Genetic Variability in *Chenopodium*

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Coefficient of variability and genetic gain for seed yield and its 10 contributing traits was worked out in 44 germplasm lines of *Chenopodium* spp. in the year 2000-2001 at National Botanical Research Institute, Lucknow. Seed yield/ plant ranged from 2.17-97.97 g with an average yield of 34.99±1.18 while leaf size ranged from 1.42-178.77 cm^2 indicating great diversity among the strains involved in the present study for these traits. Phenotypic coefficient of variation and genotypic coefficient of variation was maximum for leaf size, followed by dry weight of plant and 100 seed weight. The heritability estimates were high for all the traits, which also confirmed a great amount of variation in the lines under study. Genetic gain was high for all the traits except days to flowering and days to maturity, which indicated that all the traits were mainly governed by additive gene effects. A breeding plan was discussed to enhance the yield potential.

Key Words: Additive Gene, *Chenopodium*, Coefficient of Variability, Genetic gain, Heritability.

Introduction

Chenopodium spp. are being cultivated since centuries as a subsidiary crop, especially as leafy vegetable (*C. album*) (Singh, 1961) as well as for grain (*C. quinoa*). It can be grown under various agroclimatic situations ranging from tropical to temperate zones. The potherb is a cheap and rich source of carotenoids (78-190 mg/kg) (Prakash *et al.*, 1993). *Chenopodium quinoa* is native to the Andean region and is adapted to problems of stoniness, poor or excessively free drainage and can be cultivated in soils having a pH of 4.8 to 8.5 (Tapia, 1979). The nutritional value of quinoa seeds has been known for a long time to be superior to traditional cereals. The seeds have a protein content of 10-18%, fat content of 4.1-8.8% and traces of starch, ash and crude fibre (DeBruin, 1964). Calcium and iron are significantly higher in quinoa than in rice, maize, wheat or oats (White *et al.*, 1955; DeBruin, 1964). The seed proteins have a balanced amino acid spectrum with high lysine (5.1-6.4%) and methionine (0.4-1.00%) contents (Prakash and Pal, 1998). Inspite of its great potential, no systematic studies on various genetical aspects have been conducted. Hence an attempt has been made to initiate a crop-breeding programme on *Chenopodium* spp. The knowledge of the magnitude of variation in the available germplasm, interdependence of quantitative characters, extent of environmental influence on these factors, heritability and genetic gain in the genotypes are the prerequisite aspects for any crop-breeding programme. The present investigation was carried out to study different selection parameters in the available germplasm lines belonging to different species of *Chenopodium*.

Materials and Methods

The present investigation consisted of 44 germplasm lines of *Chenopodium* spp. of exotic and indigenous origin which included one entry each of seven spp. of *Chenopodium* namely *C. bushianum*, *C. amaranticolour*, *C. murale*, *C. opulifolium*, *C. strictum*, *C. berlandieri*, *C. ugandae and* 2 entries of *C. giganteum*, 10 lines of *C. quinoa*, 23 lines of *C. album* and two selections from 2 separate cross progenies (Table 1). The germplasm lines were selected to ensure adequate representation of germplasm lines of different ploidy levels as well as the whole distributional range of the genus. The seeds were sown in randomized block design with 3 replications in the year 2000-2001 at the experimental field of National Botanical Research Institute, Lucknow. Two rows of each entry were sown with crop geometry of 45 x 15 cm^2 row-to-row and plant-to-plant distance respectively. Five plants from each replication were randomly selected and data for 11 characters viz. days to flowering, days to maturity, plant height (cm), leaf size (cm^2), stem diameter (cm), number of primary branches/plant, inflorescence length (cm), 100 seed weight (g), dry weight of plant (g), number of inflorescence/plant and seed yield/plant (g) were recorded. Analysis of variance for each trait was done according to Panse and Sukhatme (1978) and phenotypic and genotypic coefficient of variation (PCV and GCV), heritability in broad sense and genetic advance were computed following Singh and Chaudhary (1985) and Johnson *et al.* (1955).

Results and Discussion

The analysis of variance exhibited significant differences among the strains for all the traits (Table 2) indicating

Table 1: Germplasm lines, their source, chromosome number and ploidy level

S. No.	Name of germplasm line	Source	Chromosome number	Ploidy level
1.	*C. album* PRC 9801	India	-	-
2.	*C. album* PRC 9803	India	-	-
3.	*C. album* PRC 9804	India	-	-
4.	*C. album* PRC 9802	India	-	-
5.	*C. album* IC 107295	India	-	-
6.	*C. album* IC 107297	India	-	-
7.	*C. album* IC 107299	India	-	-
8.	*C. album* IC 107296	India	-	-
9.	*C. quinoa* 587173	USDA	36	4x
10.	*C. album* local 2x Red	India	18	2x
11.	***C. bushianum* 22376**	USDA	36	4x
12.	*C. album* IOWA	IOWA, USA	54	6x
13.	*C. album* H.P	India	54	6x
14.	*C. quinoa* 510537	USDA	36	4x
15.	*C. quinoa* CHEN 92/91	Gatersleben, Germany	36	4x
16.	Progenitor of quinoa	Mexico	36	4x
17.	*C. quinoa* 478414	USDA	36	4x
18.	*C. album* (local) x *C. quinoa*	Hybrid	54	6x
19.	*C. quinoa* 584524	USDA	36	4x
20.	***C. amaranticolor***	India	54	6x
21.	*C. album* Mexico	Mexico	36	4x
22.	*C. album* x *C. album* Siliguri	Hybrid	18	2x
23.	*C. album* 'Siliguri'	India	18	2x
24.	*C. quinoa* 596498	USDA	36	4x
25.	*C. quinoa* 22158	USDA	36	4x
26.	*C. album* 'chandanbathua'	India	18	2x
27.	*C. quinoa* CHEN 67/78	Gatersleben, Germany	36	4x
28.	*C. album amaranticolor*	India	54	6x
29.	*C. quinoa* CHEN 71/78	Gatersleben, Germany	36	4x
30.	*C. album* CHEN 60/76	Gatersleben, Germany	54	6x
31.	*C. album* CHEN 85/82	Gatersleben, Germany	54	6x
32.	*C. album* Czech	Czech Republic	54	6x
33.	*C. album* x *C. quinoa* (colchiploid)	Hybrid	54	6x
34.	***C. murale* local**	India	18	2x
35.	***C. opulifolium***	Gatersleben, Germany	36	4x
36.	*C. album* PI 605700	USDA	54	6x
37.	*C. album* local 6x	India	54	6x
38.	*C. giganteum* 596371	USDA	54	6x
39.	*C. giganteum* 596372	USDA	54	6x
40.	***C. album* local**	India	18	2x
41.	***C. strictum* 47/79**	Gatersleben, Germany	54	6x
42.	***C. berlandieri* 568156**	USDA	36	4x
43.	*C. album* CHEN 63/80	Gatersleben, Germany	54	6x
44.	*C. ugandae* 77/78	Gatersleben, Germany	36	4x

a wide range of variability exists in the strains. The seed yield/plant was variable between 2.17-97.97 g with an arithmetic mean of 34.99±1.18. The character leaf size showed large variation among the strains ranging from 1.42-178.77 cm^2, with the arithmetic mean 29.48±1.02, which suggests that strains were very diverse for this trait. However, the characters dry weight of plant and number of inflorescence/plant also had large variation in the strains and varied from 3.65-289.87 g and 39.63-742.89 with an average of 65.36±2.56 and 264.12±4.80 respectively. The inflorescence length varied from 1.47-38.16 cm with an arithmetic mean of 17.98±0.49. The 100 seed weight ranged from 0.03-0.30 g with an average 0.102±0.004. The plant height and number of primary branches/plant varied from 20.55-305.00 cm and 4.20-55.33 with arithmetic mean 150.54±2.52 and 28.33±0.88 respectively. The days to flower varied from 86.00-154.67 with an average of 109.55±1.00. Days to maturity ranged from 110.10-194.33 with a mean of 143.02±1.12. The stem diameter varied from 0.37-2.30 cm with an average 1.37±0.06.

The PCV and GCV was maximum for leaf size followed by dry weight of plant and 100 seed weight (Table 2). The PCV had marginally higher estimate than corresponding GCV for all the traits, which indicates that the variability was primarily due to genotypic component.

Table 2: Genetic variability, heritability and genetic advance for different traits in *Chenopodium* spp.

Characters	F Value ± SE	Mean	Range	s^2g	s^2p	s^2e	GCV	PCV	Heritability (%)	Genetic advance	Genetic advance (%)
Days to flowering	663.77	109.55 ± 1.00	86.00-154.67	336.11	337.64	1.52	16.73	16.77	99.5	37.68	34.40
Days to maturity	835.45	143.02 ± 1.12	110.10-194.33	527.48	529.38	1.90	16.06	16.09	99.6	47.23	33.02
Plant height (cm)	2635.50	150.54 ± 2.52	20.55-305.00	8355.18	8364.70	9.51	60.72	60.75	99.9	188.19	125.01
Leaf size (cm^2)	2356.75 ± 1.02	29.48	1.42-178.77	1217.94	1219.49	1.55	118.39	118.47	99.9	71.85	243.73
Stem diameter (cm)	145.74	1.37 ± 0.06	0.37-2.30	0.26	0.27	0.005	37.29	37.67	98.0	1.04	76.03
Number of primary branches	372.98	28.33 ± 0.88	4.20-55.33	146.74	147.93	1.18	42.76	42.93	99.2	24.85	87.73
Inflorescence length (cm)	1152.30	17.98 ± 0.49	1.47-38.16	135.94	136.29	0.35	64.85	64.93	99.7	23.99	133.41
100 Seed weight (g)	951.92	0.102 ± 0.004	0.03-0.30	0.006	0.006	0.00	77.31	77.44	99.7	0.16	159.02
Dry weight of plant (g)	1301.10	65.36 ± 2.56	3.65-289.87	4257.49	4267.32	9.82	99.83	99.95	99.8	134.26	205.42
Number of inflorescence	3203.30	264.12 ± 4.80	39.63-742.89	36892.41	36926.97	34.56	72.72	72.76	99.9	395.49	149.74
Seed yield (g)	949.36 ± 1.18	34.99	2.17-97.97	656.11	658.19	2.07	73.19	73.31	99.7	52.68	150.53

s^2g = Genotypic variance, s^2p = Phenotypic variance, s^2e = Environmental variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation

The characters days to flower and days to maturity showed low estimates for PCV and GCV indicating that these traits had less scope towards improvement of yield through selection. To determine the heritable portion of variation, consideration of heritability estimates are necessary. The heritability estimates in broad sense were very high for all the characters and ranged from 99.20-99.90% (Table 2) suggesting that substantial improvement can be made using standard selection techniques. High heritability alone does not guarantee large gain through selection unless sufficient genetic advance attributable to additive gene action is present. Hence, heritability in conjunction with the estimates of genetic advance is more useful in isolating superior genotypes. The values of genetic gain were highest for leaf size (243.73%), followed by dry weight of plant (205.42%) and 100 seed weight (159.02%) (Table 2). The values of genetic advance above 100% obtained in some of the characters are due to the extreme variations present among the genotypes as evident since the genotypes belong to distinct species and are of different geographical origin. High heritability coupled with high values of genetic advance and genotypic coefficient of variation for most of the traits suggest that additive gene action played an important role for these traits. This study concludes that selection based on phenotypic performance (mass selection) for the traits namely leaf size, dry weight of plant and seed weight would be more rewarding for achieving desired gain in grain yield. Besides this, it is pertinent to discuss the crossability and the breeding potential both within and among the species. In the present study, the lines belonging to *C. quinoa*, *C. album*, and most of the species are cross compatible among themselves. Also the diploid cytotype of *C. album* found in North India is intercrossable with *C. quinoa* and the hexaploid obtained through colchicine treatment of the resultant triploid is fully fertile (Wilson 1980; Personal Communication by Dr. M Pal).

Acknowledgements

The authors are thankful to the Director NBRI, Lucknow for providing the facilities and constant encouragement to carry out the present investigation. CSIR, New Delhi is duly acknowledged for providing financial assistance.

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