Original Research Article

Genetic parameters in germplasm lines for yield and its contributing traits in grain amaranth (*Amaranthus hypochondriacus* L.)

ABSTRACT:

The present investigation was conducted to estimate the genetic variability, heritability and genetic advance of genotypes of grain amaranth during *kharif*, 2022 at Agricultural Research Station, Tornala. Fifty nine genotypes of grain amaranth along with 4 checks (Suvarna, BGA-2, GA-5 and RMA 7) were evaluated in an augmented block design for access their performances. High phenotypic and genotypic coefficient of variation were observed for grain yield/plant (82.73/82.70), no. of spikelets/plant (62.41/62.36), inflorescence length (49.72/49.66), plant height (41.54/41.47) and days to 50 % flowering (21.78/21.66) indicating the presence of high variability in germplasm for selection. The characters *viz.*, days to 50 % flowering, plant height, inflorescence length, no. of spikelets/plant and yield/plant expressed high heritability coupled with high genetic advance as percent of mean, which indicates preponderance of additive gene action in controlling the traits. . Hence, the characters having high GCA & PCA can be relied upon and simple selection can be practiced for further improvement. Based on the performance, genotypes SKGPA183,EC322998, IC 551493, IC 551496 and IC 551499 have been found superior among the genotypes which can be used in breeding programmes for crop improvement.

Key words: Grain amaranth, genetic variability, heritability and genetic advance

Introduction

“Amaranth is non-grass and is called pseudo-cereal because of their similarities to cereals in flavour and cooking. The genus amaranthus has about 60 species worldwide which is characterized by a high degree of diversity and wide spectrum of adaptability to different agro-ecological conditions” (Showemimo*et al*., 2021; Anita et al. 2022). “Grain Amaranth is an important and largely used by hilly people. Its high productive genotype can be introduced in breeding programs of amaranth to enhance the productivity. It is a short duration herb grown in almost all agro-climatic zones, mostly in temperate and tropical regions.

Amaranthus species have distinct centres of domestication and origin. These are extensively distributed in North America, Central America, and South America, where the greatest genetic diversity is found" (Xu and Sun, 2001). "It is one of those rare plants whose leaves are eaten as a vegetable while the seeds are used as cereals. Besides, it is also used as fodder, ornamental, organic red dye and for industrial purposes" (Malaghan et al., 2018). "The grains are unique and nutritionally rich. The proteins are significantly richer in essential dietary amino acids, particularly lysine, which is often limited in other cereal grains" (Oduwaye et al., 2016).

"The genetic parameters like co-efficient of variation, heritability and genetic advance as per cent of mean provide a clear insight into the extent of variability and a relative measure of the efficiency of selection of genotypes based on phenotype in a highly variable population" (Sheela et al., 2018).

"Genetic variability studies provide basic information regarding the genetic properties of the population based on which breeding methods are formulated for further improvement of the crop" (Yadav et al., 2014). "Genetic advance can be used to predict the efficiency of selection" (Showemimo et al., 2021).The objective of this study was to determine variability, heritability and genetic advance for yield and its component traits in grain amaranth.

Materials and methods

The field experiment was conducted at Agricultural Research Station, Tornala during *kharif*, 2022. The experimental material used in the present study comprised of 59 genotypes of grain amaranth including four checks*viz.*Suvarna, BGA-2, GA-5 and RMA 7. The genotypes SKGPA 180, SKGPA 181, SKGPA 182 and SKGPA 183 and check GA-5obtained from Sardarkrushinagar Agricultural University, Sardarkrushinagar, Gujarat. The checks Suvarna was obtained from GKVK, Bengaluru, RMA 7 from ARS, Mandor, Rajasthan and BGA- 2 from Odisha University of Agriculture and Technology, Bhubaneswar and remaining genotypes were obtained from National Bureau of Plant Genetic Resources, Phagli, Shimla. The experiment was conducted in an augmented block design with five compact blocks. All checks were repeated in every block while the genotypes were unreplicated. There were three rows of each germplasm in blocks with spacing 45×15 cm. Five plants were randomly selected and observations were recorded in respect to various parameters in each genotypes. The average values of observations taken from five plants were used as treatment mean in all statistical analysis. The observation included days to 50 per cent flowering, days to maturity, plant height (cm), inflorescence length (cm), number of spikelet per plant, volume weight (g/10 ml) and seed yield per plant (gm). Phenotypic and genotypic coefficient of variation was calculated as suggested by Falconer (1981). Heritability (broad sense) (Johnson et al., 1955), genetic advance (Burton, 1952) and genetic advance as percent of mean (Johnson et al., 1955) were also estimated.

Results and Discussion

The statistical analysis showed highly significant differences among the genotypes for all the characters studied, indicating considerable amount of genetic variation in genotypes. The mean, range, variance, co-efficient of variation, heritability and genetic advance for 10 traits including grain yield has been presented in the Table 1.

Table 1. Adjusted mean for different field parameters of grain amaranth

Entry	**DFF**	**Days to 80% maturity**	**Plant Height (cm)**	**Inflorescence length (cm)**	**No. of Spikelets/plant**	**Seed volume weight (g/10ml)**	**Yield/plant (g)**
GA-5	65	106	122	30	36.6	7.5	6.47
BGA-2	56	90	133	38.6	42.6	7.5	7.3
SUVARNA	55	88	114.6	32.4	34.4	7	5.1
RMA7	58	89	122	30	44.2	7	6.8
SKGPA 180	52	87	88	34.6	43.2	7	3.75
SKGPA 181	53	86	91.4	34	28	7	6.25
SKGPA 182	54	88	75	50.2	31.6	6	7.6
SKGPA 183	30	71	124	44.4	56.2	6	12.3
EC 146511	30	70	101	32.2	23.4	5.5	3.5
EC 146513	32	67	58.6	31.4	11.4	6	0.71
EC 146514	31	65	32.6	12.4	10.8	7	11.9
EC 146515	35	69	96.4	35.6	31	6.5	0.87
EC 146516	31	64	37.4	17.2	13.6	6.5	2.03
EC 146517	64	90	71	29.8	32	6	6.4
EC 146518	35	75	39	12.8	14.4	6	1.74
EC 146519	32	74	36	12.6	10.6	6	0.73
EC 146523	31	72	37.2	16.2	12.2	6.5	1.3
EC 146528	31	72	30.4	23.4	12	7	3.5
EC 146530	31	73	27	12.2	11	5	1.42
EC 146541	30	71	35.8	26.2	9.8	6.5	2.5
EC 146543	31	72	43.6	16	10.8	7	2.9
EC 322998	31	75	47.4	36	34.8	7	10.2
EC 322999	31	73	31.2	17.8	10	7	1.97
EC 323000	32	74	30.2	21.6	8	7	1.45
EC 323001	32	73	28.6	13.6	10.6	7.5	4.03
EC 323004	43	82	47	29.6	26.8	6.5	3.2
EC 328873	31	75	33	17.6	12.8	7	2.3
EC 328874	31	74	23.8	15.2	10.2	6.5	1.3

EC 328876	32	73	36.2	20.6	9.6	6.5	1.9
EC 328878	35	72	27.4	18	11.6	7	2.4
EC 328879	44	82	63.4	29.8	25.2	7.5	1.1
EC 328880	31	73	30	17.6	12.8	5.5	0.3
EC 328883	32	75	35.2	18.2	12.2	7	1.5
IC 35385	30	62	32	16.5	11.2	6	1.8
IC 547381	32	74	27	18.6	8.8	6.5	1.1
IC 547382	36	73	26.4	13.6	11.8	6.5	0.8
IC 547387	32	72	23	7.2	6.8	6	0.3
IC 547389	35	72	25.4	17.6	8.2	7	0.21
IC 547391	35	71	24.2	14.2	11	6.5	0.85
IC 547395	32	73	23	11	7.4	7	0.6
IC 547397	35	72	39.8	12.8	20	7	6.02
IC 547499	32	71	35.8	10.6	10.8	7	1.47
IC 547500	33	74	50	13.8	12.2	8	1.58
IC 547503	32	73	47.6	11.6	11.4	6.5	1.47
IC 547506	34	72	43.8	10.4	10.2	7	1.74
IC 547507	35	72	42.6	13.8	12.2	6.5	4.3
IC 547508	35	71	36.6	14.4	7.6	7.5	1.8
IC 551479	36	82	65	37.8	37.6	6.5	4.2
IC 551480	49	84	50.2	37.6	23.2	6.5	4.3
IC 551487	38	81	49	32	26	6.5	6.9
IC 551488	65	88	57	34.4	30.4	6	5.7
IC 551489	44	80	50	37.6	20.8	6	7.5
IC 551490	39	81	58	45.6	25.4	6	5.75
IC 551493	47	85	62	43.6	35.8	6	11
IC 551496	36	80	56	41.4	40.4	6.5	8
IC 551497	36	78	46.8	15	13.4	6	7.8
IC 551499	41	85	60	49.4	37.4	6.5	11.8
IC 551500	36	78	72	57	66	6	5.3
IC 551502	49	85	59	31	39.4	7	4.72

Mean	38.26	76.80	52.76	25.05	21.20	6.59	3.96
Std.Error	1.29	1.06	3.72	1.60	1.80	0.08	0.42
Std.Deviation	9.91	8.15	28.56	12.27	13.79	0.58	3.26

Phenotypic and genotypic coefficient of variation

The phenotypic coefficient of variances (PCV) were greater than their gene corresponding genotypic coefficient of variance (GCV) in respect to all quantitative traits indicating that apparent variance is not only due to genotypes but also due to influence of environment, but the difference between them is narrow indicating that the characters were less influenced by the environment. Therefore response to direct selection may be effective in improving these traits.

The characters studied in the present investigation exhibited low (less than 10%), moderate (10-20%) and high (more than 20%) phenotypic and genotypic coefficients of variation and represented in graphical form in Fig. 1.

High phenotypic and genotypic coefficient of variation were observed for grain yield/plant (82.73/82.70), no. of spikelets/plant (62.41/62.36), inflorescence length (49.72/49.66), plant height (41.54/41.47) and days to 50 % flowering (21.78/21.66) indicating the presence of high variability in germplasm for selection. Hence, these characters can be relied upon and simple selection can be practiced for further improvement. Genetic variability is the basis for any heritable improvement in the crop plants. The magnitude of PCV was high as compared to the GCV for all the characters studied, indicating the important role of environmental variation in expression of different traits in grain amaranth. The results of present investigation were within agreement to the findings of Trivedi*et al.*, (2022) for seed yield/plant, no. of spikelets/plant, Kumar *et al.,* (2021) for plant height, days to 50 % flowering and Sheela *et al.*, (2018) for inflorescence length in grain amaranth.

The estimates of phenotypic and genotypic phenotypic and genotypic coefficient of variation were low for seed volume weight (8.54/8.53) and days to 80 % maturity (8.30/8.13). Similar results were reported by Sheela *et al.,* (2018) for days to 80 % maturity.

Heritability

All the characters under investigation expressed high estimates of heritability in broad sense ranging from days to 80 % maturity (96.06 %) to yield/plant (99.94 %). High heritability for different traits indicated that large proportion of phenotypic variance was attributed to genotypic variance and therefore, reliable selection could be made for these traits on the basis of phenotypic expression. Similar results have also been reported by Sharma *et al*. (2024).

Genetic advance

Further, the heritability estimate itself may not be solely and useful index of genetic potentiality of a character. Thus, high heritability estimates coupled with high genetic advance indicate that traits are governed mainly due to additive genetic effects therefore selection may be effective for these traits.

Genetic advance as percent of mean is classified as low (less than 10%), moderate (10-20%) and high (more than 20 %). Among the traits under study, days to 50 % flowering (44.44%), plant height (85.41%), inflorescence length (102.34%), no.ofspikelets/plant (128.56%) and yield/plant (170.57%) expressed high genetic advance as percent of mean, which showed the presence of the additive gene action. Similar results were reported by Oduwaye*et al.*, (2016). Remaining two traits, days to 50 % maturity (16.44%) and seed volume weight (17.56%) recorded moderate estimates of genetic advance as percent of mean, which showed non-additive gene action.

The characters *viz.*, days to 50 % flowering, plant height, inflorescence length, no. of spikelets/plant and yield/plant expressed high heritability coupled with high genetic advance as percent of mean, which indicates preponderance of additive gene action in controlling the traits. Hence direct selection of such characters would be effective in improving the yield. The remaining two characters days to 80% maturity and seed volume weight recorded for high heritability coupled with moderate genetic advance as percent of mean, which suggested that the expression of this trait was mostly influenced by additive gene of action. Hence, response to selection is would be effective in improving the seed yield.

Table 2. Estimation of genetic parameters for yield and its contributing characters of grain amaranth

S. No.	**Traits**	**Mean**	**PCV (%)**	**GCV (%)**	**Heritability in broad sense (h^2) (%)**	**GA (5%)**	**GA as percent of mean (5%)**
1	Days to 50 % flowering	38.26	21.78	21.66	98.88	17.00	44.44
2	Days to 80% maturity	76.80	8.30	8.13	96.06	12.62	16.44
3	Plant height (cm)	52.76	41.54	41.47	99.67	45.06	85.41
4	Inflorescence length (cm)	25.05	49.72	49.66	99.79	25.64	102.34
5	No. of spikelets/plant	21.20	62.41	62.36	99.85	27.25	128.56
6	Seed volume weight (g/10 ml)	6.59	8.54	8.53	99.61	1.16	17.56
7	Yield/plant (g)	3.96	82.73	82.70	99.94	6.76	170.57

PCV- Phenotypic Coefficient of Variation; GCV - Genotypic Coefficient of Variation; GA- Genetic Advance

Average performance of genotypes

The high magnitude of genotypic and phenotypic coefficient of variation were recorded for seed yield per plant, days to 50 % flowering, plant height, inflorescence length and no. of spikelets/plant. The genotypes SKGPA 183, EC 322998, IC 551493, IC 551496 and IC 551499 showed superiority over other genotypes for these quantitative characters.

Conclusion

On the basis of experimental finding it can be concluded that the inherent variability among the amaranths accessions is useful for selection and improvement purposes. The genotypic and phenotypic coefficient of variation components are indicators of variability among the test accessions for all the traits in this study. Selection of such characters which showed high genetic advance coupled with high heritability creates scope for improvement in terms of yield. Thus, based on these traits, some of the promising genotypes in the genetic stock studied are SKGPA 183, EC 322998, IC 551493, IC 551496 and IC 551499which can be used in further breeding program for improvement of amaranth crop.

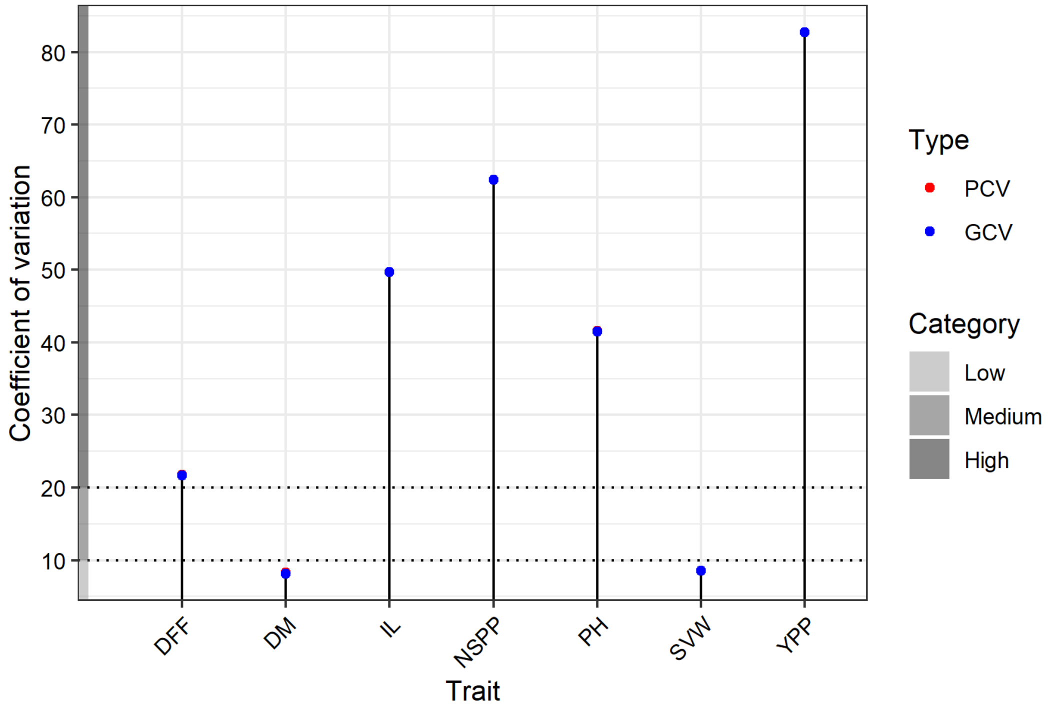

Fig. 1. Graphical representation of phenotypic and genotypic coefficients of variation for various characters in grain amaranth genotypes

DFF- Days to 50% flowering; DM - Days to maturity; IL - Inflorescence length; NSPP - No. of spikelets/plant; PH -Plant Height; SVW - Seed volume weight ; YPP - Yield per plant

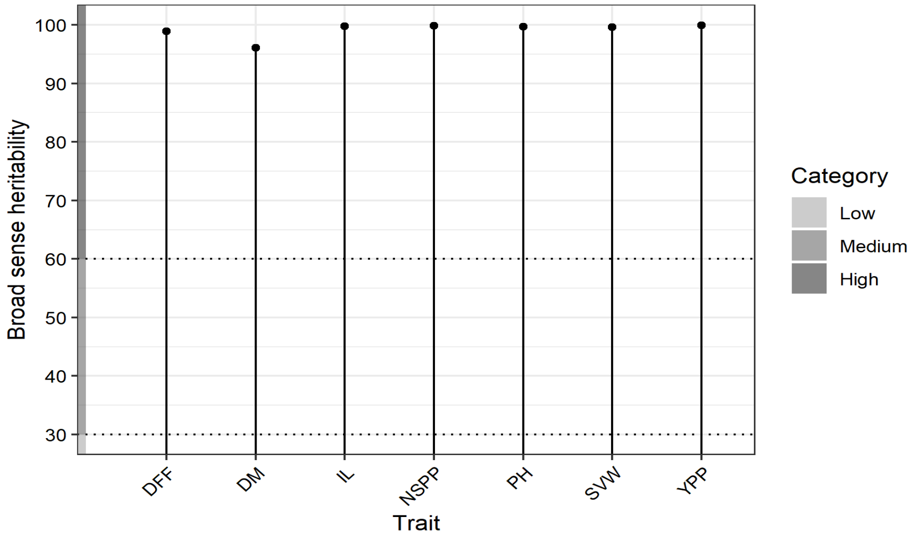

Figure 2. Graphical representation of heritability in broad sense for various characters in in grain amaranth genotypes

DFF- Days to 50% flowering; DM - Days to maturity; IL - Inflorescence length; NSPP - No. of spikelets/plant; PH -Plant Height; SVW - Seed volume weight ; YPP - Yield per plant

Disclaimer (Artificial intelligence)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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