



Studies on Genetic Divergence in Buckwheat (*Fagopyrum Esculentum* Moench) Germplasm

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ABSTRACT

Buckwheat is one of the most important pseudo cereal crop of the mountain region widely cultivated in the middle and higher Himalayas during kharif season. The thirty diverse germplasm of buckwheat including four checks i.e. PRB-1, Himpriya, VL-7 and Shimla-B1 was laid out in Randomized Block Design with three replication. Presence of wide genetic diversity among the germplasm was revealed by Mahalanobis D^2 analysis. Among 30 germplasm were group into six different non-overlapping clusters. Cluster I was highest number of 9 germplasm followed by cluster II with 6 germplasm. The maximum inter-cluster genetic distance was observed between cluster I and cluster IV (367.82) followed by cluster I and cluster III (313.09). Cluster mean revealed that Cluster IV having 4 germplasm exhibited highest cluster mean for plant height (112.05 cm), number of primary branches per plant (3.55), number of leaves per plant (27.85), 100-seed weight (1.96 g) and seed yield per plant (3.16 g) these characters can be used for improvement of a large number of seed yield and yield per plant. Characters contributing to total divergence are number of leaves per plant (22.30%), seed yield per plant (20.69%), days to 50% flowering (18.62%), plant height (17.47%), 100-seed weight (8.28%), number of internodes per plant (7.59%), days to maturity (3.45%) and number of secondary branches per plant (1.61%). Based on high inter-cluster distance of cluster I with cluster IV, cluster I with cluster III and cluster II with cluster VI such as IC-13507 × IC-412762, IC-341661 × IC-412762, Shimla-B1 × IC-412762, IC-13507 × IC-412733, IC-341661 × IC-412733, IC-294344 × IC-107988, RSR/SKS-104 × IC-107988, Himpriya × IC-107988 and VL-7 × IC-107988 are recommended for hybrid breeding programmes in mid hills of Uttarakhand.

Key-words: Buckwheat, Genetic Divergence, Mahalanobis D^2 , Seed Yield and Yield Attributes

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INTRODUCTION

Common buckwheat (*Fagopyrum esculentum* Moench) is herbaceous erect annual plant with diploid chromosome number ($2n=16$) it belongs to the family Polygonaceae. Buckwheat is one of the most important pseudo cereal crop of the mountain region widely cultivated in the middle and higher Himalayas between 1800 m and 4500 m asl in kharif season. Buckwheat is originated in temperate Central Asia. In India this crop is grown on large scale in Jammu and Kashmir, Himachal Pradesh and Uttarakhand and to some extent in Northern states i.e. Sikkim, Assam, Arunachal Pradesh, Nagaland, and Manipur. It is also sporadically cultivated in the Nilgiris and Palni hills in Southern India [5]. Systematic research work in India on pseudocereals was started with the identification and strengthen of programme under the All India Coordinated Research Network Project on Underutilized Crops taking into consideration the potential of these crop the new name of the project in All India Coordinator Research Network Project on Potential Crop when it 2013-14 onwards. Buckwheat is having high nutritive value, It contains 11 to 15% protein which is deposited in the embryo and in the aleurone layer [8]. It has excellent protein quality in terms of essential amino-acid like lysine that are deficient in cereal crop. The tender shoots are used as leafy vegetables [16]. Assessment of available genetic diversity for important economic traits to develop high yielding varieties is an important function in crop breeding. As genetic diversity refers to the variation of genes within species, that is, the heritable variation within and

between populations of organisms. Genetic diversity is necessary to be present in the base population from which potential parents are to be selected as diverse parent for hybridization. For this purpose, various multivariate analytical techniques, which simultaneously analyze multiple measurements on each individual under investigation, are widely used in analysis of genetic diversity irrespective of the dataset. Moreover knowledge on genetic diversity, its nature and degree is useful for selecting desirable parents from genotypes for the successful breeding programme. Mahalanobis D^2 techniques appears to be a fruitful approach which is based on multivariate analysis and serves to be a good index of genetic diversity. A great extent of diversity present in various quantitative traits among the germplasm of buckwheat suggested good scope for improvement in economic traits through conventional breeding.

MATERIALS AND METHODS

Planting Material

The present investigation was carried out during *kharif* season-2013-2014 at the Crop Improvement Research Block of Veer Chandra Singh Garhwali Uttarakhand University of Horticulture and Forestry, College of Forestry, Ranichauri, Tehri Garhwal, Uttarakhand. The experimental materials for present investigation comprised of 30 germplasms viz., IC-13507, IC-294344, IC-412733, IC-412762, IC-13446, IC-13454, IC-13458, IC-13533, IC-13544, RSR/SKS-71, RSR/SKS-84, RSR/SKS-104, RSR/SKS-106, IC-26598, IC-26599, IC-36805, IC-36914, IC-37265, IC-42426, IC-107988, IC-108516, IC-109309, IC-204020, IC-329200, IC-341661, IC-276627 of Buckwheat (*Fagopyrum esculentum* Moench) including four check varieties *i.e.* Himpriya, VL-7, Shimla-B1 and PRB-1. The seed material of 30 germplasm including four check varieties used in the study was procured from Project Coordinator Unit of All India Coordinated Research Project on Under Utilized crop, NBPGR, regional station, Shimla.

Experimental Design

The field experiment was conducted in Randomized Block Design with three replications. Each of the germplasm was sown in two continuous rows length. The replications were located in three adjacent terraces. The row length was 3 meter and spacing was done in row to row 30 cm and plant to plant 10 cm. Observation was recorded on Days to 50% flowering, Days to maturity, Plant height at maturity (cm), Number of primary branches per plant, Number of secondary branches per plant, Number of internodes per plant, Number of leaves per plant, Leaf length (cm), 100-seed weight (g), Seed yield per plant (g).

Genetic divergence (Mahalanobis ' D^2 ' statistics)

The genetic divergence in twenty one genotypes was estimated by Mahalanobis ' D^2 ' statistics (generalised distance as suggested by [14] and canonical variate analysis. The calculation of D^2 values involved following steps [9].

- i. A set of uncorrelated linear combinations (Y 's) was obtained by pivotal condensation of the common dispersion matrix [14] of a set of correlated variable (X 's) and this matrix was arranged with the help of error mean sum of squares and sum of products.
- ii. Using the relationship between Y 's and X 's the mean values of different genotypes for different characters (X_1 to X_{13}) were transformed into the mean values of asset of uncorrelated linear combinations (Y_1 - Y_{13}).
- iii. The D^2 values between i^{th} and j^{th} genotypes for P^{th} characters was calculated as under

$$D^2_{ij} = \sum_{t=1}^P (Y_{it} - Y_{jt})^2$$

Where

Y_{it} is uncorrelated mean value of i^{th} genotype for ' t ' characters

Y_{jt} is uncorrelated mean value of j^{th} genotype for ' t ' characters

D^2_{ij} is D^2 between i^{th} and j^{th} accessions.

In all combinations each character was ranked based on their contribution towards divergence between two entries ($d_i = Y_{it} - Y_{jt}$). Rank 1 is given to the highest mean difference and rank P to the lowest difference, where, P is the total number of characters.

(a) The ' P ' component and D^2 for each combination were ranked in descending order of magnitude.

(b) The ranks were added up for each component D^2 over all combination and the rank totals were obtained.

RESULT AND DISCUSSION

Genetic divergence (Mahalanobis's D^2 statistics)

The 30 germplasm were grouped into six different non-overlapping clusters are presented in **Table-1**. Cluster I was highest number of 9 germplasm (IC-13507, IC-341661, Shimla-B1, IC-26598, IC-109309, IC-

13454, IC-42426, IC-13544 and IC-204020), followed by cluster II with 6 germplasm (IC-294344, RSR/SKS-104, Himpriya, VL-7, IC-13458 and IC-13533) and cluster V with 5 germplasm (RSR/SKS-84, IC-36805, IC-36914, IC-37265 and IC-26599). Cluster IV possessed 4 germplasm (IC-412762, RSR/SKS-71, IC-276627 and PRB-1) while cluster III and VI consist 3-3 germplasm viz., (IC-412733, RSR/SKS-106 and IC-13446) and (IC-107988, IC-108516 and IC-329200). The discrimination of germplasm lines in so many discrete clusters, suggested presence of high degree of genetic diversity in the material evaluated. Earlier workers have also reported existence of substantial genetic divergence in buckwheat materials Rana and Joshi [13]; Rana [11]; Rana and Sharma [12]; Kapila *et al.* [6]; Debnath *et al.* [3] and Cepkova *et al.* [2] and Ahmmed *et al.* [1] and Hasan *et al.* [4] in amaranth. Presence of substantial genetic diversity among the germplasm lines screened in the present study indicated that these materials may serve as good source for selecting the diverse parents for hybridization programme aimed as isolating desirable segregates for developing high yielding varieties of buckwheat.

Table-1: Clustering pattern of 30 germplasm of buckwheat on the basis of genetic divergence

Clusters	Number of genotypes	Genotypes
I	9	IC-13507, IC-341661, Shimla-B1, IC-26598, IC-109309, IC-13454, IC-42426, IC-13544, IC-204020
II	6	IC-294344, RSR/SKS-104, Himpriya, VL-7, IC-13458, IC-13533
III	3	IC-412733, RSR/SKS-106, IC-13446
IV	4	IC-412762, RSR/SKS-71, IC-276627, PRB-1
V	5	RSR/SKS-84, IC-36805, IC-36914, IC-37265, IC-26599
VI	3	IC-107988, IC-108516, IC-329200

Intra-and Inter cluster genetic distance ($\sqrt{D^2}$)

As far as intra-cluster distance (**Table-2**) is concerned, out of six clusters, cluster II had maximum intra cluster distance (119.33) followed by cluster I (118.13), cluster IV (106.62), cluster V (94.91), cluster VI (94.44) and cluster III (84.84). High intra-cluster genetic distance is a measure of genetic heterogeneity of genotypes included in that cluster. In general, it is observed that more number of genotypes included in a cluster may lead to high intra-cluster distance with exceptions. High intra-cluster genetic distance in cluster II was because of heterogeneous composition of that cluster

Maximum inter-cluster genetic distance was observed between cluster I and cluster IV (367.82) followed by cluster I and cluster III (313.09), cluster II and cluster VI (239.42), cluster I and cluster II (234.93), cluster IV and cluster V (234.82), cluster I and cluster V (233.22), cluster III and cluster V (229.88), cluster I and cluster VI (225.07), cluster III and cluster VI (220.02), cluster II and cluster IV (215.25), cluster II and cluster III (208.39), cluster II and cluster V (201.16), cluster IV and cluster VI (173.56), cluster III and cluster IV (163.42) and cluster V and cluster VI (159.35). The clusters with higher inter-cluster distances indicated that the genotypes included in those clusters had high genetic variation and hybridization between genotypes that may result heterotic hybrids because of convergence of diverse genes scattered in parents to progeny. Selection of genotypes belonging to clusters with maximum inter-cluster distance for hybridization had also been reported by Rana and Joshi [13]; Rana [11]; Rana and Sharma [12]; Kapila *et al.* ([6] and Debnath *et al.* [3] and Verma *et al.* [17]; Kusuma *et al.* [7]; Pandey and Singh (2011) and Ahmmed *et al.* [1] in amaranth.

Table-2: Intra and inter cluster distance $\sqrt{D^2}$ values among 30 germplasm of buckwheat

	I	II	III	IV	V	VI
I	118.13	234.93	313.09	367.82	233.22	225.07
II		119.33	208.39	215.25	201.16	239.42
III			84.84	163.42	229.88	220.02
IV				106.62	234.82	173.56
V					94.91	159.35
VI						94.44

Cluster means

Cluster group means for all 10 characters are given in **Table-3**. A close perusal of these clusters means for different characters indicated that considerable differences existed among the clusters for all the characters. Cluster I having 9 germplasm, showed lowest cluster means for plant height (85.41 cm) and

100-seed weight (1.42 g). Cluster II, having 6 germplasm exhibited lowest cluster mean for number of secondary branches per plant (9.83). Cluster III, having 3 germplasm exhibited highest cluster mean for number of internodes per plant (11.22) and leaf length (6.30 cm) but, exhibited lowest cluster mean for days to 50% flowering (43.77 days), days to maturity (116.11 days) and seed yield per plant (2.26 g). Cluster IV having 4 germplasm exhibited highest cluster mean for plant height (112.05 cm), number of primary branches per plant (3.55), number of leaves per plant (27.85), 100-seed weight (1.96 g) and seed yield per plant (3.16 g). The 5 germplasm of cluster V resulting highest cluster mean for days to maturity (121.33 days) and number of secondary branches per plant (10.98). Cluster VI, having 3 germplasm exhibited highest mean for days to 50% flowering (64.77 days) but, exhibited lowest cluster mean for number of primary branches per plant (3.06) and leaf length (4.89 cm).

On the basis of above results it is evident that cluster IV had maximum cluster means for most of desirable characters *viz.*, plant height, number of primary branches per plant, number of leaves per plant, 100-seed weight and seed yield per plant. Therefore genotypes (IC-412762, RSR/SKS-71, IC-276627 and PRB-1) including this cluster can be used for improvement of seed yield and yield attributes. Variable cluster means for different plant growth and seed yield characters have also been reported by Rana and Joshi [13]; Rana [11]; Rana and Sharma [12] and Debnath *et al.* [3] in buckwheat and Verma *et al.* [17] in Amaranth.

Table-3: Intra cluster group means for various components of buckwheat germplasm

S.N.	Characters	Cluster Means					
		I	II	III	IV	V	VI
1	Days to 50% flowering	59.77	49.05	43.77	49.41	62.93	64.77
2	Days to maturity	117.40	118.38	116.11	121.00	121.33	118.88
3	Plant height at maturity (cm)	85.41	94.36	105.91	112.05	108.25	105.64
4	No. of primary branches per plant	3.34	3.45	3.24	3.55	3.37	3.06
5	No. of secondary branches per plant	10.54	9.83	9.95	10.40	10.98	10.33
6	No. of internodes per plant	9.56	10.82	11.22	9.43	10.46	11.00
7	No. of leaves per plant	23.32	21.75	26.08	27.85	21.66	26.48
8	Leaf length (cm)	5.66	5.75	6.30	5.71	6.23	4.89
9	100-seed weight (g)	1.42	1.67	1.76	1.96	1.75	1.75
10	Seed yield per plant (g)	2.62	3.08	2.26	3.16	2.68	2.97

Contribution of different characters to total divergence

The relative contribution of different quantitative characters in (Table-4) depicted that number of leaves per plant contributed maximum (22.30%) towards genetic divergence followed by seed yield per plant (20.69%), days to 50% flowering (18.62%), plant height (17.47%), 100-seed weight (8.28%), number of internodes per plant (7.59%), days to maturity (3.45%) and number of secondary branches per plant (1.61%) exhibited low contribution towards genetic divergence, while remaining 2 characters played negligible role less (<1%) in contributing genetic diversity. The low contribution was however measured on other characters, *viz.*, number of primary branches (0.00%) and leaf length (0.00%). These were considered to be the most important characters for the genetic diversity.

Table-4: Contribution of different plant growth and seed yield characters to total divergence in buckwheat

S.N.	Characters	Number of times appearing first in ranking	Per cent contribution (%)
1	Days to 50% flowering	81	18.62
2	Days to maturity	15	3.45
3	Plant height at maturity (cm)	76	17.47
4	No. of primary branches per plant	0.01	0.00
5	No. of secondary branches per plant	7	1.61
6	No. of internodes per plant	33	7.59
7	No. of leaves per plant	97	22.30
8	Leaf length (cm)	0.01	0.00
9	100-seed weight (g)	36	8.28
10	Seed yield per plant (g)	90	20.69

The characters that appeared maximum number of times first, greater was its contribution to genetic divergence. In present investigation, an assessment of the contribution of different characters indicated that number of leaves per plant, seed yield per plant, days to 50% flowering, plant height, 100-seed weight, number of internodes, days to maturity and number of secondary branches had maximum

contribution to genetic divergence as these traits appeared maximum times first rank viz., 97, 90, 81, 76, 36, 33, 15 and 7, respectively. These characters could be used to assess the genetic diversity among the population of buckwheat and also for selecting diverse parents for hybridization programme with view to develop transgressive segregants while working in buckwheat, Rana and Sharma [12] and Debnath *et al.* [3], also reported maximum contribution to total divergence in buckwheat and Shukla and Singh [15] in Amaranth.

CONCLUSION

Keeping in the view, inter-cluster distance and cluster means, it could be concluded that the information high inter cluster distances and cluster means could be useful for developing future hybridization programme in the seek of heterotic hybrids in buckwheat. Based on high inter-cluster distance of cluster I with cluster IV, cluster I with cluster III and cluster II with cluster VI such as IC-13507 × IC-412762, IC-341661 × IC-412762, Shimla-B1 × IC-412762, IC-13507 × IC-412733, IC-341661 × IC-412733, IC-294344 × IC-107988, RSR/SKS-104 × IC-107988, Himpriya × IC-107988 and VL-7 × IC-107988 are recommended for hybrid breeding programmes. Contribution of different characters indicated that number of leaves per plant, seed yield per plant, days to 50% flowering, plant height, 100-seed weight, number of internodes, days to maturity and number of secondary branches had maximum contribution to genetic divergence. These characters could be used to assess the genetic diversity among the population of buckwheat and also for selecting diverse parents for hybridization programme with view to develop transgressive segregants in mid hills of Uttarakhand.

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