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## Studies on Genetic Diversity for Quantitative Characters in Quinoa (*Chenopodium quinoa* Willd.)

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### ABSTRACT

The 30 genotypes of Quinoa (*Chenopodium quinoa* Willd.) were studied for genetic diversity for nine different quantitative traits. Genotypes were grouped into eleven clusters. Cluster I was the largest cluster with 11 genotypes followed by cluster II with 7 genotypes, cluster V, IX, XI with 2 genotypes each while, cluster III, IV, VI, VII, VIII and X were solitary. The calculated  $D^2$  values varied from 2.37 to 12.05. The maximum intra cluster distance was observed for cluster XI and inter cluster distance was maximum between cluster X and V. Highest mean values showed by cluster IX for characters inflorescence length, inflorescence per plant, plant height, branches per plant, Seed volume weight, seed yield days to flowering and maturity. Cluster III showed highest mean value for characters branches per plant, inflorescence per plant, inflorescence length, inflorescence width and Seed volume weight.

The character days to maturity (28.97 %) showed maximum contribution towards the total divergence. It was followed by inflorescence width (20.00 %), no of branches per plant (14.94 %), days to 50 % flowering (14.48 %), seed volume weight/10 ml (7.13 %) and inflorescence length (5.98). Based on inter-cluster distance, intra-cluster distance and per se performance the genotypes viz., EC-896097, EC-896108, EC-896212, EC-896209 and IC-411824 can be used for future breeding programme.

**Keywords:** Quinoa, Divergence, Cluster,  $D^2$  and Monogenotypic.

### INTRODUCTION

Over past decades, agriculture has achieved monumental increase in food production but these have been paralleled by serious overuse of non-renewable inputs and natural resources, loss of biodiversity and changes in lifestyle. Today, out of more than 7000 species used for food only four crops viz., rice, maize, wheat and potato contribute over 60 per cent of calories obtained by human. This dramatic shrinkage of food basket brought a negative impact on nutrition security and dietary diversity, which caused the health-related problems like micronutrient deficiencies or "hidden hunger". Hence there is an urgent need to include a much wider range of crop species in current agriculture system and for this purpose "Neglected and Underutilized Crops" or "Orphan Crops" can be appropriate solution for above problems [1, 2].

Quinoa (*Chenopodium quinoa* Willd.) is an annual herbaceous species belonging to family *Amaranthaceae*, but formerly placed in *Chenopodiaceae* family, domesticated staple food in Andean South America. It is principally a grain crop harvested and consumed in a manner similar to that for cereal grain, although its leaves are also used as potherb. Quinoa was domesticated ancient Andean civilization in region surrounding the Bolivian and Peruvian altiplano. Nevertheless, cultivation of quinoa extends to south central zone of Chile in fragmented pattern.

Genetic diversity is one of the criteria for parent's selection in hybridization programme. Plant characteristics advantageous for the adaptation of quinoa to other growth regions of the world are available but are scattered throughout the existing germplasm. The availability of transgressive segregant in any breeding programme depends upon the diversity between the parents involved. Recent work indicated that the Mahalanobis generalized distance ( $D^2$  statistic) may be an efficient tool in the quantitative estimation of genetic diversity [3]. The divergence analysis has a definite role to play in an efficient choice of divergent parents for hybridization to exploit maximum heterosis or transgressive segregants for improving grain yield. Keeping all these aspects in view, the present study was done for genetic diversity for yield and yield contributing traits in thirty different genotypes of quinoa (*Chenopodium quinoa* Willd.).

## MATERIAL AND METHODS

The experimental material for the study consisted of 30 genotypes of Quinoa obtained from AICRN on Potential Crops, Mahatma Phule Krishi Vidyapeeth Rahuri- 413 722 Dist. Ahmednagar, Maharashtra (India). The experiment was conducted at Agricultural Botany Research Farm, Post Graduate Institute, MPKV, Rahuri-413 722 Dist. Ahmednagar, Maharashtra during *Rabi*, season, 2019. The experiment was conducted in a randomized block design (RBD) with three replications with spacing 30cm x 10cm. Each entry was represented by single row of 5.00-meter length. All the cultural practices such as fertilizer application, inter culturing, weeding etc., were followed to raise good crop. Observations were recorded on nine different quantitative characters *viz.*, days to 50 per cent flowering (no.), days to maturity (no.), plant height (cm), branches per plant (no.), inflorescence per plant (no.), inflorescence length (cm), inflorescence width (cm), seed volume weight (g/ 10 ml) and seed yield/ plant (g). Observations were recorded on five randomly selected plants, from each treatment in each replication and averages were worked out and used for statistical analysis. Genetic divergence was measured by the procedure [3]. The genotypes were grouped according to the method [4].

## RESULT AND DISCUSSION

### Genetic Divergence:

In the present investigation, D<sup>2</sup> values between all possible pairs of 30 genotypes ranged between 1.94 and 12.05. This high range for D<sup>2</sup> values indicates high amount of genetic diversity present in the genotypes. The lowest value was between the cluster V while, the highest was between cluster V and X.

The 30 genotypes were grouped into eleven clusters suggesting, the presence of substantial amount of genetic diversity in the material under investigation. The Cluster I with 11 genotypes followed by clusters II with 7 genotypes, cluster V, IX and XI with 2 genotypes each. While, remaining all other clusters *viz.*, III, IV, VI, VII, VIII and X were solitary (Table 1). Similar results were obtained in grain amaranth (*Amaranthus hypochondriacus* L.) [5] and in barn yarn millet [6].

### Intra and Inter-cluster Distance:

The averages inter and intra cluster 'D' values are presented in Table 2. The maximum intra cluster distance was registered between cluster

XI (2.70) followed by cluster II (2.56), I (2.29) and IX (2.11). The high intra cluster distance values revealed the presence of genetic diversity between genotypes which were grouped together in those clusters. The maximum inters cluster distance showed by cluster X and cluster V (12.05) followed by cluster IX and V (10.68) and cluster XI and V (10.31). Suggesting that genotypes present in these clusters might have different genetically architecture. However, lowest intra cluster distance was observed in cluster V indicating that genotypes present in these cluster might have genetically similarities with one another and appeared to have evolved from the common gene pool. Cluster III, IV, VI, VII, VIII and X showed no intra cluster distance due to its monogenotypic nature.

### Cluster Means for Different Characters:

The genotypes in cluster IX were early for days to 50 per cent flowering (43.50 days) followed by cluster X (43.67 days). Cluster X (100.67 days) matured earliest followed by cluster IX (101.00 days). Likewise, cluster IX (169.10 cm) and cluster IV (168.93 cm) cluster mean maximum for plant height, Cluster IX (42.95) and cluster III (40.47) was maximum for branches per plant.

Cluster mean for inflorescence per plant was maximum for cluster IX (37.83) followed by cluster III (35.78) Likewise, Cluster IV (30.90) and cluster VII (30.13). Cluster IX (26.17 cm) and cluster X (25.68 cm) for inflorescence length. Cluster X (21.10 cm) and cluster IX (20.90 cm) for inflorescence width cluster III (7.52 g) and cluster IX (7.42 g) for seed volume weight / 10 ml and Cluster IV (25.77 g) and cluster IX (25.48 g) exhibited highest seed yield per plant. Similar results were coincided by [7, 8].

### Per cent contribution of 9 characters for divergence:

Looking to the per cent contribution for total divergence, the character days to maturity (28.97%) showed maximum contribution towards the total divergence. It was followed by inflorescence width (20.00%), no of branches per plant (14.94%), days to 50 % flowering (14.48%), seed volume weight/10 ml (7.13%), inflorescence length (5.98), plant height (5.52%). Results were coinciding by [9]. While, the magnitude of contribution by inflorescence per plant and seed yield per plant was low.

Based on inter-cluster distance, intra-cluster distance and per se performance the genotypes *viz.*, EC-896097, EC-896108, EC-896212, EC-896209 and IC-411824 can be used for future breeding programme.

**Table 1:** Distribution of 30 genotypes of quinoa into eleven clusters

Clusters	No. of genotypes included	Genotypes
I	11	EC-896215, EC-896271, EC-896229, EC-896237, EC-896275, EC-896088, EC-896210, EC-896087, EC-896203, EC-896109, EC-896112.
II	7	EC-896059, EC-896083, EC-896206, EC-896086, EC-896105, EC-896115, EC-896098.
III	1	EC-507747
IV	1	EC-896097
V	2	EC-896108, EC-896212
VI	1	EC-896089
VII	1	EC-507139
VIII	1	EC-896207

IX	2	EC-896209, IC-411824
X	1	EC-896114
XI	2	EC-896116, EC-896202

**Table 2:** Average intra (bold) and inter cluster D values for eleven clusters in thirty quinoa genotypes

Cluster No	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	2.29	3.33	3.10	3.81	7.82	3.43	3.45	2.75	4.38	5.56	4.52
II		2.56	4.92	3.65	9.91	3.15	3.70	3.27	3.95	3.89	3.64
III			0.00	4.89	7.55	4.52	3.95	3.89	4.61	7.00	5.98
IV				0.00	9.97	2.53	3.47	2.58	4.22	6.06	4.84
V					1.94	10.19	9.71	8.88	10.68	12.05	10.31
VI						0.00	3.04	2.37	4.37	5.20	5.19
VII							0.00	3.19	5.17	6.11	5.26
VIII								0.00	4.39	5.85	5.13
IX									2.11	4.36	4.06
X										0.00	3.92
XI											2.70

**Table 3:** Mean values of the eleven clusters for nine characters in thirty Quinoa genotypes

Cluster No.	Days to 50 % flowering (No.)	Days to maturity (No.)	Plant height (cm)	Branches/ plant (No.)	Inflorescences/ plant (No.)	Inflorescence length (cm)	Inflorescence width (cm)	Seed volume weight (g/10ml)	Seed yield/ plant (g)
I	49.45	106.06	145.04	30.93	26.24	21.95	17.10	6.77	20.03
II	48.34	102.80	142.89	27.64	23.63	21.85	17.61	6.49	19.40
III	49.07	106.00	153.43	40.57	35.78	25.23	19.17	7.52	20.69
IV	50.00	102.00	168.93	37.42	30.90	23.40	17.40	7.30	25.77
V	55.17	122.33	145.47	30.40	25.85	20.92	17.43	6.59	21.05
VI	49.33	101.23	144.40	28.53	23.87	23.90	16.05	7.05	20.50
VII	52.00	101.33	148.33	35.63	30.13	22.40	17.53	6.74	20.47
VIII	49.33	103.67	153.13	31.90	26.30	22.11	15.33	6.58	19.13
IX	43.50	101.00	169.10	42.95	37.83	26.17	20.90	7.42	25.48
X	43.67	100.67	139.67	28.13	24.10	25.68	21.10	6.06	22.33
XI	45.33	102.50	150.87	31.72	25.87	17.40	17.38	6.58	24.36

**Table 4:** Per cent contribution of 9 characters for divergence

Sr. No.	Source	Times ranked first	Contribution (%)
1.	Days to 50 % flowering (no.)	63	14.48
2.	Days to maturity (no.)	126	28.97
3.	Plant height (cm)	24	5.52
4.	Branches per plant (no.)	65	14.94
5.	Inflorescence per plant (no.)	3	0.69
6.	Inflorescence length (cm)	26	5.98
7.	Inflorescence width (cm)	87	20.00
8.	Seed volume weight /10 ml (g)	31	7.13
9.	Seed yield per plant (g)	10	2.30
	<b>Total</b>		100

## CONCLUSION

All the thirty genotypes were grouped into eleven clusters. The maximum intra cluster distance was observed for cluster XI and inters cluster distance between cluster X and V. Out of 9 characters studied, the days to maturity showed maximum contribution towards divergence followed by inflorescence width, branches per plant, days to 50 % flowering, seed volume weight/10 ml, inflorescence length and plant height. Based on inter-cluster distance, intra-cluster distance and *per se* performance the genotypes viz., EC-896097, EC-896108, EC-896212, EC-896209 and IC-411824 can be used for future breeding programme.

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