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Genetic diversity in potato (*Solanum tuberosum* L.) genotypes grown in Bangladesh

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Abstract

Using biometrical methods of the genetic parameter, the present study was investigating the genetic diversity of 31 potato genotypes grown in Bangladesh. Thirty-one genotypes, year and interaction (G×Y) items were well differentiated by the analysis of variance. Greater variability observed among the varieties was due to genetic causes according to genetic parameter study. The results also indicate that plant height, number of leaflets/compound leaf, leaf area, foliage coverage/plant, fresh weight/compound leaf, number of tuber/plant, single tuber weight/plant and tuber weight/plant exhibited high GA, high heritability as well as high GAM (% of mean), therefore, these characters might be advocated to improve the tuber yield by effective selection. Five different cluster might be included 31 genotypes according to cluster analysis and these cluster analysis comment that cluster II and III was far diverse from genotypes of the cluster I where as it was least diverse from the genotypes belonging to V and IV. Heterogeneous and homogeneous nature between and within groups were suggested for higher inter cluster distance than intra-cluster respectively. Considering all the characters, it might be suggested for developing high yielding varieties of potato through breeding programs using the genotypes of cluster I and II.

Keywords: Potato, Genotype, Genetic diversity, Genetic parameter, Cluster analysis.

Introduction

Among the flowering plants, potato (*Solanum tuberosum* L.) belongs to the Solanaceae family. After rice and wheat potato is the third most important food crop in the world in terms of human consumption and it grown extensively in tropical and temperate countries. Potato is eaten more than a billion people worldwide, and global total potato production exceeds 374 million metric tons[1]. Potato ranks first among the vegetables in terms of area and production in Bangladesh. It occupies 11,41,727 acres (4,62,032 hectares) area of land in Bangladesh and the total production has been estimated 89,50,024 metric tons in the year of 2014. Farmer cultivated potato for not only food but also uses as animal feed, in industries and seed production purposes. Potato is the leading non-cereal crop among all roots and tuber-based food. The improvement of yield potential (25%) of cultivated crop like potato obtained through conventional breeding program.

Breeding progress conditioned by the magnitude, nature and interrelationship of genotypic and environmental variation in different characters. In that case, it becomes necessary to partition the observed variability into its heritable and non-heritable components with the help of suitable genetic parameter such as genotypic coefficient of variation (GCV), heritability estimates and genetic advance etc.[2-4]. It is also beneficial to make a comparative study of a few characters to select the desirable ones in different strains. The important factor that may consider as genetic variability with respect to genetic diversity, it is also essential prerequisite for crop improvement program for obtaining high yielding progenies. Using biometrical procedure quantification of genetic diversity made it possible to choose genetically diverse parents for a successful hybridization program. It is important to know the genetic diversity and the source of genes of a trait within the available genotype. Thus, genetic diversity in between the segregating population may helps to selecting the suitable types for commercial cultivation.

In spite of the commercially importance crop, the genetic data of the potato genotypes in Bangladesh are relatively scarce. For the genetic improvement of plants, it is important to know germplasm diversity among breeding materials and varieties. Breeders also know the genetic background of the breeding materials and varieties that is useful. Therefore, an experiment were conducted with thirty-one diverse genotypes of potato with a view to finding out a variety or varieties, which grow very well give high yield and show the most desirable characteristics under the existing conditions of Bangladesh.

Materials and methods

Plant materials used in this study were 31 (released, exotic and local) potato (*Solanum tuberosum* L.) genotypes that gain from Plant Breeding and Gene Engineering Lab, Department of Botany, Rajshahi University, Rajshahi, and Akafuji Agrotechnologies, Rajshahi, Bangladesh. It was conducted at the research field of the Department of Botany, University of

Rajshahi, Rajshahi, Bangladesh in three robi crop seasons of 2011, 2012 and 2014. The texture of the soil was fertile and silty loam having pH 5.2-6.4. The total rainfall is above 28.40 mm, average minimum-maximum temperatures were 12.74°C and 25.63°C, and relative humidity during the crop period was 82%. Potato genotypes were grown in RCBD (Randomized Complete Block Design) design and total field area was 12×18 sq m having 3 replications. Each replication consisted of 31 lines. Each line had 15 plants. The genotypes randomly assigned in each line of the replicated plot. Replication to replication distance was 1 m. The experimental land prepared by mechanical means. Ploughing and laddering continued until a good tilth was obtained upto a depth of 6-8 inches. Basal fertilizer doses applied at the time of seed sowing in furrows at both the sides of seed rows. The rest half of the urea applied in the time of top dress of 35 days after sowing of the seed tubers. Manures and fertilizers were applied after land preparation[5].

Seed tubers sown in 3 m × 3 m plots maintaining row-to-row spacing at 60 cm and plant-to-plant spacing at 25 cm. After 35 days of plantation, weeding and earthing up were done manually. After spading the soil between the rows, weeds were removed. Then urea was broad casted between the rows, which was followed by earthing up at a light of 20 cm from the base. Irrigation was applied in four times, first one was one week after planting, second one was just after earthing up, third one was at 52 days and the last one was at 65 days after sowing. A general dose of 0.2% Asataf (systemic insecticide) used at every 15 days and 0.02 % Dithane M-45 was used at 10 days interval, starting at 35 days to prevent any late blight infection. The potato tuber harvested on 90 days from the date of sowing to maturity. When the colour of leaf turned yellow and dropped off then plants of individual orientation as tagged previously separately harvested. Cured harvested potato tubers and slotted properly. Collecting different quantitative characters on individual plant basis from 10 plants selected randomly in each line of each replication. Every measurement was taken in CGS system.

Mean data of three years were analyzed for Analysis of Variance (ANOVA) following the biometrical techniques[6] based on mathematical model[7] and Genetic parameter were estimated[8] using OPSTAT of the online-based software. Multivariate analysis was done based on Mahalanobis analysis, D^2 –statistics[9] using GENSTAT 513 software (Copyright 1987, Lawes Agricultural Trust, Rothamsted Experimental Station, UK).

Results and discussion

Statistical analyses were done for analysis of variance, genetic parameters, and genetic diversity with D^2- statistics. The results obtained in this investigation are discussed under the following subheads with an endeavor to justify them.

Means square: The ANOVA studies of the ten quantitative characters were performing separately. Replication items were non-significant for all of the quantitative characters. Highly significant genotypic items for all the characters at 1% level, which meant significant differences, remain within the genotypes for the characters considered in this study. Year/environment item was also significantly influence for most of the characters except in number of stems per plants and number of tuber per plant. The interaction items (G×Y) were also highly significant for all the characters at 1% level, which reveals that different genotypes respond differently in different years (Table-1). In Chickpea[10], in sugarcane[11] and in potato obtained similar results[3,4,12].

Table-1: Mean squares in the analysis of variance (ANOVA) in tuber yield and yield related characters of 31 potato genotypes.

	Source				
	Mean sum of squares				
Characters	Replication	Genotypes	Year	G×Y	Error
Degrees of freedom	2	30	2	60	184
Plant height (cm)	62.73	3645.65 **	400.50 **	4349.28 **	264.29
Number of stems per plant	0.12	72.70 **	8.80 ns	5377.91 **	8.29
Number of leaflets/compound leaf	311.27	7623.91**	19288.27 **	7553.13 **	4691.02
Leaf area (cm^2)	181.01	14776 **	56579.92 **	403886.4 **	1005.36
Foliage coverage per plant	2353.01	57500.18 **	46984.06 **	691717.7 **	28172.67
Fresh weight of compound leaf (g)	14.69	52659.03 **	1049.58 **	558725.7 **	186.75
Tuber dry matter (%)	1551.59	675.36 **	936.09 **	8307.01**	116.24
Number of tubers per plant	51.66	159.41 **	30.45 ns	6124.7 **	26.33
Single tuber weight per plant (g)	1049.99	739.79 **	2194.41 **	9799.92 **	438.63
Total tubers weight per plant (g)	76.93	57866.52 **	3204.67 **	239394.7 **	432.51

ns and ** indicate significant at 1 % level and non-significant.

Genetic Parameters: It is prior condition for initiating high yielding variety development is to know the genetic variability and careful analysis of genetic variability of any crop species. For the identification of useful yield, respecting characters of crops it is essential to study the variability, heritability, phenotypic and genotypic coefficient of variation. The population nature and magnitude of variation and prolong environmental influence on the indication of characters is the basic requirements for effective success in breeding programme. Genetic parameters helps in calculating possible genetic advance through selection based on phenotypic value. In the present study, phenotypic variability considered as a reliable measure of genetic variability as the genotypic variance followed the same trend of phenotypic variance for all the characters studied.

Not only that the environmental influences were negligible as the environmental variance was lower than genotypic and phenotypic variance for most of the characters studied except in number of stems/plant. In case of genotypic co-efficient of variation (GCV%) and phenotypic co-efficient of variation (PCV %) the better part of the traits was quite close in both the cases indicate environmental role was less responsive and well-adapted genotypic performance. The value of GCV as well as PCV percentage was high (Table-2) for most of the characters. Greater variability for these characters among the varieties was due to genetic causes, thus less affected environmental cause that could improve in selection methods. Some researcher[13-20] also observed high GCV and PCV percentage for tuber numbers/plant, average tuber weight/plant and tuber weight/plant.

However, they observed moderate GCV and PCV percentage for plant height and tuber dry matter content. Same results were observed in different crops for yield and yield related characters[21-26].

Heritability estimates in broad sense were relatively high for almost all the characters studied. Although high heritability estimates have found to be helpful in making selection of superior genotypes because of phenotypic performance. Heritability estimates along with genetic gain were more useful in predicting the effect for selecting the best individual[27].

The present finding, therefore, are in agreement with the earlier finding[14,17,20,28,29]. They have also observed high heritability for tuber yield, average tuber weight, tuber number, and plant height and tuber dry matter content.

Table-2: Components of variance, coefficients of variability, board sense heritability (H^2b), genetic advance (GA) and expected genetic advance in percentage of mean (GA%) for ten characters of 31 potato genotypes.

Genetic parameters	Different characters									
	PH	NS	NLCL	LA	FC	FWCL	TDM	NT	STW	TTW
Genotypic variance	1.53	7.16	182.6	50.66	33.45	6.02	150.24	106.27	493.19	14.86
Phenotypic variance	265.8	15.45	727.70	149.7	87.80	72.40	296.74	165.39	552.26	447.38
Environmental variance	1.46	19.71	157.00	7.57	42.27	5.27	8.81	0.04	18.87	9.80
Genotypic coefficients of variation	34.09	47.11	32.70	36.18	34.94	53.63	26.56	32.51	22.29	42.32
Phenotypic coefficients of variation	38.74	54.43	35.62	41.76	36.38	55.18	31.36	36.16	25.84	44.95
Environmental coefficients of variation	3.86	0.17	19.66	27.43	16.72	9.88	53.48	0.75	9.60	37.05
Heritability (%)	77.43	74.91	44.27	75.05	52.21	64.46	11.72	80.87	74.39	88.62
Genetic Advance (GA)	17.98	2.04	20.55	14.69	63.90	76.60	6.61	43.17	56.82	62.90
GA % of mean	61.80	84.01	61.84	64.57	69.12	107.38	5.33	60.24	39.60	82.07

PH= Plant height (cm), NS= Number of stem per plant, NLCL= Number of leaflets per compound leaf, LA= Leaf area (cm^2), FC= Foliage coverage per plant (cm^2), FWCL= Fresh weight of per compound leaf (g), TDM= Tuber dry matter content, NT= Number of tuber per plant, STW= Single tuber weight per plant (g), TTW= Total tuber weight per plant.

However, the evaluation may be reliable through studies of GCV percentage and heritability, still more concrete basis formed by studying the performance through genetic advance. It is therefore, necessary to estimate the broad-sense heritability in conjunction with the genetic advance. High heritability estimates for plant height/plant, number of stems/plant, leaf area, fresh weight/compound leaf, number of tubers/plant, single tuber weight/plant and tuber weight/plant. Which associated with high to moderate genetic advance as percentage of mean, suggested that these characters were more influenced by the environment and improvement of these genotypes could be practiced following simple selection methods in future breeding strategy (Table-2). Several scientists agreed with the present results[13,17-20,29]. High heritability dose not necessarily mean that the characters will show high genetic advance. However, whenever this association exists, it is important from the breeding point of view. Tuber dry matter content had less scope for further improvement by selection because of high heritability but low genetic advance (% of men). Similar results have also been reported[16,20] in potato. They also reported low genetic advance for tuber dry matter and starch content. High genetic advance in tuber yield/plant and number of stems/plant[14,17,20] is in agreement with the result of the present study. In another study found low heritability and low amount of genetic advance for tuber dry matter content[13], which is in contrast with the results of the present study.

Thus, the results of the present study indicated that plant height, number of leaflets/compound leaf, leaf area, foliage coverage/ plant, fresh weight/compound leaf, number of tubers/plant, and single tuber weight/plant and tuber weight of plant exhibited high GCV%, high heritability as well as high GAM (% of mean) (Table-2). Alternate systems like random mating, intermating, biparental mating, crossing of selected sibs in early generation and dialel selective mating systems may therefore, be advocated to improve the tuber yield by effective selection.

Genetic diversity of potato: According to principal component analysis, the positive characters were plant height, number of stems/plant, number of leaflets/compound leaf, fresh weight/compound leaf, tuber dry matter content, single tuber weight/plant and total tuber weight/plant. Maximum contributions towards diversity were these characters. These characters extended greater diversity, which has the scope for improvement of potato yield through proper selection of parent's genotypes (Table-3).

Thirty-one potato genotypes grouped into five different clusters according to cluster analysis in which cluster IV had the maximum number of genotypes (each containing 11 genotypes). The lowest number of genotypes (only two) had in cluster I. Similar opinions reported in potato[16] and in okra[31]. Between the clusters III and I had higher inter cluster divergence, and minimum in between clusters V and III. The maximum intra-cluster distance was observed in cluster II and minimum in cluster V. Heterogeneous and homogeneous nature between and within groups were due to lower intra-cluster distance than the inter cluster one. Cluster means results were supported these variations. Among single as well as multi-genotypic clusters, variation had the wide range of for several characters. So, the total divergence largely contributed for plant height, number of stems/plant, number of leaflets/compound leaf, leaf area, foliage coverage/plant, fresh weight/compound leaf, tuber dry matter content, number of tubers/plant, single tuber weight of plant and tuber weight/plant. Similar results have also been reported[16,20,30] by total divergence in cluster for tuber yield, plant height, fresh weight of plant, number of leaves/plant and number of tubers/plant. Hence, the present study suggested that genotypes should be selected from clusters II, III and IV (Table-4 and Table-6) for the improvement of different characters *viz*., tuber numbers/plant, single tuber weight/plant, tuber weight/plant, fresh weight/plant under.

Table-3: Eigen values and percentage of variation for corresponding 10 component characters in 31 genotypes of potato.

Principal component axis	Initial Eigen values		
	Total	% of Variance	Cumulative %
Plant height(cm)	2.400	23.999	23.999
Number of stems per plant	2.122	21.221	45.221
Number of leaflets/compound leaf	1.266	12.658	57.879
Leaf area (cm^2)	1.039	10.386	68.265
Foliage coverage per plant	0.893	8.926	77.191
Fresh weight per plant (g)	0.759	7.590	84.781
Tuber dry matter (%)	0.481	4.811	89.592
Number of tubers per plant	0.460	4.603	94.195
Single tuber weight per plant (g)	0.386	3.859	98.054
Total tubers weight per plant(g)	0.195	1.946	100.000

Vector I the important characters responsible for genetic divergence in the major axis of differentiation were plant height, number of stems/plant, number of leaflets/compound leaf, leaf area, and fresh wt/plant, tuber dry matter content, single tuber weight/plant and total tuber weight/plant (yield) from the principal component analysis. In vector, II had the same,

characters that of axis I which was the second axis of differentiation. Positive across two axes indicating the important components of genetic divergence in the characters of plant height, number of stems/plant, number of leaflets/compound leaf, leaf area, fresh wt/plant, tuber dry matter content, single tuber weight/plant and total tuber weight/plant (yield) for both the vectors (Table-3). No reports in potato crop on genetic divergence using principal component analysis. In plant height, number of tubers/plant and tuber weight/plant were the major traits in contribution towards divergence in potato which was reported by another study[30]. It is important to clustering D^2 - statistics for selecting varieties from the already chosen groups, other important characteristics may considered like disease resistance, earliness, quality or even performance of particular character.

Table-4: Genotypic grouping of thirty-one potato genotypes based on morphological characters.

Cluster (Group)	Number of Genotypes	Genotypes
I	2	Quence, Haita red
II	7	Shepody, Lady rosety, Febula, Jamalu, Akira, Atlas, Diamont
III	6	Granula, Petroneous, Banana, Blondy, Chieftan, Indurkani
IV	11	All blue, Carage, Baraka, JPR, Altra, Hipita, Dumini, Shilbilati, All red, Asterix, Lalpakri
V	5	Shita white, Innovator, Atlantic, Hagri, Voyager

Table-5: Inter and intra (bold) cluster distances (D^2) in potato obtained by Canonical variate analysis.

Cluster	I	II	III	IV	V
I	8.549	103.84	103.87	66.95	67.009
II		22.05	94.358	76.523	95.818
III			9.545	82.447	64.136
IV				17.259	73.083
V					6.851

Table-6: Cluster means for 10 characters of 31 potato genotypes.

Characters	Cluster				
	I	II	III	IV	V
Plant height(cm)	44.40	37.94	34.18	37.72	36.62
Number of stems per plant	2.43	3.04	3.31	3.29	3.14
Number of leaflets/compound leaf	28.08	45.51	42.65	51.31	61.24
Leaf area (cm^2)	46.25	26.08	26.89	27.78	17.34
Foliage coverage per plant	138.90	118.71	59.68	95.42	113.10
Fresh weight per plant (g)	97.69	101.63	53.28	125.71	57.85
Tuber dry matter (%)	12.91	16.16	15.51	16.56	17.27
Number of tubers per plant	4.41	6.14	7.14	5.47	5.42
Single tuber weight per plant (g)	16.87	19.15	14.99	16.84	17.87
Total tubers weight per plant(g)	37.04	134.96	79.83	66.47	51.87

Table-7: Latent vectors for 10 characters of 31 potato genotypes.

Characters	Vector I	Vector II
Plant height(cm)	0.0265	0.1156
Number of stems/plant	0.0243	0.0154
Number of leaflet/compound leaf	0.0075	0.0262
Leaf area (cm^2)	0.0095	-0.0121
Foliage coverage/plant	-0.0897	-0.0567
Fresh weight/compound leaf	0.0256	0.0539
Tuber dry matter content	0.0342	0.0253
Number of tuber/plant	-0.0426	0.0291
Single tuber weight/plant	0.0362	0.0535
Total tuber weight/plant(g)	0.1241	0.1362

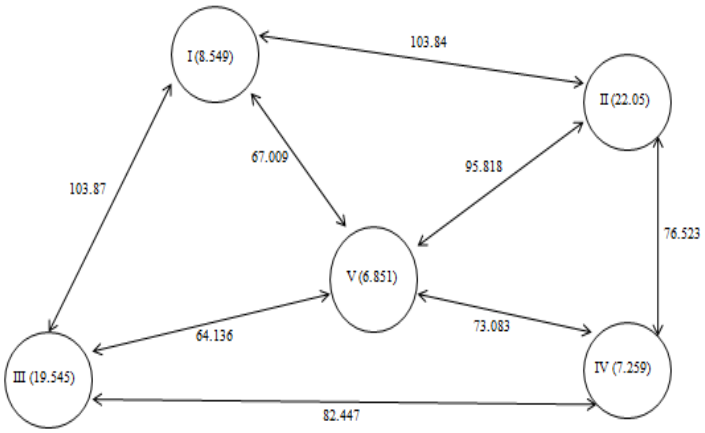

Figure-1: Diagram showing intra and inter cluster distances of 31 potato genotypes.

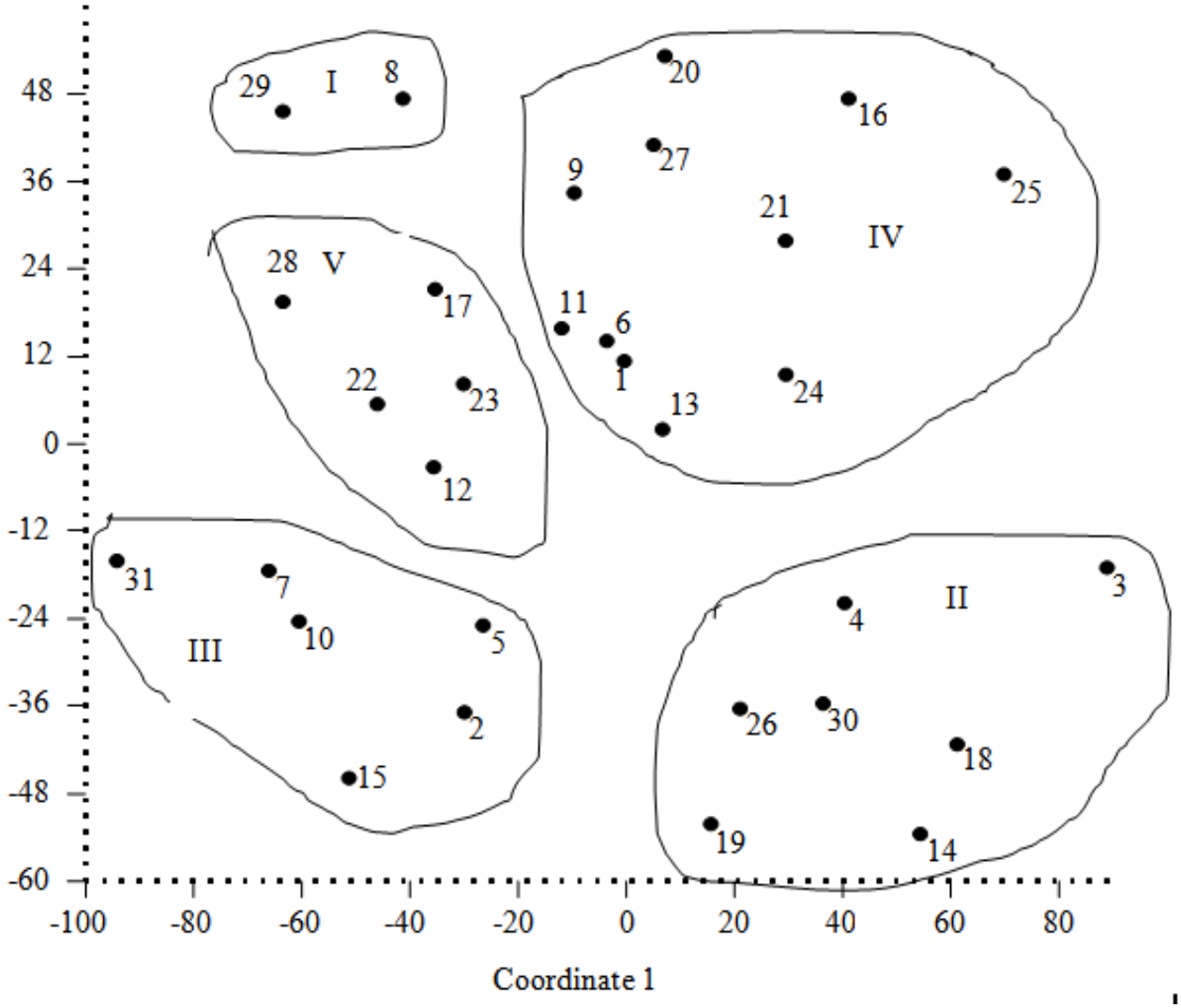

Figure-2: Scatter distribution of 31 potato genotypes based on their principal component scores superimposed with clustering.

Conclusion

The present investigation amplifies that 31 potato genotypes were genetically diverse according to diversity study. In addition, greater variability observed among the genotypes was due to genetic causes. The results also indicate that the characters plant height, number of leaflets/compound leaf, leaf area, foliage coverage/plant, fresh weight/compound leaf, number of tuber/plant, single tuber weight/plant and tuber weight/plant might be work to improve the tuber yield by effective choice. Therefore, following cluster study, it may be concluded that cluster II and I should be used for developing high yielding varieties of potato through breeding programs.

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