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Genetic variability, heritability (bs) and genetic advance for various qualitative characters of potato

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Abstract

Genetic Variability, heritability and genetic advance for different qualitative characters were studied in 38 genotypes of potatoes. The study indicated the existence of considerable amount of genetic variability for all the traits under study. Analysis of variance revealed significant differences among genotypes for almost all the traits studied. The maximum range was recorded for dry matter content (17.41-23.94%), followed by vitamin C (17.41 -22.21 mg 100g⁻¹), TSS (4.16 - 6.26 °Brix) and specific gravity (0.99-1.32 g). The highest phenotypic and genotypic coefficients of variability were observed for specific gravity followed by dry matter content, vitamin C and TSS. In general the phenotypic coefficients of variation were slight higher than genotypic coefficients of variation for most of the quality contributing traits which indicates the minor role of environment in the expression of these traits. The estimates of heritability in broad sense was high for most of the characters indicating a great scope in the improvement of these traits as these characters in general possessed high estimates of heritability coupled with high genetic advance except for vitamin C content indicating preponderance of additive gene action for control of these traits.

Keywords: Genetic variability, heritability, genetic advance, various qualitative characters, potato

Introduction

Potato (*Solanum tuberosum* L.) is an imported temperate vegetable that has adapted well for cultivation under subtropical conditions of India and the world. This tuber crop of the family solanaceae comprises about 200 species mostly confined to American continent. The large variability available among the species has not yet been fully exploited. India is the second largest producer of potato after China. It produces more food and edible protein per unit area and time as compared to any other major food crop and as such it plays an important role in food and nutritional security of the world. In India crop occupies an area of 1.97 million hectares, with a production and productivity of about 41.55 million tones and 21.10 tones of potato per hectare respectively (Anonymous, 2014a) ^[2]. The development of an efficient plant breeding programme is dependent upon the existence of genetic variability as the efficiency of selection largely depends upon the magnitude of genetic variability, heritability and association between quality contributing traits present in the available germplasm. Potato exhibits considerable variation for a number of traits which provide greater scope for improving this crop through selection.

Material and Methods

The present investigation entitled "Genetic variability and divergence studies for various qualitative characters of potato (*Solanum tuberosum* L.)" was conducted on the experimental field of the Division of Vegetable Sciences, Sher-e-Kashmir University of Agricultural Sciences & Technology of Kashmir during *Kharief* 2017-18. The experimental field located at the main campus, Shalimar, Srinagar which is 15 km away from Srinagar city on the foot hills of Mahadev. The altitude of the location is 1685 meter above mean sea level and situated 34.1' North of latitude 74.89 East of longitude. The climate is temperate, characterized by mild summers. June and July are the hottest months while January and February are the coldest. The maximum rainfall is received during March to April. Thirty eight varieties/genotypes of potato

maintained by Division of Vegetable Sciences, SKUAST-K were evaluated for various yield and yield attributing traits at the Experimental field of the Division of Vegetable Sciences, SKUAST-K Shalimar Srinagar, during Kharief 2017.The experimental was planted in RCBD with three replications. The plot size was kept 2.4 x 1.2 m (2.88 m²), each plot consisted of 3 rows of each genotype in each replication at spacing of 60 x 20 cm. Observations were based on 5 randomly selected plants in each replication. The experimental fields were well prepared and standard cultural, manural and plant protection practices were followed to ensure a healthy crop growth. The analysis of variance were carried out as suggested by Panse (1957) ^[12] and were used for calculating other genetic parameters. The magnitude of phenotypic co-efficient of variation (PCV) and genotypic coefficient of variation (GCV) existing in a trait was worked out by the formula given by Burton (1952)^[7]. Heritability (b.s) was calculated as per the formula given by Burton and Johnson et al. (1955)^[9]. Genetic advance explains the degree of gain obtained in a character under a particular selection pressure. It also indicates the presence of additive genes in the trait and further suggest reliable crop improvement through selection of such traits. It was estimated by using the formula given by Lush (1949) ^[10] and Johnson et al. (1955) ^[9]. The equations are given as under:

$$GCV\% = \sqrt{\frac{\sigma^2 g}{\overline{x}}}$$
$$PCV\% = \sqrt{\frac{\sigma^2 p}{\overline{x}}}$$

Where, \bar{x} = general mean for the character under consideration. The estimates of PCV and GCV were classified as low (< 10%), moderate (10-20%) and high (> 20%) as per classification given by Sivasubramanium and Madhavamanon (1973) ^[17].

$$h^2$$
 bs % = $\frac{\sigma^2 g}{\sigma^2 p} \times 100$

H2 = Estimate of heritability in broad sense, $\sigma 2$ g = Genotypic variance, and $\sigma 2$ p = Phenotypic variance

The broad sense heritability estimates were classified as low (<50%), moderate (50-70%) and high (>70%) as suggested by Robinson (1966).

Genetic advance = $K.\sigma p.h^2$ Where, K = Constant value of 2.06 at 5% selection intensity σp = Phenotypic standard deviation of the character

 h^2 = Heritability of the character

GA as percentage of mean $=\frac{GA}{\bar{x}} \times 100$

Where, GA = Genetic advance

 $\bar{x} = Mean$

The magnitude of genetic advance as percentage of mean was classified as low (<10%), moderate (10-20%) and high (>20%).

Results and Discussion

Analysis of variance revealed that mean sum of squares due to genotypes/varieties was found to be highly significant indicating genetic differences among genotypes. The extent of variability present in 38 genotypes of potato was measured in terms of range, mean, phenotypic variance, genotypic variance, genotypic coefficient of variation, phenotypic coefficient of variation, heritability in broad sense and genetic advance (Tables 1-2). Observation was recorded from ten randomly selected tubers of each genotype, on the basis of which the mean performance of genotypes/varieties for different traits was calculated. The mean performance (Table-2) of thirty eight genotypes/varieties for different traits under consideration. However genotypes/varieties like HB/90-45 (1.17), C-1 (1.32), C-8 (1.15), P-16 (1.21), HB/85-50 (1.16), C-11 (1.14), Chipsona-2 (1.14) for Specific gravity; K-Sindhuri (5.56), C-1 (5.87), K-jyoti (6.27), Shalimar Potato-2 (6.05), HB/85-50 (5.85), Chipsona-2 (5.69), Hirpora (6.49) for TSS (°B); K- Himalini (21.48), C-1 (22.04), P-18 (21.57), P-15 (21.67), Gulmarg Special (21.57), PH-2 (21.54), for Vitamin C (mg100g⁻¹) and for number of tubers plant⁻¹; K-Shailja, C-20, CP-30, Chipsona-2, Red Hybrid-17, Red hybrid-20 and Shalimar Potato-1 for average tuber weight; K-Shailja, CP-30, Chipsona-2, Red hybrid-20, HB/82-185, Shalimar potato-1 and LB-4 for tuber yield plant⁻¹ and tuber vield plot⁻¹; K- Shailja, CP-30, Chipsona-2, Red hybrid-20, CP-2035, Shalimar Potato-1 and Red Hybrid-17for tuber yield hectare-1; HB/90-45, C-1, C-8, P-16, HB/85-50, C-11 and Shalimar Potato-1 (22.31), C-11 (21.71), CP-2035 (22.93), CP-30 (23.94), HB/82-185 (21.94), Chipsona-2 for specific gravity;. The range in the values reflect the amount of phenotypic variability, which is not very reliable since it includes genotypic, environmental and genotype X environmental interaction components and does not reveal as to which character is showing higher degree of variability. Further, the phenotype of crop is influenced by additive gene effect (heritable), dominance (non-heritable) and epitasis (non-allelic interaction). Hence, it becomes necessary to split the observed variability into phenotypic coefficient of variation and genotypic coefficient of variation, which ultimately indicates the extent of variability existing for various traits.

The estimates of phenotypic and genotypic coefficients of variation of all the characters studied are presented in (Table 1). In general the phenotypic and genotypic coefficients of variation were almost similar with slight higher phenotypic coefficients of variation, which indicates the role of environment in the expression of traits under observation. This was in agreement with the study of Rangare and Rangare (2013) ^[14] and Asefa et al. (2016) ^[4]. The role of genetic variability is selecting the best genotypes for making rapid improvement in quality characters as well as to select most potential parent for making the hybridization programme successful. According to Vavilov (1951) ^[19], a large amount of variability always provides a better chance of selecting desired genotypes. Since the genetic variability is the basis of all plant improvement programmes, sufficient genetic variability, if present, can be exploited to develop superior genotypes.

The analysis of variance revealed highly significant differences among genotypes/varieties for all the eleven characters which proved adequacy of material for the study. Since the genotypes/varieties used for study have sufficient amount of variation for all the characters, selection will be very effective. The maximum range was recorded for dry matter content (17.41-23.94%), followed by vitamin C (17.41 -22.21 mg $100g^{-1}$), TSS (4.16 - 6.26 °Brix) and specific gravity (0.99-1.32 g).

The estimates of phenotypic coefficients of variability were slightly higher than corresponding genotypic coefficients of variation for all the characters under study indicating the predominant role of environment in the expression of traits. All the characters exhibited a narrow range between phenotypic and genotypic coefficients of variability, which indicate that genotypes have predominance in the expression of their phenotype. Phenotypic coefficients of variation and genotypic coefficients of variation varied from 8.44 to 22.47 and 7.80 to 20.51 percent respectively. The highest phenotypic and genotypic coefficient of variability was recorded for specific gravity (22.47 and 20.51 respectively); followed by dry matter content (12.73 and 12.61 respectively), TSS (11.80 and 11.11 respectively) and specific gravity (8.44 and 8.11 respectively). These results confirm the earlier findings of Ahmad *et al.* (2005) ^[1], Biswas *et al.* (2005) ^[6], Barik (2007) ^[5], Singh (2008) ^[15], Ara *et al.* (2009) and Pradhan *et al.* (2014)

Table 1: Analysis of Variance with respect to MSS for various Quality traits in potato (Solanum tuberosum. L)

S. No.	Source of variation	d.f	Mean sum of Squares				
			Specific gravity	TSS (°B)	Vitamin C (mg 100 ⁻¹ g)	Dry matter (100g ⁻¹)	
1.	Replication	2	0.0045	0.125	0.1887	0.082	
2.	Treatments	37	0.0150**	0.9940**	7.3030**	9.2013**	
3.	Error	Error 74 0		0.0379	0.3917	03219	
	CD ($p \le 0.05$)		0.0421	0.3231	1.0217	0.9213	
** 8:: 6:							

** Significant 1%, *Significant at 5%

Heritability and genetic advance (as percent of mean): The genotypic coefficient of variation does not offer full scope to estimate the variation that is heritable and, therefore estimation of heritability becomes necessary. The heritability estimate facilitates the evaluation of hereditary and environmental effects in phenotypic variation. Therefore, genotypic coefficient of variation together with heritability estimates would give the best picture expected for selection. In order to understand the proportion of variability that is heritable and how much gain one can achieve through selection, it is desirable to consider the estimates of heritability and genetic advance because high heritability estimate could not be the only guideline for improvement work unless associated with genetic advance. Johnson et al. (1955) [9] have pointed out that in selection programme heritability values as well as estimates of genetic advance are more useful than the heritability alone in predicting the resultant effect for selection. Therefore, the effectiveness of selection is realized more quickly in those characters which have high heritability and high genetic advance. The relative amount of the heritable portion of the variation was therefore, estimated with the help of heritability estimates and genetic advances. A perusal of the Table -2 indicated that heritability in broad sense was high for all characters except for specific gravity which exhibited moderate heritability. The range of heritability varied from 75 percent (days taken to flowering) to 99 percent (tuber yield plot⁻¹) which suggested major role of genetic constitution in the expression of the characters and least effect by environmental modifications, hence considered to be dependable from breeding point of view and, selection based on phenotypic expression could be relied upon. High heritability estimates for various characters in potato have also been reported by Mishra *et al.* (2006) ^[11] for specific gravity of tubers; Rangare and Rangare (2013) ^[14] dry weight of tubers.

Effectiveness of selection is considered more reliable when heritability is coupled with genetic advance. High heritability along with high genetic advance was observed in the characters for high heritability and moderate to low genetic advance was found in the rest traits. High estimates of heritability and high genetic advance were also reported by Biswas *et al.* (2005) ^[6], Chandrakar (2007) ^[8] and Singh *et al.* (2015) ^[16].

Although high heritability was recorded for almost all the traits except days taken to flowering and number of tubers plant⁻¹ which recorded moderate estimates of heritability, the genetic gain did not exhibit the same trend which indicates that the traits were subjected to certain degree of non-heritable components of variability. In the present study high heritability associated with high genetic gain was recorded for the traits namely plant height, plant spread, leaf area number of stems hill⁻¹, days taken to flowering, yield plant⁻¹ and yield ha⁻¹. The value of genetic gain varied from 4.83 to 56.18 percent for all traits.

High heritability coupled with high genetic gain for the above stated characters was also reported by Ahmad *et al.* (2005) ^[1], Mishra *et al.* (2006) ^[11], Ummyiah *et al.* (2010) ^[18] and Asefa *et al.* (2016) ^[4]. From the above discussion it is obvious that the characters which exhibited high estimates of heritability along with high genetic gain could be considered reliable tools for selection as such characters indicate dominance of additive gene effect.

 Table 2: Estimates of mean, range, phenotypic variance, genotypic variance, phenotypic and genotypic coefficients of variation, heritability (bs) and genetic advance (as % of mean) for different quality parameters in Potato (Solanum tuberosum L.)

S. No.	Parameters	Mean	Range	Phenotypic variance (PV)	variance	Phenotypic coefficient of variation (PCV)	Genotypic coefficient of variation (GCV)	Heritability (bs)	Genetic advance (as % of mean)
1.	specific gravity	1.09	0.99 - 1.32	0.06	0.05	22.47	20.51	75	34.71
2.	Total soluble solids (°B)	5.01	4.16 - 6.26	0.35	0.31	11.80	11.11	89	21.64
3.	Vitamin C (mg 100g ⁻¹)	19.44	17.21 - 22.03	2.69	2.30	8.44	7.80	86	14.94
4.	Dry matter (100g ⁻¹)	20.21	17.41 - 23.94	6.62	6.50	12.73	12.61	99	25.96

Table 3 revealed that genotypes like C-1 for specific gravity and vitamin C and Hirpora and Gulmarg Special for TSS and

Vitamin C. The highest dry matter content was for CP-30 followed by Chipsona-2 and CP-2035.

S. No.	. Genotype specific gra		TSS(°B)	vitamin C (mg 100 ⁻¹)	Dry Matter (%)	
1.	Kufri Shailja	1.06	5.56	17.66	21.34	
2.	Kufri Himalini	1.00	5.06 21.48		18.80	
3.	Kufri Jyoti	1.01	6.27	20.85	20.55	
<u> </u>	Kufri Giriraj	1.13	5.45	20.83	18.43	
5.	Kufri Sindhuri	1.17	5.37	18.80	20.18	
6.	C-1	1.32	5.87	22.04	17.83	
7.	C-8	1.15	4.18	18.44	19.92	
8.	C-11	1.14	5.01	17.65	21.71	
9.	C-13	1.05	4.28	20.94	18.33	
10.	C-14	1.03	4.45	20.21	19.77	
11.	C-20	1.04	4.26	17.92	20.98	
12.	CP-30	1.09	5.27	17.22	23.94	
13.	CP-2035	1.11	5.00	17.51	22.93	
14.	CP-2187	1.07	5.12	21.17	20.09	
15.	Chipsona-2	1.14	5.69	17.21	23.74	
16.	P-1	1.02	4.60	19.73	19.98	
17.	P-12	1.04	5.01	19.90	19.81	
18.	P-15	1.04	5.28	21.67	18.41	
19.	P -16	1.21	4.75	18.81	19.61	
20.	P -18	1.13	5.02	21.57	17.80	
21.	P -20	1.04	4.20	18.47	19.84	
22.	PH-2	1.12	4.17	21.54	17.41	
23.	PH-3	1.02	4.59	20.28	18.93	
24.	PH-4	1.14	4.16	20.53	19.21	
25.	Red Hybrid-17	1.12	4.93	18.19	21.34	
26.	Red Hybrid-1	1.01	4.99	19.62	20.18	
27.	Red Hybrid-2	1.03	4.86	18.92	20.88	
28.	Red Hybrid-20	1.11	5.08	17.58	21.43	
29.	HB/82-185	0.99	4.47	17.36	21.94	
30.	HB/85-50	1.16	5.85	18.67	20.84	
31.	HB/62-18	1.00	5.02	21.86	18.21	
31.	HB/90-45	1.17	5.15	21.30	17.10	
33.	Shalimar Potato-1	1.06	5.32	19.10	22.31	
33. 34.	Shalimar Potato-1	1.16	6.05	18.18	20.90	
34. 35.	Shannar Potato-1 SM-855	1.10	4.41	17.88	20.90	
35. 36.	LB-4	1.10	4.41 5.07	17.88	22.62	
30. 37.		1.09	5.07 6.49	20.38		
	Hirpora				18.60	
38.	Gulmarg Special	1.07	5.13	21.57	20.52	
Mean		1.09	5.01	19.44	20.21	
C.V.		2.05	3.89	3.22	2.75	
S.E.		0.01	0.11	0.36	0.33	
C.D. 5%		0.04	0.32	1.02	0.92	
	Range Lowest	0.99	4.16	17.21	17.41	
	Range Highest	1.32	6.26	22.03	23.94	

Table 3: Mean performance of genotypes for different quality traits

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