GENETIC DIVERGENCE IN HIMALAYAN CHENOPOD

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Fifty three genotypes of Himalayan chenopod (*Chenopodium album* L.) including 3 exotic introductions (*C. quinoa*) were grouped into eleven clusters following multivariate analysis on a set of ten characters related to yield and its contributing characters. The multivariate analysis studies indicated that geographical isolation might not be the only factor causing genetic diversity. Leaf length, days to maturity, leaves on main shoot and leaf width were the most potnetial traits contributing to the total genetic divergence. Clusters IV, V and VII were important because they comprised genotypes with high grain yield/plant, high inflorescence length, high number of leaves on main shoot, long leaf length and bold grain types. Utilizing genotypes from these clusters, there is a sufficient scope for varietal improvement through hybridization.

Chenopod (*Chenopodium album* L.) is the most important under-utilized food crop of Indian Himalayas and *C. quinoa* is an important crop of the Andean region, which originated near Lake Titicaca in the Andean region. Chenopod local land races account for all the produce in the Himalayan region and no improved variety is available for cultivation to the farmers. The grain yield improvement work in this crop is meager in the Himalayan region, though a wide range of genetic diversity is available in chenopod collections (Joshi, 1991 and Partap, 1990). The utility of these collections in genetic improvement programme is limited unless they are systematically evaluated. An attempt has been made to evaluate and group fifty-three genotypes of chenopod germplasm based on their genetic distance.

MATERIALS AND METHODS

The experiment was conducted with fifty accessions of chenopod originating from Kulu, Shimla, Chamba, Kinnaur (Himachal Pradesh); Jammu and Kashmir; Uttarkashi, Almora (Uttaranchal) and Lucknow (Uttar Pradesh); Darjeeling and three accessions originating from Bolivia, Mexico and Guatemala. These 53 accessions were sown during Kharif season of 1993 and 1994 in an augmented design (Federer, 1956). The seeds were drilled in rows 50 cm apart first followed by thinning and plant to plant distance was kept 20 cm within rows. Five competitive plants of each accession were selected at random. Data were recorded on ten characters viz. plant height (cm), number of branches, number of leaves on main shoot, inflorescence length (cm), leaf length (cm), leaf width (cm), days to flower, days to mature, 1000-grain weight (g) and yield per plant (g). The average values of 5 plants for each character were subjected to multivariate analysis, using Mahalanobis (1949) generalized distance D^2. The genotypes were grouped into different clusters according to Tocher's method as described by Rao (1952). The contribution of different characters towards divergence was estimated.

RESULTS AND DISCUSSION

Fifty-three accessions of chenopod collections were grouped into eleven clusters (Table 1). Cluster I was largent, comprising 15 accessions and clusters IX, X and XI were the smallest with one accession only. Among others clusters cluster II with 9 accessions, cluster III with 8 accessions, cluster IV and V having 5 accessions each, cluster VI with 4 accessions all originating from South America except one from Chamba. Cluster VII and VIII with 2 accession each both originating from NBRI, Lucknow. The exotic material received from Mexico, Bolivia and Guatemala got grouped together with one Himalayan collection from Chamba in cluster VI. All the exotic introductions maintained their geographic isolation by falling together in one and the same cluster. falling of one accessions in cluster VI from Chamba suggested that there is no firm relationship between genetic divergence and geographical distance. genetic drift and selection under diverse environment could cause greater diversity than geographical distance. While classifying the large germplasm of chenopod into different ecotypes according to information on their origin, Risi and Galwey (1989) reported a considerable overlap with respect to the origin between ecotypes. The results therefore, suggest that genotypes belonging to the same location may yield better transgressive segregates than the genotypes originating from different areas. There is also a need to evaluate the genotypes originating from different areas, There is also a need to evaluate the genotypes on the basis of their individual merit and genetic diversity and only those genotypes, which stand top and highly diverse, should be chosen for breeding work.

Intra and inter-cluster D^2 values are presented in Table 2. Intra cluster values ranged 0.00 to 15.47. The highest intra-cluster value was recorded in cluster VI (15.47) followed by cluster I (12.32) and cluster VIII (12.10). Inter cluster D^2 values ranged from 16.62 to 55.08. Highest inter-cluster D^2 value was observed between XI and X (49.70) indicating that these clusters are highly divergent. The least inter-cluster D^2 value was recorded between these two clusters.

Table 1. Cluster composition based on D^2 values in chenopod

Clusters	No. of Genotypes	Name of genotypes	Geographical origin
I	15	IC108088, IC108089, IC109025, IC109480, IC109732, IC109734, IC109736, IC109738, IC109740, IC109758, IC100355, P1123, P1171, P1212, CH/LKW-10	Kulu, Chamba, Uttarkashi, Shimla
II	9	T45-87, T87, TP30, T2-87, CH/LKW-16, CH/LKW-49, IC109739, T3-87, CH/LKW-5	Almora, Kulu, Lucknow, Shimla
III	8	NC58224, NC58229, NC58230, NC58230, NC58231, NC58232, IC15022, CH/LKW-16, CH/LKW49	Chamba, Kinnaur, Darjeeling
IV	5	IC107297,IC107854,IC107808,IC109733,IC109737	Kulu,Shimla
V	5	IC107185,IC107263,IC107295,IC107396,IC108086	Shimla
VI	4	NC58233,EC180010,EC180011,EC180012	Chamba,Bolivia,Gautamala,Mexico
VII	2	CH/LKW-66,CH/LKW-100	Lucknow
VIII	2	CH/LKW-60,CH/LKW-62	Lucknow
IX	1	NC58014	Jammu & Kashmir
X	1	T-87	Kulu
XI	1	CH/LKW-6	Lucknow

Table 2. Average intra and inter cluster D^2 values

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	12.32	27.43	25.32	37.31	34.10	29.00	30.00	20.45	29.62	32.50	37.46
II		11.19	19.42	32.72	27.30	27.32	31.56	33.70	31.95	37.97	39.35
III			8.39	16.62	27.50	32.76	22.83	37.37	21.97	26.14	32.10
IV				10.97	47.62	48.02	38.26	25.60	44.60	50.69	40.14
V					9.31	39.30	24.39	24.63	40.72	30.81	36.32
VI						15.47	30.00	28.73	37.43	31.27	31.44
VII							10.03	39.21	40.20	42.54	39.77
VIII								12.10	39.64	23.46	37.75
IX									0.00	49.70	55.08
X										0.00	41.03
XI											0.00

Table 3. Average cluster means of 53 genotypes belonging to different clusters

Traits/ Cluster	Plant height	Branches/ plant	No. of leaves on main shoot	Inflore- scence Length	Leaf length	Leaf width	Days to flower	Days to mature	1000 seed weight	Yield/plant
I	107.23	26.22	32.36	17.48	5.25	4.28	62.15	119.20	0.73	7.40
II	118.83	32.16	33.41	7.59	4.20	5.21	60.75	125.08	0.72	7.01
III	123.40	24.20	34.61	18.49	5.54	4.00	60.00	123.70	0.67	8.39
IV	106.40	67.90	89.58	29.30	7.98	6.51	38.40	99.10	0.99	10.25
V	205.90	36.00	27.56	25.29	4.52	3.13	61.40	38.40	99.10	0.99
VI	97.00	45.62	50.50	8.53	6.50	4.58	37.25	97.57	0.87	5.91
VII	88.00	27.75	28.25	8.10	8.20	3.85	34.75	59.06	1.01	8.35
VIII	84.24	31.50	37.75	8.15	8.10	4.12	49.50	148.00	0.94	6.45
IX	194.00	52.45	34.00	9.10	8.25	4.10	40.50	98.51	0.81	8.25
X	107.50	22.30	24.50	9.45	3.75	4.60	65.00	133.00	0.60	8.60
XI	79.00	32.24	38.26	16.40	4.62	4.42	56.50	119.40	1.77	7.20

The inter-cluster distance was higher than the intra-cluster distances in all the cases indicating more divergence of genotypes between the clusters. The maximum cluster mean (Table 3) was observed in cluster IV for yield per plant, number of branches/plant, number of leaves on main shoot, inflorescence length and leaf width; cluster VII for 1000-grain weight, leaf length, early maturity and plant height. These clusters could be regarded as useful sources of genes for different traits and there is sufficient scope for varietal improvement through hybridization. These results also indicate that if we take one representative genotype from each cluster and make a diallel, then in the progeny we can get better heterotic effects and more variability in F_2 population which will be helpful in selection and breeding programme of chenopod for the Himalayan region.

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