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Agronomic and genetic performance of quinoa (*Chenopodium quinoa*) genotypes in rainfed conditions of Garhwal Hills of Uttarakhand

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Abstract

Nutritional value is enticing the cultivation of quinoa (*Chenopodium quinoa* Willd.) at the global level. One field experiment was planned for the assessment of different genotypes of quinoa under the rainfed hilly condition of Uttarakhand. The experiment was conducted with thirteen entries of *Chenopodium quinoa*, in silty clay loam under low input, rainfed organic conditions. The experiment was laid out in a Randomized Block Design along with 3 replications. Data on yield and other parameters were recorded using standard procedure. Significant variation was observed in the growth and yield parameters of *Chenopodium quinoa* genotypes. Thus based on the experiment, NIC022506 recorded significantly higher seed yield in the mid-hill rainfed conditions of Uttarakhand. The days to maturity have high heritability coupled with high genetic advance and days to 50% flowering and No. of leaves having high heritability along with moderate genetic advance can be used for selection in quinoa breeding programs.

Keywords: *Chenopodium quinoa*, Quinoa, genetic diversity, agronomic performance, heritability, food security

Introduction

At present, global climate change is readily affecting traditional agriculture. However, some non-traditional crops have a higher ability to withstand normal under abiotic stress. Quinoa, being one such crop, has the potential to yield abundant seed despite adverse climatic conditions such as frost, chilling, drought, freezing, salinity, and nutritional stress that has made it attractive for introduction in arid, semiarid, saline, and highland regions throughout the world (Choukr-Allah, 1996^[10]; Jacobsen, 2003^[16]; Schabes and Schabes, 2005^[22]; Erley *et al.*, 2005^[11]; Bonifacio, 2006^[5]). Quinoa is considered among the crops selected for future food security during the 21st century (FAO, 1998)^[12]. Quinoa (*Chenopodium quinoa* Willd.), considered a super food, is an ancient crop that has a vast genetic diversity resulting from its fragmented and localized production over the Andean region (Latijnhouwers *et al.*, 2003)^[18]. The family *Chenopodiaceae* comprises about 250 species (Giusti, 1970)^[14]. *Chenopodium quinoa* Willd. originated from Andean Plateau, around Lake Titicaca, 3800 m above sea level on the Peruvian-Bolivian border (Jacobsen, 2003)^[16]. It is being cultivated since 7000 years ago (Bazile, *et al.*, 2013)^[2]. It is grown in a wide range of environments in the South American region around the Andes latitudes and altitudes are 20^oN in Columbia to 40^oS in Chile, and from sea level to 3800 m (Risi and Galwey, 1989)^[21]. The grain belongs to the pseudo cereals and has high-protein content (14 to 20%) with an abundance of essential amino acids, and a wide range of vitamins and minerals (Repo-Carrasco *et al.*, 2003)^[20]. Further value composition of the nutritional seed of *Chenopodium* has high fats and antioxidants, which are at least fivefold greater than other cereals flours (Koziol, 1993^[17]; Jacobsen, *et al.*, 2003^[16]; Bhargava, *et al.*, 2006)^[4]. Also, quinoa products are categorized under gluten-free cereals that are beneficial for consumption by people suffering from celiac diseases as well as those who have an allergy to wheat consumption (Gambus, *et al.*, 2002^[13]; Chillo, *et al.*, 2009^[9]). Taking into consideration the nutritional benefit, and climate resilience of quinoa, the field experiment was planned for the assessment of different genotypes of quinoa under the rainfed hilly condition of Uttarakhand.

Materials and Methods

The *Chenopodium quinoa* genotypes were evaluated during *Kharif* 2018 in terraced fields at the Crop Improvement Block of College of Forestry, VCSG Uttarakhand University of

Horticulture and Forestry, Ranichauri, Uttarakhand, India. The experiment was conducted in silty clay loam under low input, rainfed organic conditions, situated between altitudes of about 1600 to 2200 m AMSL. The soil of the experimental block is largely acidic (pH 5.7) in nature, having available nitrogen 210 kg/ha, available phosphorus of 17 kg/ha, and available potassium of 390 kg/ha. The crop season experienced continuous high rainfall throughout the season, particularly during May (126.9 mm) but a short spell of the drought was experienced particularly during the end of the season Oct 2018 (9.4 mm in one day). Pre-monsoon showers in May were received resulting in timely sowing of experiments. The maximum and minimum temperature throughout the crop season was recorded as 16.6 to 25.5 °C and 5.1 to 16.2 °C respectively. The field was ploughed followed by harrowing and leveling. Thirteen entries of *Chenopodium quinoa* viz. EC507738, EC507739, EC507740, EC507741, EC507742, EC507743, EC507744, EC507746, EC507747, EC507748, EC507749, IC363733 and NIC022506 received from NBPGR, Shimla were used as treatments. The experiment was laid out in a Randomized Block Design along with 3 replications having 4 rows per treatment of 3 m row length. The row-to-plant spacing was 30 cm x 10 cm. The experiment was sown on 28, May 2018 and harvested as per the maturity of the treatments. Data on yield and other parameters were recorded using standard procedures including plant height, the number of branches per plant, days to 50% flowering, inflorescence length (cm), days to maturity, and seed volume weight (g/10 ml), and seed yield (q/ha). The data observed were analyzed by STPR-3 statistical software of the Department of Mathematics and Statistics, CBSH, GBPUA & T, Pantnagar. The analysis of the data was done by the STPR software developed by GBPUAT Pantnagar and the genetics components analysis was done on Microsoft excel manually using the different formulae taken from Bhagasara, *et al.*, (2017) [3].

Results and Discussion

Agronomic performance

Significant variation was observed in the plant height of *Chenopodium quinoa* genotypes (Table 1). IC363733 registered significantly higher plant height (148.80 cm) which was statistically at par with NIC022506, EC507749, and EC507746. It was might be due to the better nutrient utilization ability of the germplasm. Chen, *et al.* 2018 [8], also suggested that a better supply of nitrogen increases the plant height of the rice. A significantly lower plant height of quinoa was recorded in EC507740 (117.97 cm). The days taken to 50% flowering and maturity of quinoa genotypes were significantly influenced by each other. EC507739 was found to be significantly early in flowering (47.7 days) and maturity (84.7 days), while IC363733 takes maximum time to achieve 50% flowering (61 days) and maturity (110.7 days). Sajjad *et al.* 2014 [22] also reported the range of 50% flowering from 46.56 to 55.89 days. However, IC363733 registered a significantly higher inflorescence length (25.07 cm) which was statistically at par with EC507749, EC507746, EC507741, EC507742, EC507743 and EC507748 while EC507740 obtained the lowest inflorescence length (18.27 cm). The significant variation in the number of branches per plant of quinoa genotypes was registered to be significantly maximum in NIC022506 (5.07) and minimum in EC507746 (3.60). The seed volume weight was found significantly maximum in EC507749 (6.20 g/10 ml) which was statistically at par with all the genotype treatments except EC507739 and EC507740, which recorded the lowest seed volume weight.

The seed yield among different quinoa genotypes varies between 10.19 to 16.67 q/ha (Table 1). A significantly higher seed yield was recorded in NIC022506 (16.67 q/ha) followed by IC363733, EC507746, EC507744, and EC507747. Minimum seed yield (10.19 q/ha) was recorded in EC507738 and EC507740. Sajjad, *et al.* 2014 [22] also reported variability in the yield of quinoa genotypes when tested against two dates of sowing. NIC022506 registered a 63.6% higher seed yield in comparison to EC507738 and EC507740.

Table 1: Variation in agronomic performance of different *Chenopodium quinoa* genotypes

S. No	Genotypes	Plant height (cm)	Days to 50% flowering	Days to maturity	Inflorescence length (cm)	No. of fingers/plant	No. of branches/plant	No. of leaves/plant	10 ml seed weight (g)	Seed yield (q/ha)
1	EC507738	120.87	48.67	87.67	20.20	6.33	4.27	18.67	6.07	10.19
2	EC507739	121.50	47.67	84.67	19.13	7.30	4.20	19.10	3.17	12.04
3	EC507740	117.97	48.00	85.33	18.27	6.13	3.80	19.53	4.17	10.19
4	EC507741	132.10	49.67	91.33	22.87	8.53	3.73	15.27	5.00	12.04
5	EC507742	123.10	50.00	94.00	22.13	6.60	3.87	16.73	5.33	10.65
6	EC507743	132.07	49.67	92.00	22.23	5.47	3.67	15.00	5.27	12.04
7	EC507744	123.70	49.33	92.33	21.53	6.20	4.00	14.87	6.00	12.50
8	EC507746	135.73	48.00	92.00	23.27	7.07	3.60	13.33	6.07	12.96
9	EC507747	130.87	49.33	92.67	21.67	7.00	3.93	14.47	5.97	12.50
10	EC507748	126.73	49.00	88.00	22.13	7.13	4.07	13.73	6.00	11.58
11	EC507749	140.50	49.00	100.33	24.93	8.67	3.80	20.53	6.20	10.65
12	IC363733	148.80	61.00	110.67	25.07	8.87	4.40	23.53	5.40	13.43
13	NIC022506	141.27	59.33	106.67	21.47	9.00	5.07	21.33	6.00	16.67
	Mean	130.40	50.67	93.67	21.92	7.25	4.03	17.39	5.43	12.11
	CD (0.05)	16.54	1.85	2.57	3.35	0.98	0.60	2.34	0.87	2.31
	CV	7.53	2.17	1.63	9.06	8.03	8.85	7.98	9.50	11.30

Analysis of Variance

The results of the analysis of variance for Randomized Block Design for nine characters of the thirteen *Chenopodium quinoa* genotypes have been presented in Table 2. The mean sum of squares due to genotypes were showed a highly

significant difference for all the characters, it indicates that sufficient variability present among all the genotypes.

Genetic Component

Statistically, workout the computation of genotypic,

phenotypic and environmental variances, genotypic coefficient of variance (GCV), phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV) to understand the nature and extent of variability in different character's expression prevailed in population and that led to facilitating selection for various traits for identifying desired genotypes suitable for hills (Guleria *et al.*, 2019) [15]. The genetic variability in different field parameters is presented in Table 2.

Genetic components

There were statistically worked out to know the nature and extent of variability through computation of genotypic, phenotypic, and environmental variances, genotypic coefficient of variance (GCV), phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV) in the expression of various characters prevailed in population and that led to facilitating selection for various traits for identifying desired genotypes which are suitable in hills. The genetic variability in different field parameters is presented in Table 2. The estimates of phenotypic (PCV) and genotypic coefficient (GCV) of variation indicated that the values of PCV were higher than of GCV, but the difference was closer between these two estimates for most of the cases. This indicates that the greater role of genetic components and expression of characters under study was less influenced by the environmental factors. The perusal of the data revealed that higher PCV and GCV were recorded for 10 ml seed weight (g) followed by the number of leaves per plant, seed yield (q/ha), and the number of fingers per plant. Two characters can be included in the average PCV values such as inflorescence length (cm) and the number of branches per plant. This indicates that the selection with these characters may be a good approach for enhancing seed yield for these genotypes. Such kind of information was given by Guleria *et al.*, (2019) [14] in soybean.

Heritability and genetic advance

The genotypic coefficient of variation alone cannot determine the extent of variation which is heritable. The information about heritability helps to plant breeders in the prediction of

genetic advances for any quantitative characters and exercising selection procedure (Baraskar *et al.*, 2014) [1]. The best picture expected for selection than the heritability value alone can be obtained by the genotypic coefficient of variation together with the heritability estimate (Burton, 1952) [6].

The heritability estimates can be divided into three categories which are low heritability ($h^2 < 0.2$), medium heritability ($0.2 > h^2 < 0.5$), and high heritability ($h^2 > 0.5$) (MacWhirter, 1979) [19]. The estimates of heritability (Table 2) were observed to be high for all the characters except plant height (cm) and inflorescence length (cm) which showed average heritability. This indicated that selection based on phenotypic levels would be useful for the improvement of the traits.

According to Baraskar *et al.*, (2014) [1] genetic advance estimates can be divided into three classes, high (>20%), moderate (10-19%), and low (<10%). The magnitudes of genetic advance were observed to be high in days to maturity, moderate for plant height, days to 50% maturity and the number of leaves per plant whereas other characters showed low genetic advance. The magnitude of high genetic advance is useful in the identification and selection of appropriate characters.

The genetic architecture of the population can be measured by the idea of estimates of heritability and genetic advance (Baraskar *et al.*, 2014) [1]. High heritability along with high genetic advance was observed for days to maturity which indicates the presence of additive gene action for improvement of this trait by various selection methods. The moderate genetic advance accompanied by high heritability was observed for days to 50% flowering and number of leaves per plant which indicates the presence of both additive and non-additive gene action for these traits. High heritability coupled with low genetic advance found for other characters, indicates the presence of non-additive gene action, and selection is not rewarding for such traits. For such types of traits, recombination breeding and recurrent selection may be used for population improvement. Such kind of information was also reported by Chandrawat *et al.*, (2017) [7]; Guleria *et al.*, (2019) [15] on soybean.

Table 2: Analysis of variance and Genetic components for different parameters of *Chenopodium quinoa* genotypes

Source of Variation	DF	Plant height (cm)	Days to 50% flowering	Days to maturity	Inflorescence Length (cm)	No. of fingers/plant	No. of branches/plant	No. of leaves/plant	10 mL seed weight (g)	Seed yield (q/ha)
Replication	2	93.37	0.79	2.02	45.56	1.75	0.60	8.18	0.04	11.50
Treatment	12	257.30*	55.17**	183.72**	11.59*	4.06**	0.46*	31.93**	2.40**	9.02**
Error	24	96.31	1.21	2.33	3.95	0.34	0.13	1.93	0.27	1.93
CV		7.53	2.17	1.63	9.06	8.03	8.85	7.98	9.50	11.30
CD at 5%		16.54	1.85	2.57	3.35	0.98	0.60	2.34	0.87	2.31
Mean		130.40	50.67	93.67	21.92	7.25	4.03	17.39	5.43	12.11
Vg		160.99	53.96	181.39	7.64	3.72	0.33	30.00	2.13	7.09
Vp		353.61	56.38	186.05	15.54	4.40	0.59	33.86	2.67	10.95
Ve		96.31	1.21	2.33	3.95	0.34	0.13	1.93	0.27	1.93
GCV		12.30	14.66	14.47	15.51	27.72	16.87	32.49	28.55	24.77
PCV		14.42	14.82	14.56	17.97	28.97	19.11	33.47	30.02	27.33
ECV		7.52	2.17	1.63	9.08	8.00	8.93	7.99	9.58	11.48
h ²		45.53	95.71	97.50	49.16	84.55	55.93	88.60	79.78	64.75
GA		17.63	14.81	27.39	3.99	3.66	0.89	10.62	2.68	4.41
Genetic gain		13.52	29.22	29.25	18.20	50.45	22.01	61.08	49.33	36.46

CV = Coefficient of variation, CD = Critical difference, VG = environmental variance, GCV = Genotypic coefficient of variation, VP = phenotypic variance, VE = variation, PCV = phenotypic coefficient of variation, ECV =

environmental coefficient of variation, h^2 = heritability, GA = Genetic advance

Conclusion

Based on the experiment, NIC022506 recorded significantly higher seed yield in the mid-hill rainfed conditions of Uttarakhand. Based on the result, the characters having high heritability followed by high genetic advance can be used in the quinoa breeding programmer to obtain a high yield. The characters having high heritability alone can also be used in the breeding programmer for improving yield. Those genotypes have performed variability such kinds of genotypes can be included in the identification of good general combiner to produce good specific combining ability hybrids in quinoa breeding program.

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