % respectively. The actual genetic gain depends on the genetic coefficient of variation and heritability values of the traits. The genetic advances of tuber yield (0.19) was reported by Tekalign (2009), for tuber number (3.4), plant height (8.8), plant yield (117.79) and dry matter content (4.6 %) by Regassa and Basavaraj (2005) and for plant height (27.4 %), tuber number (45.3 %), tuber weight (21.1 %) and plant yield (62.1 %) by Sattar et al. (2007).

The discrepancies between the reported genetic advance values might be due to the differences in sampling the genotypes and environments. In general, it has been accepted that the Genetic Coefficient of Variation was not sufficient to test heritable variation so

more reliable procedures need to estimate the heritability and the genetic advance.

Estimates of heritability, genetic coefficient of variation and genetic advance would be helpful to the breeder during the application of selection in the breeding programmes. The heritabilities estimated by the variance components method would be useful in making these decisions. Mishra et al. (2006) also concluded that high heritability and high genetic advance would be valuable in selection programmes.

To recapitulate, the estimates of heritabilities based on the growing potato genotypes at several locations for several years will help to the potato breeders in deciding about the breeding strategy. Potato clones could have the additive, dominant and epistatic type genetic variability due to their stable genetic structure. For that reason, estimation of heritabilities by using the variance components method might be more dependable in potatoes in comparison to the generatively producing crops.

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