

Genetic Variability Analysis in Germplasm Collections of Buckwheat

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ABSTRACT

Buckwheat is an important pseudo-cereal with a better nutritional and medicinal value than many common cereals. The present investigation was undertaken to estimate the phenotypic coefficient of variation (PCV) and genetic coefficient of variation (GCV), heritability and genetic advance as per cent mean. Fifty-four diverse buckwheat genotypes (involving exotic, indigenous and local collection) were evaluated in a replicated completely randomized block design during Kharif 2017. Analysis of variance revealed highly significant differences between the genotypes for all characters studied suggesting the presence of adequate variability for selection. Moderate PCV and GCV coupled with high heritability were recorded for days to 50 per cent flowering while, high genotypic and phenotypic coefficients of variation coupled with high heritability and genetic advance as per cent mean were observed for seed yield and number of secondary branches indicating the more additive gene action hence the selection for these traits could be effective. However, days to maturity exhibited low PCV, GCV and genetic advance indicating selection will be ineffective for such traits.

Keywords

Pseudo-cereal,
Variability, GCV,
PCV, Heritability,
Genetic advance.

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Introduction

Buckwheat (*Fagopyrum esculentum*. Moench) is the plant of dicot family Polygonaceae, a native of Northern or Central Asia being largely cultivated in the United States. However, the cultivation of buckwheat is more widespread in the high altitude areas of the north-western Himalaya where it is grown mainly as a food grain crop, is eaten on 'Bart' or fast days, being one of the lawful foods for such occasions. It is a multi-food-use pseudocereal with a better nutritional value than many common cereals and a functional food with industrial applications.

The multipurpose use of buckwheat coupled with early maturity, low nutrient demand and

ability to adapt well to marginal and degraded lands makes it an ideal candidate for future sustainable agriculture (Dutta, 2004). Buckwheat is a short season crop that does well on low-fertility or acidic soils, but the soil must be well drained. It is thriving in the poorest soil.

Buckwheat contains rutin, a medicinal chemical that strengthens capillary walls, reducing hemorrhaging in people with high blood pressure and increasing microcirculation in people with chronic venous insufficiency (Ihmel *et al.*, 2003). Dried buckwheat leaves for tea were manufactured in Europe under the brand

name "Fagorutin". Buckwheat contains no gluten, and can thus be eaten by people with coeliac disease or gluten allergies. Buckwheat contains D-chiro-inositol, a component of the secondary messenger pathway for insulin signal transduction found to be deficient in Type II diabetes and Polycystic Ovary Syndrome (PCOS). It is being studied for use in treating Type II diabetes (Kawa *et al.*, 1996). Research on D-chiro-inositol and PCOS has shown promising results (Nestler *et al.*, 1999; Iuorno *et al.*, 2002). A buckwheat protein has been found to bind cholesterol tightly. It is being studied for reducing plasma cholesterol in people with an excess of this compound (Tomotake *et al.*, 2001). Hence the crop is nutritionally rich with enormous medical importance in pharmaceutical industries.

Buckwheat is boon to both industry and to farmers as well. It is boon to the farmer because of the factors like Short duration (70-80days), good yield (5-6q/ha), low input requirement, good market price, it can be grown under rainfed or with restricted irrigation and marginal farmers can get good income (appx. 2.5 Lakh/acre @ rate of Rs 500/kg in the national and international market)

It is also boon to the industry as it has the advantages like good pharmaceutical value (drug industry), good health benefits (food industry), many Nutri-rich products and several other value added products can be developed and it has good market value for grains and by-products.

However, the productivity of Indian buckwheat is quite low as compared to that of Korea (Joshi and Paroda, 1991 and Bhag Mal, 1994) and other buckwheat growing countries. For achieving increased production in buckwheat, it is essential to develop new high yielding varieties. Planning of any

breeding programme requires information on the extent and nature of genetic variability available among the existing genotypes. The effectiveness of selection and identification of superior genotypes depends on the magnitude of inherent variability for a particular character. Hence it is prerequisite to study the estimates of genetic parameters such as coefficients of genotypic and phenotypic variability, heritability and genetic advance.

Improvement of any characters in a crop depends upon the amount of variability present in the base population, in absence of which there shall be no response to selection. Thus, the present study, therefore, was undertaken to estimate the extent of genetic variation, heritability and genetic gain present for various quantitative characters including seed yield in a set of buckwheat genotypes.

Materials and Methods

The present investigation was conducted at Botanical Garden, Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, Karnataka, India during *Kharif*, 2017 using 54 diverse genotypes belonging to both *Fagopyrum esculentum*, received from NBPGR, Regional Station, Shimla, Himachal Pradesh. The genotypes evaluated comprised local collections (Himachal Pradesh), indigenous and exotic collections along with Himapriya, VL7 and PRB-1 as the checks. The experiment was laid out in a randomized block design with two replications. The experiment was conducted with 4 rows of each genotype in 3 meter long plots with a spacing of 30 cm × 15 cm respectively between row to row and plant to plant. Recommended agronomical practices were followed with a fertilizer dose of 20:40:0 N: P: K kg/ha and no plant protection measures were undertaken since no insect and disease problems were encountered.

Observations were recorded on 5 randomly selected representative plants/plot. Data on days to 50% flowering, days to maturity (days), plant height (cm), number of primary branches, number of secondary branches, weight of 100 seeds (test weight) (g) and seed yield (q/ha) were recorded. Analysis of variance was done from the mean data obtained for each character. Both genotypic and phenotypic coefficients of variation (GCV and PCV, respectively) were estimated as suggested by Burton (1952). Heritability (h^2) in broad sense was estimated as suggested by Hanson *et al.*, (1956) and expressed in per cent. Genetic advance as per cent mean was calculated following Johnson *et al.*, (1955).

Results and Discussion

The analysis of variance for all the characters revealed the significant differences among the clones studied (Table 1) indicating the existence of adequate variability and considerable improvement can be achieved in these characters by selection. However, the analysis of variance by itself is inconclusive in explaining all the inherent genetic variability in the collection. This is evident by partitioning the total variability inherent in the genotypes from the phenotypic variance.

The scope for improvement through selection is enhanced by the range of variability in the population. The comparison of results revealed higher range values for plant height, number of racemes, days to maturity and days to 50 % flowering. Similar results were also observed by Dutta *et al.*, (2008).

From this, it can be inferred that the genotypes used in the present study possessed wide variability for most of the traits. Higher estimates of phenotypic and genotypic coefficients of variations were observed for seed yield per plant, number of secondary

branches and number of primary branches indicating the scope of improvement through selection in these traits while low to medium estimates were observed for plant height, days to 50% flowering, number of racemes and test weight (Table 2).

However, days to maturity exhibited low estimates of PCV and GCV (Dutta *et al.*, 2008). High estimates of PCV and GCV for seed yield was reported by Gohil and Misri (1986) and for seed yield and number of branches by Joshi and Rana (1995) in buckwheat.

The amount of genetic variation alone may not be of more relevance unless it is supplemented with the information on estimates of heritability. It has been suggested by Burton and De Vane (1953) that the GCV along with heritability estimate could provide a better picture of degree and magnitude of improvement that can be expected by phenotypic selection. High estimate of broad sense heritability was recorded for all the characters investigated except for primary and secondary branches which showed moderate heritability (Table 2).

This suggests that selection of genotypes for these characters with high heritability will be effective as it indicates the heritable portion of the total variation. These results are in agreement with (Dutta *et al.*, 2008). Knowledge on the heritability of characters is important to the breeders since it indicates the possibility and extent of improvement that can be achieved through selection for a particular trait. Since the genetic advance is dependent on phenotypic variability and heritability in addition to selection intensity, the heritability estimates in conjunction with genetic advance values will be more effective and reliable in predicting the response to selection by providing more genetic information on the character.

Table.1 Analysis of variance for different quantitative characters in Buckwheat

Source of Variation	Degrees of Freedom	Plant Height (cm)	Days to 50 per cent flowering	Days to maturity	Number of Primary braches	Number of Secondary branches	Number of racemes	Test weight (g)	Seed Yield (q/ha)
Replicate	1	2.28	0.75	3.34	0.03	4.92*	8.03*	0.19	0.12
Treatments	53	583.97**	42.08**	36.72**	3.02**	5.90**	470.69**	0.48**	6.54**
Error	53	11.23	0.43	0.72	1.06	1.12	1.70	0.03	0.41
SEm		2.35	0.46	0.59	0.72	0.74	0.91	0.12	0.45
CD at 5%		6.72	1.31	1.70	2.06	2.13	2.62	0.33	1.29

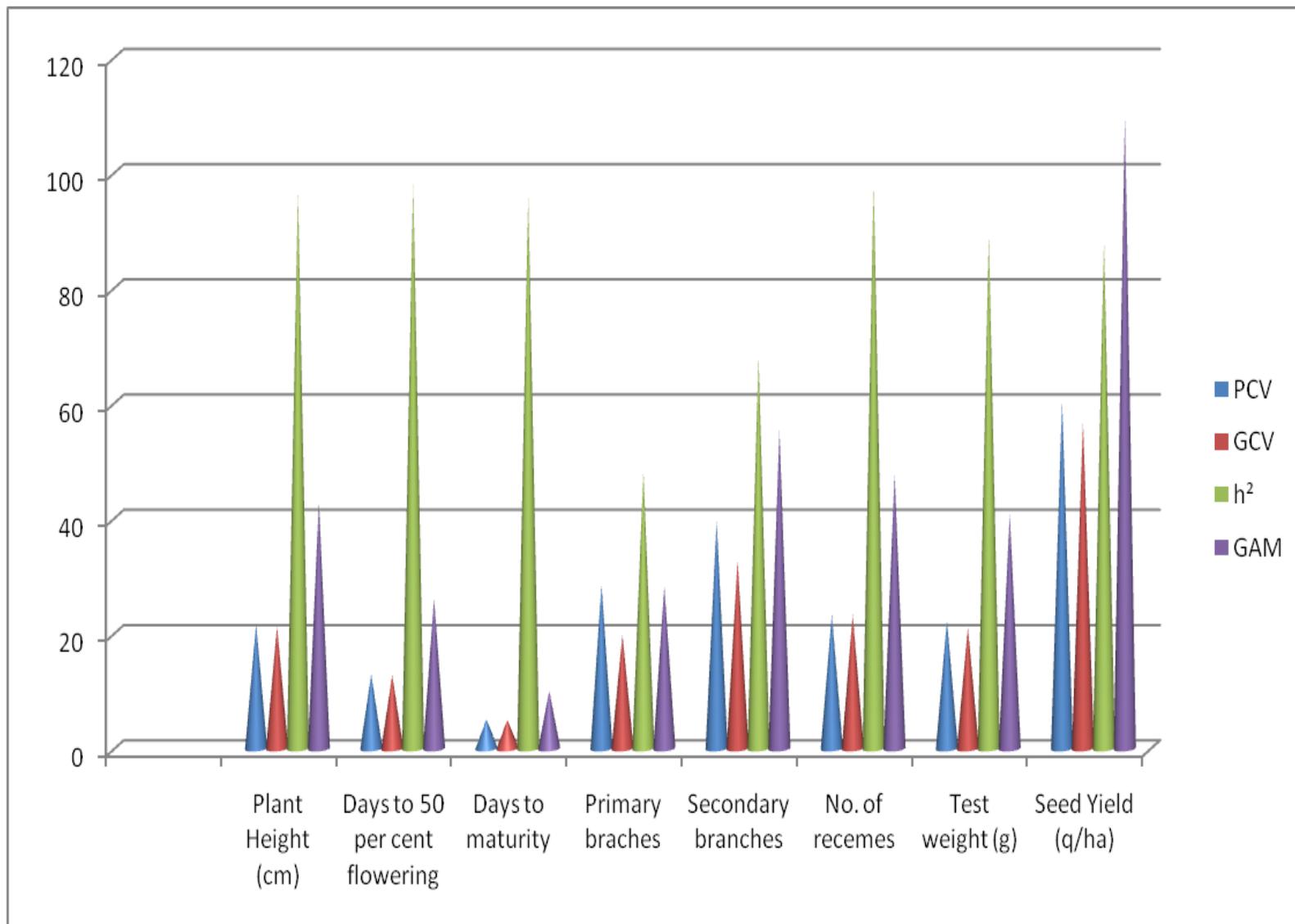
* = 0.05 probability level

**= 0.01 probability level

Table.2 Estimates of Genetic variability parameters for different quantitative traits in Buckwheat

Character	Mean	Range		Phenotypic Variance	Genotypic Variance	PCV	GCV	h ²	GA	GAM
		Lowest	Highest							
Plant Height (cm)	79.86	45.24	109.98	297.60	286.37	21.60	21.19	96.20	34.20	42.82
Days to 50 per cent flowering	35.82	27.50	44.00	21.25	20.83	12.87	12.74	98.00	9.31	25.98
Days to maturity	85.68	74.50	95.00	18.72	18.00	5.05	4.95	96.20	8.57	10.00
Primary braches/plant	5.03	2.58	8.54	2.04	0.98	28.43	19.72	48.10	1.42	28.16
Secondary branches/plant	4.75	2.17	9.02	3.51	2.39	39.46	32.54	68.00	2.63	55.29
Number of racemes/plant	66.02	27.19	86.09	236.20	234.49	23.28	23.19	99.30	31.43	47.61
Test weight (g)	2.27	1.32	3.41	0.25	0.23	22.22	20.98	89.10	0.93	40.80
Seed yield (q/ha)	3.09	0.40	8.84	3.48	3.07	60.40	56.71	88.10	3.39	109.67

Fig.1 Graphical representation of genetic variability parameters for different quantitative traits in Buckwheat



High heritability coupled with high genetic advance observed for seed yield, number of secondary branches, number of racemes, plant height and test weight (Table 2 and. Fig. 1) (Gohil and Misri, 1986; Dutta *et al.*, 2008) indicated that these characters may be controlled by additive gene action; hence, phenotypic selection could be effective in improvement of such traits (Panse and Sukhatme, 1967). Moderate genetic advance was exhibited by day to 50% flowering and number of primary branches while, days to maturity showed high heritability coupled with low genetic advance suggesting that selection will be less effective for such traits.

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