DIRECT AND INDIRECT EFFECTS OF QUANTITATIVE CHARACTERS IN QUINOA (*Chenopodium quinoa* Willd.) GENOTYPES

Pawar S.V.[1], Shinde P.Y[2] Rajput H.J.[2] and Katore T.D.[2]

[1&2]Botany Division, College of Agriculture, Pune, Maharashtra, India, 411 005

---***---

Abstract - *The present study was conducted for association of characters and path analysis in thirty genotypes of Quinoa. Greater amount of variability was observed among the genotypes for all characters studied. The magnitude of genotypic coefficient of variation was lower than phenotypic coefficient of variation. The estimates of heritability (b.s.) ranged from 76.09 to 95.55 per cent. The highest heritability was observed for days to maturity (95.55 %) followed by inflorescence per plant (90.80 %), days to 50 % flowering (89.84 %), branches per plant (88.44 %), inflorescence length (87.06 %), inflorescence width (86.60 %), seed volume weight/ 10 ml (81.25 %), seed yield per plant (76.36 %) and plant height (76.09 %). High heritability coupled with high genetic advance as percent mean was observed for branches per plant, inflorescence per plant, inflorescence length, inflorescence width and seed yield per plant.*

The character seed yield per plant had highest significant positive correlation with plant height (0.785) followed by branches per plant (0.705), inflorescence per plant (0.682), seed volume weigh/10 ml (0.590), inflorescence width (0.520) and inflorescence length (0.235) respectively. Branches per plant, Inflorescence per plant, inflorescence length, inflorescence width, yield per plant, seed volume weight/10 ml showed highly positive association with each other.

The path analysis revealed the character inflorescence width (0.956) showed highest direct positive effect on seed yield per plant followed by plant height (0.836), seed volume weight/10 ml (0.431) and inflorescence per plant (0.400), indicating, true and perfect relationship between them. Hence, direct selection based on these characters would help in selecting the high yielding genotypes in quinoa.

Key Words: GCV, Correlation, path analysis, Quinoa and association,

1. INTRODUCTION

Quinoa (Chenopodium quinoa Wild.) is an annual herbaceous species belonging to family Amaranthaceae, but formerly placed in Chenopodiaceae family, and belongs to a complex of allotetraploid (2n = 4x = 36). It is domesticated staple food in Andean South America. It contain high amount of Ca, Fe, Cu, Zn and Mn. The oil content is 1.8 to 9.5 per cent and rich in essential fatty acids like linoleate and linolenate (55-65% of lipid fraction). In addition, quinoa seed is rich in folic acid (78.1 mg), vitamin C (16.4 mg), thiamine (0.4 mg), riboflavin (0.39 mg) and carotene (0.39 mg) in 100 g seeds, respectively. The calorific value is 350 cal per 100 g grains and is greater than that of other cereal and legume foods. Quinoa is qualified as a functional food (Filho et al., 2017; Abugoch, 2009) because its nutritional quality is superior to other grains like rice and wheat (Vilcacundo and Hernandez, 2017; Navruz- Varli and Sanlier, 2016).

In developing countries of Africa and Asia quinoa may be a crop able to provide highly nutritious crop under dry conditions. Population demands an increase in food production along with sustainable agriculture. There is need for cultivation of crops that require minimum input, but can counter the nutritional deficiency prevalent in general population of this region in developing countries. Very little research work has been done on the adoptability and standardization of package of practices of quinoa in India.

The success of breeding programme means development superior varieties/ hybrids depend on the magnitude of genetic variability and heritability present in the source material. The extent of variability is measured by GCV and PCV which provides information about relative amount of variation in different characters. Since the estimates of variability alone will not be much use for selection based on phenotypic basis, genetic gain should also be considered. So keeping all these aspects, the present investigation was carried out to study the *association of yield and yield contributing characters in thirty genotypes of Quinoa.*

2. MATERIAL AND METHODS

The experiment was conducted on 30 genotypes of Quinoa at Agricultural Botany Research Farm, Post Graduate Institute, MPKV, Rahuri-413 722 Dist. Ahmednagar, Maharashatra during Rabi, season, 2019. The Material was obtained from AICRN on Potential Crops, Mahatma Phule Krishi Vidyapeeth Rahuri- 413 722. The experiment was laid in a randomized block design (RBD) with three replications and spaced at 30cm x 10cm. Each entry was

represented by single row of 5.00 meter length. All the inter-culturing operations 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. The genotypic and phenotypic correlation coefficients were worked out by the method suggested by Singh and Chaudhary (1977) and path analysis by Dewey and Lu (1959).

3.   RESULT AND DISCUSSION

Wide range of variation was observed for all characters under study. Analysis of variances exhibited significant treatment mean square for all the characters studied. It revealed the presence of considerable amount of variability evaluated.

The parameters of genetic variability for 30 genotypes in quinoa are presented in Table 1. The magnitude of genotypic coefficient of variation was lower than phenotypic coefficient of variation. The GCV and PCV both were observed high for inflorescence per plant. Thus, this character provide good source of variation and hence inflorescence per plant useful in crop improvement programme in quinoa. However, moderate amount of GCV and PCV observed for branches per plant, inflorescence length, inflorescence width and seed yield per plant. The estimates of heritability (b.s.) ranged from 76.09 to 95.55 per cent. The highest heritability was observed for days to maturity (95.55 %) followed by inflorescence per plant (90.80 %), days to 50 % flowering (89.84 %), branches per plant (88.44 %), inflorescence length (87.06 %), inflorescence width (86.60 %), seed volume weight/ 10 ml (81.25 %), seed yield per plant (76.36 %) and plant height (76.09 %). Therefore, it can be concluded that environmental effects are least on the characters studied. High heritability coupled with high genetic advance as percent mean was observed for branches per plant, inflorescence per plant, inflorescence length, inflorescence width and seed yield per plant. Similar results were observed by Sravanthi et al. (2012) and Venkatesh et al. (2014) for heritability (high) with genetic advance as per cent mean (high) in amaranths for majority of characters.

In correlation study, (Table 2) seed yield per plant had positive and significant correlation with plant height (0.785) followed by branches per plant (0.705), inflorescence per plant (0.682), seed volume weigh/10 ml (0.590), inflorescence width (0.520) and inflorescence length (0.235). It had negative and highly significant

correlation with days to maturity (-0.226) and days to 50 per cent flowering (-0.493). This indicates the dependency of these characters on each other. Days to 50 % flowering showed positive and significant correlation with days to maturity. Plant height showed positively significant correlation with branches per plant, inflorescence per plant, inflorescence length, inflorescence width, seed volume weight/10 ml both at phenotypic and genotypic level. The association between seed yield and its component traits in this study are accordance with the findings of Bhargava et al. (2007) and Mhada et al. (2014). Jacobsen et al. (1996) reported that the grain yield had a positive association with plant height, length and diameter of inflorescence in quinoa.

Branches per plant, Inflorescence per plant, inflorescence length, inflorescence width, yield per plant, seed volume weight/10 ml showed highly positive association with each other. Spehar and Santos (2005) reported that inflorescence length and diameter were positively associated with grain yield. Szilagyi and Jornsgard (2014) also reported that the seed yield had significant and positive association with plant height, biological yield and harvest index in quinoa.

The path analysis (Table 3) revealed the character inflorescence width (0.956) showed highest direct positive effect on seed yield per plant followed by plant height (0.836), seed volume weight/10 ml (0.431) and inflorescence per plant (0.400). Exhibited high direct effects in the desirable direction and also confirmed their strong association with seed yield per plant indicating, the true and perfect relationship between them and it suggested that, direct selection based on these characters would help in selecting the high yielding genotypes in quinoa. The characters branches per plant (-0.842), inflorescence length (-0.704) and days to maturity (-0.050), showed significant negative direct effect on seed yield per plant. Khurana et al. (2013) reported that the number of leaves per plant had highest positive direct effect (0.493) on total green yield followed by leaf area index (0.427), leaf length (0.099), plant height (0.092) and leaf width (0.049) in amaranth. Venkatesh et al. (2014) also reported positive direct effect of seed weight, panicle length and plant height on grain yield in grain amaranth.

Looking to the indirect contributors, the plant height showed significant indirect positive association via inflorescence /plant (0.325) followed by seed volume weight/10 ml (0.318) and inflorescence width (0.182).

Likewise, branches per plant showed maximum indirect significant positive effect via plant height (0.702) followed by inflorescence width (0.456), seed volume weight /10 ml, inflorescence/plant (0.400) and days to maturity (0.354). The inflorescence per plant showed indirect positive effect

was observed via plant height (0.679) followed by inflorescence width (0.518) and seeds volume weight/10 ml (0.347). Seed volume weight/10 ml showed indirect positive effect was observed via plant height (0.616) followed by inflorescence per plant (0.322) and inflorescence width (0.257). The inflorescence width showed indirect positive effect was observed via inflorescence per plant (0.217) followed by plant height (0.159) and seed volume weight/10 ml (0.116). The inflorescence length via inflorescence width (0.713) followed by inflorescence per plant (0.214) and seed volume weight/10 ml (0.207). So, it could be concluded that the traits seed volume weight/10 ml, inflorescence width, inflorescence /plant, plant height, inflorescence

width, and days to maturity were major yield contributing traits and that traits will help in improving seed yield. So, emphasis should be given on selecting these characters in breeding programme to develop desirable varieties.

In present study residual effect at genotypic level was 0.276, which suggested that there might be few more component traits responsible to influence the green fodder yield/plant than those studied.

Table 1. Parameters of genetic variability in 30 genotypes in Quinoa

Sr. No.	Character	Mean	Range	GCV (%)	PCV (%)	ECV(%)	h² % (B.S)	Genetic Advance	Gen. Adv. as % of Mean
1.	Days to 50 % flowering (No.)	48.79	43.33-55.33	6.76	7.13	2.27	89.84	6.44	13.20
2.	Days to maturity (No.)	105.09	101.33- 122.33	5.80	5.93	1.25	95.55	12.27	11.68
3.	Plant height (cm)	147.81	131.33- 174.20	5.52	6.33	3.10	76.09	14.67	9.92
4.	Branches per plant (No.)	31.53	20.66-43.03	19.77	21.03	7.15	88.44	12.08	38.31
5.	Inflorescence per plant (No.)	26.80	17.13-38.29	23.50	24.66	7.48	90.80	12.37	46.13
6.	Inflorescence length (cm)	22.20	17.14-27.60	16.19	17.35	6.24	87.06	6.91	31.12
7.	Inflorescence width (cm)	17.64	14.30-21.73	17.88	19.21	7.03	86.60	6.05	34.27
8.	Seed volume weight/10 ml (g)	6.74	5.98-7.52	8.74	9.69	4.20	81.25	1.09	16.22
9.	Seed yield per plant (g)	20.89	15.66- 25.76	16.28	18.63	9.06	76.36	6.12	29.31

Table 2   Estimates of genotypic (above diagonal) and phenotype correlation coefficients (below diagonal) among seedyield and yield contributing characters in thirty quinoa genotypes

Sr. No.	Character	Days to 50 % flowering	Days to maturity	Plant height (cm)	Branches /plant (No.)	Inflorescences/ plant (No.)	Inflorescence length(cm)	Inflorescencewidth (cm)	Seed volume weight (g/10 ml)	Seed yield/ plant (g)
1.	Days to 50 % flowering (No.)	**1.000**	0.729**	-0.329**	-0.232*	-0.240*	-0.265*	-0.499**	-0.019	-0.493**
2.	Days to maturity (No.)	0.682**	**1.000**	-0.244*	-0.119	-0.115	-0.214*	-0.158	-0.091	-0.226*

3.	Plant height (cm)	-0.236*	-0.167	**1.000**	0.841**	0.813**	0.248*	0.190	0.738**	0.785**
4.	Branches/plant (No.)	-0.182	-0.094	0.087	**1.000**	0.991**	0.523**	0.477**	0.821**	0.705*
5.	Inflorescences / plant (No.)	-0.189	-0.086	0.830**	0.975**	**1.000**	0.599**	0.542**	0.806**	0.682**
6.	Inflorescence length (cm)	-0.084	-0.086	0.373**	0.534**	0.564**	**1.000**	0.745**	0.496**	0.235**
7.	Inflorescence width (cm)	-0.216*	-0.042	0.369**	0.544**	0.571**	0.837**	**1.000**	0.268**	0.520*
8.	Seed volume weight (g/10 ml)	-0.001	-0.085	0.442**	0.487**	0.462**	0.298**	0.188	**1.000**	0.590**
9.	Seed yield/plant (g)	-0.291*	-0.106	0.760**	0.708**	0.681**	0.365**	0.500**	0.247*	**1.000**

*and ** significant at P= 5 and P = 1 level of significance, respectively

Table 3.   Estimates of   genotypic direct (diagonal) and indirect effects (above and below diagonal) of componentcharacters on seed yield in thirty quinoa genotypes. Residual effect (R) = 0.276

Sr. No.	Character	Days to 50 % flowering	Days to maturity	Plant height (cm)	Branches /plant (No.)	Inflorescences/ plant (No.)	Inflorescence length (cm)	Inflorescence width (cm)	Seed volume weight (g/10 ml)	Genotypic correlation with Seed yield/ plant (g)
1.	Days to 50 % flowering (No.)	**0.018**	-0.037	-0.275	0.195	-0.096	0.186	-0.477	-0.008	-0.493**
2.	Days to maturity (No.)	0.013	**-0.050**	-0.204	0.100	-0.046	0.151	-0.151	-0.039	-0.226*
3.	Plant height (cm)	-0.006	0.012	**0.836**	-0.707	0.325	-0.175	0.182	0.318	0.785**
4.	Branches/plant (No.)	-0.004	0.006	0.702	**-0.842**	0.400	-0.368	0.456	0.354	0.705**
5.	Inflorescences /pl ant (No.)	-0.004	0.006	0.679	-0.842	**0.400**	-0.422	0.518	0.347	0.682**
6.	Inflorescence length (cm)	-0.005	0.011	0.207	-0.440	0.239	**-0.704**	0.713	0.214	0.235*
7.	Inflorescence width (cm)	-0.009	0.008	0.159	-0.402	0.217	-0.525	**0.956**	0.116	0.520**

| 8. | Seed volume weight (g/10ml) | 0.000 | 0.005 | 0.616 | -0.691 | 0.322 | -0.349 | 0.257 | **0.431** | 0.590** |

3. CONCLUSIONS

- High heritability (b.s.) with high genetic advance as present mean was recorded for inflorescence per plant, branches per plant, inflorescence width, inflorescence length, seed yield per plant indicate that these traits were predominantly governed by additive gene action and selection of these traits would be more effective for desired genetic improvement.

- Seed yield per plant exhibited positive correlation with plant height, branches per plant, inflorescence per plant, Inflorescence length, inflorescence width, seed volume weight per 10 ml.

- Path analysis showed direct selection based on character inflorescence width, plant height, seed volume weight /10ml, inflorescence per plant and days to 50 per cent flowering can help in the improvement of seed yield in quinoa.

ACKNOWLEDGEMENT

REFERENCES

[1] Abugoch James, L.E. 2009. Quinoa (Chenopodium quinoa Willd.) composition, chemistry, nutritional, and functional properties. Adv. Food Nutr. Res. 58 :1-31.https://doi.org/10.1016/S1043-4526(09)58001-1

[2] Bhargava, A., Shukla, S. and Ohri, D. 2007. Genetic variability and interrelationship among various morphological and quality traits in quinoa (Chenopodium quinoa Willd.). Field Crops Res., 10:104-116.

[3] Dewey, D.R. and Lu, H.K. 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. Agron, J., 51(6):515-518.

[4] Filho, A.M.M., Pirozi, M.R., Borges, J.T.D.S., Pinheiro Sant'ana, H.M., Chaves, J.B.P. and Coimbra, J.S.D.R. 2017. Quinoa: Nutritional, functional and antinutritional aspects. Critical Reviews in Food Science and Nutrition.57(8):1618-1630.https://doi.org/10.1080/ 10408398.2014. 100181.

[5] Jacobsen S.E., Hill, J. and Stolen, O. 1996. Stability of quantitative traits in quinoa (Chenopodium quinoa). Theor. Appl. Genet., 93:110–116.

[6] Khurana, D.S., Singh, J. and Kaur, B. 2013. Genetic variability, correlation and path coefficient analysis in Amaranthus. Veg. Sci., 40(2): 238-240.

[7] Mhada, M., Jellen, E.N., Jacobsen, S.E. and Benlhabib, O. 2014. Diversity Analysis of a Quinoa (Chenopodium quinoa Willd.) Germplasm during Two Seasons. Int. J. Agric. and Biosystems Engi., 8 : 108-112.

[8] Navruz-Varli, S. and Sanlier, N. 2016. Nutritional and health benefits of quinoa (Chenopodium quinoa Willd.). J. Cereal. Sci. 69: 371-376. https://doi.org/10.1016/j.jcs.2016.05.004.

[9] Singh, R.K. and Chaudhary, B.D. 1977. Variance and covariance analysis in Biometrical methods in quantitative genetic analysis . Kalyan Publ., New Delhi. pp. 39-68.

[10] Spehar, de Barros and Santos, R.L. 2005. Agronomic performance of quinoa selected in the Brazilian Savannah. Pesq. Agropec, Bras., Brasilia, 40(6): 609-612.

[11] Sravanthi, V., Begum, H., Sunil, N. and Reddy, M.T. 2012. Variance component analysisfor grain yield and agro economic traits in grain amaranths (Amaranrhus spp.). Advances fn. Boric. Sct. and Res., 2(7) : 233-244.

[12] Szilagyi, L. and Jornsgard, B. 2014. Preliminary agronomic evaluation of (Chenopodium quinoa Willd). Under climatic conditions of Romania. Scientic Papers. Series A. Agronomy, Vol. VII.

[13] Venkatesh, L., Murthy, N., Nehru, S.D. and Manjappa, N. 2014. Genetic variability, heritability and genetic advance in grain amaranth (Amararnthus spp.) Asian. Bio. Sci. 9(1): 67-70.

[14] Vilcacundo, R. and Hernandez, B. 2017. Nutritional and biological value of quinoa (Chenopodium quinoa Willd.). Current Opinion in Food Science. 14 : 1-6.