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Genetic Variance Estimates in Heterogeneous Potato Populations Propagated from True Potato Seed（TPS）

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Abstract: Twenty nine cross populations developed according to line × tester mating design along with their twelve parents raised from true potato seeds, were used to study variability and correlation for seven characters. The range of variation for all the characters were found to be wide and pronounced which indicated that characters were quantitative in nature and were under polygenic control. For all the characters, greater portion of the total δ^2p was mostly contributed by the δ^2g. Among the seven characters, tuber weight per plant showed the highest δ^2g, PCV, GCV, H^2b, GA and expected GA%. On the other hand, dry matter contents(%) showed the lowest H^2b. Phenotypic and genotypic correlation coefficients of plant height with no. of tubers per plant and tuber weight per plant; no. of branches per plant with no. of tubers per plant and tuber weight per plant were found to be significant and positive.

Key Words: variability; correlation; true potato seed(TPS); potato(*Solanum tuberosum* L)

True potato seed(TPS) is the actual botanical seed produced by the potato plant(*Solanum tuberosum* L.) found in tiny seed balls resembling tomatoes. TPS is occasionally formed after the potato has finished flowering. Potato crops are usually planted from the potato(or tuber) itself, but planting from TPS has several advantages. In Bangladesh, out of total land area, for potato cultivation 62% is covered by high yielding varieties [1]. The average yield of potato in Bangladesh is only 11.2 ton·ha^{-1}, which is very low in comparison to western countries and even in our neighboring country India(18.22 ton·ha^{-1}) [2]. The causes of such low yield and non-profitability of potato cultivation might be due to lack of quality seeds of good varieties, unavailability and uneven distribution of certified seeds, inadequate less cost storage facilities, use of local low yield potential cultivars(42% of total land), high production cost and short growing season. Potato is propagated by tuber seeds. So once when any variety is infested by virus or other disease, these pathogens have high chance to transmit to next generation. Beside these, the tuber seeds used for propagation involve high amount money and bulb amount of seeds. The use of true potato seeds(TPS) has provided many opportunities for varietal improvement of potato and its production technology. The TPS technology has proved itself to be highly promising and has been well accepted by the progressive farmers all over Bangladesh and other countries like India. In order to increase yield potential, information about genetic variability is necessary. The degree of success of genetic study and progress in the breeding work depends upon the magnitude of genetic variability in the available materials. To get idea of the genetic variability existing among the varieties with regard to the

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quantitative characters of economic importance, it becomes necessary to study them under an array of distinguishable environments. The concept of multiple gene inheritance or of quantitative inheritance is now one of the most important principles of genetics which require refined statistical method. Smith[3] proposed polygenic concept of quantitative characters and Mather[4] on the basis of this concept elaborated the statistical method of Fisher *et al*[5] to study genetic components of variance as well as environmental variance. As yield is the main object of a breeder, it is important to know the relationship between various characters that have direct and indirect effect on yield. The degree of relationship or association of these characters with yield can be ascertained by correlation studies. Determination of correlation coefficients among the yield and yield components is, therefore, prime importance in selecting suitable plant types and in designing effective breeding programme. The objectives of the present study were therefore, carried out to study the variability and correlation coefficient among seven quantitative characters in twenty nine populations of potato.

1 Materials and Methods

Twelve genetically diverse genotypes of potato were used in line × tester mating design. Of these, ten genotypes (Lal Pakri, Ausha, Patnai, Lal Sil, Chamak, Hera, Dhera, Lal Sil Bilaty, MF-II, and TPS-13) were used as female parents (lines) and the three (TPS-13, TPS-64, TPS-67) were used as male parents (testers). TPS-13 was used as both male and female parent. All the lines were crossed to each tester to produce true seeds at Plant Breeding and Gene Engineering Lab, Department of Botany, University of Rajshahi, during the years 1999-2000. For flower induction, artificial lighting was performed to extend photoperiod up to 17 hours with the help of high pressure sodium bulb. True seeds of twenty nine crosses were pre germinated in Petri plates at 20℃ during September 2000. The pre germinated true potato seeds were individually transplanted into the polythene bags filled with the mixture of soil, sand and compost in 1∶1∶1 proportion. The seedlings at 5-6 leaf stage were transplanted in the field following randomized block design with three replications. A spacing of 60 and 30 cm between rows and within the rows, respectively was maintained. Each of the crosses was planted in single row plots, having 40 seedlings/replication. Fertilizer dose was used at the rate of 100-160-100 kg of NKP·ha^{-1}, respectively. Cowdong was also used at the rate of 10 tons per ha. Recommended agronomic practices were followed to raise the crop under irrigated conditions. Observations were recorded and calculated on ten randomly selected plants from each plot/replication on plant height per plant at 40 days after planting (PH), number of leaves per plant at 50 days after planting (NLPP), number of branches per plant at 100 days after planting (NBPP), foliage coverage at 50 days (FC), tuber number per plant at 100 days after planting (TNPP), tuber weight per plant at 100 days after planting (TWPP) and dry matter content % (DMC). The collected data were analyzed following biometrical techniques developed by Mather[4] based on the mathematical methods of Fisher *et al*[5] and those of Hayman[6], Dewey and Lu[7] and Allard[8].

2 Results and Discussion

The mean square estimates of ANOVA for different quantitative characters have been shown in Table 1. The item variety for all the characters was found to be highly significant except NBPP indicating the existence of a great deal of variations among the varieties used. The estimates of different statistics like range, mean with standard error and component variations for different characters are presented in Table 2. Wide range of variability observed in the traits in this study would help in detecting the range of genetic diversity for these traits in a population. The highest range of variation was found in TWPP and variation was found in NBPP. The phenotypic variation was always greater than the genotypic and environment variations, as expected. The results show that there was a major portion of the phenotypic variations which were genotypic in nature in all the characters and a pronounced variation in all phenotypic, genotypic and environmental co-efficient of variability for most of the characters. For all characters, the difference between phenotypic and genotypic coefficient of variability was found low except for TWPP. These indicate pronounced genetic control on these characters. Phenotypic coefficient of variability was found to be the highest for TWPP. TNPP displayed moderately high phenotypic coefficient of variability. It was successively followed by FC, NLPP and PH. The least phenotypic coefficient of variability was estimated for NBPP. The highest genotypic coefficient of variability was noted for TWPP. It was followed by TNPP, FC, NLPP and PH. The lowest genotypic coefficient of variability was estimated for NBPP. Estimates of environmental coefficient of variability was also high for TWPP and the lowest was noted for NBPP. All the characters showed a wide and pronounced range of variation. The wide variation in the studied characters supported the idea that they were quantitative in nature and under the control of polygene. Similar results were also reported by Desai and Jamini[9], Hossain *et al*[10], and Biswas[11].

Table 1 Analysis of variance for various characters in true potato seed (TPS) population

Characters^1	Mean sum of square		
	Variety(28)^2	Replication(2)^2	Error(56)^2
PH(cm)	81.491**	10.442**	1.675
NLPP	112.439**	4.657	2.370
NBPP	2.351	0.010	0.107
FC	263.383**	219.253**	1.991
TNPP	209.001**	11.174	5.305
TWPP(g)	16938.145**	537.410	119.527
DMC%	11.419**	0.712	1.319

** Significant at 1%.

1 PH: Plant height; NLPP: number of leaves per plant; NBPP: number of branches per plant; FC: foliage coverage; TNPP: tuber number per plant; TWPP: tuber weight per plant; and DMC: dry matter content. The same below.

2 Denotes degree of freedom.

Table 2 Range, mean, components of variation, coefficient of variability, broad sense heritability (H^2b), genetic advance (GA) and expected genetic advance in percentage of mean (GA%) for seven characters

Characters	Range	Mean±SE	$\delta^2\rho$	δ^2g	δ^2e	PVC	GCV	ECV	H^2b	GA	GA%
PH	43.70-64.20	51.62±0.98	28.280	26.605	1.675	54.905	51.653	3.252	94.078	10.306	20.009
NLPP	23.20-51.20	34.94±1.18	39.059	36.690	2.370	114.055	107.136	6.919	93.933	12.093	35.313
NBPP	3.00-6.90	4.56±0.16	0.855	0.748	0.107	18.748	16.411	2.338	87.532	1.667	36.568
FC	50.00-85.00	64.92±1.68	102.319	84.339	17.980	239.295	197.245	42.051	82.427	17.176	40.169
TNPP	15.40-59.30	30.65±1.55	73.204	67.899	5.305	238.825	211.517	17.308	92.753	16.348	53.334
TWPP	130.50-440.20	236.96±14.32	5725.733	5606.206	119.527	2425.142	2374.514	50.626	97.912	152.623	64.644
DMC	14.06-24.99	20.24±0.36	4.686	3.367	1.319	23.169	16.647	6.522	71.850	3.204	15.842

The genetic coefficient of variability is not only sufficient to determine the amount of heritable portion of variation, but also can be measured by the heritability estimates and genetic gains [12]. The estimations of heritability and genetic advance give the heritable portion of variation. Heritability estimate along with genetic gain is more useful than the heritability value alone in predicting the result for selection of the best individuals[13]. In the present investigation, a comparatively high heritability accompanied by high genetic advance was recorded for the character PH, NLPP, TNPP and TWPP, indicating the importance of additive gene effects for these traits[14]. It also indicated a wide range of genetic diversity, which could be used in a breeding programme, and phenotypic selections would be effective. Similarly, Singh *et al*[15] reported high heritability and high genetic advance for these traits. High heritability does not always give high genetic advance as was indicated by Johonson et al[13]. In this study, NBPP exhibited high heritability and low genetic advance, indicating that non-additive gene systems were also involved. This might happen due to the intra or interalletic interactions. In such situations a recurrent selection may be adopted to improve these traits.

Yield is a complex and important quantitative character. It is the gross product of a number of characters. Accurate determination of correlation between yield and its component characters in genotypic level is of great importance in planning and designing an efficient breeding programme for the improvement of yield. Correlation between agronomic and yield contributing characters is very important because this association helps select a suitable character for the breeding experiment. The estimates of correlation coefficient between all possible pairs of characters were analyzed separately. The phenotypic and genotypic correlation coefficients between different pairs of characters are presented in Table 3.

Table 3 Phenotypic and genotypic correlation coefficients among the seven characters of twenty nine TPS progenies

Characters		PH	NLPP	NBPP	FC	DMC	NTPP	TWPP
PH	P		0.3834***	0.297	0.5415**	-0.235	0.406*	0.3243
	G		0.6829**	0.299	0.7419***	-0.241	0.477*	0.670***
NLPP	P			0.331	0.2895	0.0744	0.2223	0.5159**
	G			0.330	0.3923*	0.0755	0.219	0.366*
NBPP	P				0.35	0.0798	0.450**	0.4159**
	G				0.48**	0.0819	0.4507**	0.423**
FC	P					0.0963	0.168	0.2103
	G					0.1341	0.196	0.2379
DMC	P						0.5496**	-0.376*
	G						0.4798**	-0.3771*
NTPP	P							0.6336***
	G							0.695***

Note: df=27, *, ** and *** significant at 5%, 1% and 0.1% level, respectively. P=Phenotype, G=Genotype.

Correlation analyses among tuber yield and yield contributing characters revealed that the genotypic correlation coefficients in most of the cases were higher than their phenotypic correlation coefficients. In few cases, however, phenotypic correlation coefficients were higher than their genotypic correlation coefficients, suggesting that both environmental and genotypic correlation in these cases act in the same direction and finally maximize their expression at phenotypic level. The higher genotypic correlation than the corresponding phenotypic correlation in this experiment in most cases confirms with the results of Weber and Moorthy[16], Swarup and Chaugale[12], Salehuzzaman *et al*[17]. The correlation coefficients of TWPP with NLPP, NBPP and NTPP both at genotypic and phenotypic levels were significant and positive. These characters had also strong positive association among themselves (Table 3). The present results are also in agreement with the findings of Patel *et al*[18], Desai and Jamini[9] and Pandita *et al*[19]. PH showed high positive and significant association at genotypic as well as at phenotypic level with NLPP, FC and NTPP but showed negative correlation with DMC. NLPP showed high and positive correlation with FC at genotypic level. Positive correlation of NBPP with NTPP at phenotypic and genotypic level suggests that selection for higher number of tubers might be done by selecting higher number of branches. Dayal *et al*[20], Patel *et al*[18], Mishra and Gautam[21], Singh and Sing[22], Desai and Jamini[9], and Mondal *et al*[23] have also reported positive correlation between the number of branches and number of tuber. DMC showed high positive correlation with NTPP at both phenotypic and genotypic level, but the character was significantly and negatively correlated with TWPP. This result suggests that selection for high dry matter content (DMC) may be done by selecting lower TWPP and/or high TNPP.

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