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Prediction of adaptability and yield stability of elite grain amaranth genotypes under different population densities (*Amaranthus hypochondriacus* L.)

S. Ramesh Kumar[1]* and G. Mohamed Yassin[2]

[1]Department of Horticulture, Vanavarayar Institute of Agriculture, Manakkadavu, Pollachi-642103, TNAU, Tamil Nadu, India.
[2]Department of Horticulture, Pandit Jawaharlal Nehru College of Agriculture and Research Institute, TNAU, Karaikal-609603, Puduchery, India.

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The study was conducted to assess the yield stability across the plant densities. Amaranth genotypes were evaluated for yield characters under very high (D_1), high (D_2), normal (D_3) and low (D_4) plant density levels to determine stability parameters. The study was conducted at Karaikal, Puduchery, India during November, 2007 to February, 2008. The results revealed that genotype Annapurna was stable for grain yield in all plant density levels. Genotypes BGA 2, GA 2 and IC 415290 were stable for total carbohydrates and protein content, and could be utilized for improvement of these traits in breeding programs. Genotype GA 2 was stable for weight of the inflorescence in all plant density levels. Similarly, SKNA 601 was stable for leaf area at 50% flowering in all plant density levels. Among the characters studied, length of the rachis per inflorescence, total carbohydrates and protein content were found to be relatively stable in all plant density levels. Therefore, the above said traits are important, while exercising selection for different density levels.

Key words: *Amaranthus hypochondriacus*, grain yield, stability parameters, selection.

INTRODUCTION

Amaranthus hypochondriacus L. is cultivated as a monocrop in different spacings. The performance of genotypes varies widely over densities due to the genetics of varieties. It is necessary to identify stable genotypes. Information on genotypes and density will allow for a better measure of evaluating varietal stability. Grain amaranth production has declined mainly due to a lack of producer awareness of its nutritive value, non-availability of suitable high yielding varieties and lack of improved production techniques. Varietal improvement is needed to increase yield potential of this crop. Adoption of scientific cultivation practices including proper plant densities and other inputs are essential in maximizing grain yield (Henderson et al., 1993). Exploitation of heterosis and success in obtaining desirable segregants through breeding depends to a greater extent on the degree of genetic divergence between the parents. Genotypes should be stable for seed yield and other contributing characters under different plant densities. Realization of normal yields in grain amaranth depends on

*Corresponding author. E-mail: rameshamar06@gmail.com or ramesh_amar06@yahoo.co.in.

Table 1. Genotypes source and availability, National Bureau of Plant Genetic Resources.

Genotype	Source	Status
RMA 3	Rajasthan	Released variety
BGA 2	NBPGR	Released variety
E C 519554	NBPGR	Breeding line
SKNA 21	Gujarat	Released variety
Annapurna	New Delhi	Released variety
SKNA 601	Gujarat	Released variety
GA 2	Gujarat	Released variety
RMA 4	Rajasthan	Released variety
I C 415290	NBPGR	Breeding line
PRA 2004 - 2	NBPGR	Breeding line

Table 2. Plant densities.

	Density			
Character	**D_1 (very high)**	**D_2 (high)**	**D_3 (normal)**	**D_4 (low)**
Spacing	30 × 20 cm	30 × 30 cm	45 × 20 cm	45 × 30 cm
Plant population/m^2	50	33	30	22
Plant population·ha^{-1}	500,000	333,000	330,000	2,22,222

and optimum population density. Grain amaranth genotypes capable of stable yield under different population densities are lacking. Thus, it becomes imperative for a breeder to evaluate and select generally adapted and stable grain amaranth genotypes that can produce normal yields under different population densities. Studies on the influence of different population densities over the stability parameters would help the breeder to formulate appropriate selection strategies.

MATERIALS AND METHODS

Grain amaranth genotypes were obtained from the germplasm collection of National Bureau of Plant Genetic Resources (NBPGR) maintained at the University of Agricultural Sciences, Bangalore and Forestry College and Research Institute, Mettupalayam, India (Table 1). Plants were grown from November, 2007 to February, 2008 in a randomized complete block design with three replications. The soil was a well drained sandy loam with pH > 6. The soil was prepared and cultivated three times to obtain a loose, friable, soil. Farm yard manure (cow manure) was applied along with urea, diammonium phosphate (DAP) and muriate of potash as per Tamil Nadu Agricultural University crop production guide (2005). Irrigation was applied at a 7-day interval during the growing season. The insecticides chloriphyriphos or dimethoate were applied at 1.5 ml·L^{-1}. Genotypes were grown in beds of 2 × 1.5 m. Seeds were sown in a single line in the middle of the bed. Plants were thinned 15 days after sowing to maintain very high (30 × 20 cm), high (30 × 30 cm), normal (45 × 20 cm) and low (45 × 30 cm) densities (Table 2). Observations were recorded from five randomly selected plants of each genotype in each replication and population density for plant height, leaf area at 50% flowering, weight of the inflorescence, number of rachis per inflorescence, rachis length per inflorescence, number of secondary branches per inflorescence, grain yield per plant, grain yield per plot, and total grain carbohydrate and protein contents. For quality traits, composite samples drawn from five random plants per genotype grown under different population densities were used for analysis.

Stability analysis

The method of Eberhart and Russell (1966) was followed to estimate the parameters of stability: mean (x), regression coefficient (b) and mean square deviation (S^2d) for each genotype. In addition, the density index (I_j) and phenotypic index (Pi) were also estimated from mean data averaged over replications in the densities.

RESULTS AND DISCUSSION

A stable genotype is one that has low genotype (G) × environment (E) interaction for agronomically important characters. Assessment of the G × E interaction is necessary to identify phenotypically stable genotypes. Regression analysis of G × E interaction is used to characterize genotypic responses to densities (Sharma et al., 1998). Eberhart and Russell (1966) extended this approach and included deviation from the regression coefficient as an additional parameter, an approach widely used by breeders to detect high yielding stable genotypes.

Density indices (Table 3) computed for characters indicated that the normal density favored expression of all characters in the desirable direction except days to 50% flowering and total carbohydrates. The protein content was

Table 3. Values of environmental indices for different traits.

	Density[a]			
Character	**Very high**	**High**	**Normal**	**Low**
Plant height	4.64	-4.06	4.35	-4.95
Leaf area at 50% flowering	-10.69	-1.67	27.92	-15.57
Fresh weight of the inflorescence	-3.66	2.55	4.77	-3.82
Number of rachis per inflorescence	-1.80	0.31	2.28	-0.78
Length of the rachis per inflorescence	-2.15	-0.85	1.93	1.10
Number of secondary branches per inflorescence	-0.28	-0.24	0.47	0.07
Grain yield per plant	0.21	0.90	2.04	0.87
Grain yield per plot	-8.16	107.90	48.68	-148
Total carbohydrate content	0.39	0.34	-0.23	-0.50
Protein content	-0.06	0.02	0.04	0.01

[a]See Table 2 for description.

Table 4. Analysis of variance for stability for different characters.

Source	df	Mean square									
		Plant height	Leaf area at 50% flowering	Fresh weight of the inflorescence	Number of rachis per inflorescence	Length of the rachis per inflorescence	No. of secondary branches per inflorescence	Grain yield per plant	Grain yield per plot	Protein content	Total carbohydrate content
Genotype (G)	9	633.77**	1089419.28**	3091.02**	192.90**	208.40**	11.55**	148.58**	112285.54**	11.34**	236.99**
D + G × D	30	111.64**	5061.27**	395.23**	40.11**	13.50**	0.46**	6.56**	17296.53**	0.02	0.50
Density (D) (linear)	1	814.85**	11388.21**	400.10**	91.57**	102.88**	3.59**	53.53**	360577.96**	0.05	5.73
G × D (linear)	9	107.36**	2782.23**	54.44**	36.58**	17.95**	0.63**	23.08**	8447.46**	0.02	0.72
Pooled deviation (non linear)	20	78.41**	5770.47**	548.34**	39.12**	7.02**	0.23**	5.78**	4114.53**	0.02	0.14
Pooled error	80	36.94	2408.96	106.77	14.23	3.41	0.08	1.56	2219.52	0.11	0.85

** Significant at 1% level.

favorable at all plant densities except the very high density level. The length of the primary inflorescence, weight of the inflorescence, number of rachis per inflorescence, grain yield per plant, grain yield per plot and protein content were favorable under normal and high plant densities. Sharma et al. (2001) observed significant differences for densities as well as for G × E interaction for yield and its component traits in grain amaranth. In the present investigation, pooled analysis of variance (Tables 4 and 5) indicated that plant density and the G × E interaction were significant for the characters studied; plant height, leaf area at 50% flowering, weight of the inflorescence, number of rachis per inflorescence, rachis length per inflorescence, grain yield per plant, and grain yield per plot. The G × E interaction effect was further partitioned into linear (predictable) and nonlinear (unpredictable) components through analysis of variance for stability. The E + (G × E) interaction was significant

Table 5. Pooled analysis of variance over four plant density levels for different characters.

Source	df	Mean squares									
		Plant height (cm)	Leaf areaat 50% flowering	Fresh weight of the inflorescence	Number of rachis per inflorescence	Length of the rachis per inflorescence	Number of secondary branches per inflorescence	Grain yield per plant	Grain yield per plot	Protein content	Total carbohydrate
Genotype (G)	9	633.77**	108949.28**	3091.02**	192.90**	208.40**	11.55**	1337.29**	112285.54**	11.34**	236.99**
Density (D)	3	271.62**	3797.74**	133.42**	30.51**	34.29**	1.19	53.53**	120192.35**	0.02	1.91
G × D	27	93.87**	5201.668**	424.32**	41.18**	11.19**	0.38	143.46**	5863.66**	0.02	0.34
Error (Pooled)	80	34.94	2408.96	106.77	14.23	3.41	8.71	1.56	2219.52	0.11	0.85

**Significant at 1% level.

for all characters, except total carbohydrates and protein content.

Differential effects of density on genotypes were significant for all characters, except plant height, leaf area at 50% flowering, weight of the inflorescence, number of rachis per inflorescence, rachis length per inflorescence, grain yield per plant, and grain yield per plot, as indicated by density (linear) mean squares. The linear component of G × E interaction was significant for plant height, leaf area at 50% flowering, weight of the inflorescence, number of secondary branches per inflorescence, number of rachis per inflorescence, length of the rachis per inflorescence, grain yield per plant and grain yield per plot, indicating predictions about performance of most genotypes appeared feasible for these characters. The significant mean squares due to pooled deviation- observed for plant height, leaf area at 50% flowering, weight of the inflorescence, number of rachis per inflorescence, rachis length per inflorescence, grain yield per plant, and grain yield per plot indicated that genotypes differed with respect to their stability, representing the unpredictable component of G × E interaction.

Eberhart and Russell (1966) used the stability parameters (i) genotypic mean (g_i), expressed as phenotypic index (Pi), (ii) regression value (b) (predictable linear response) and deviation from linearity (S^2d) (unpredictable non-linear response) for identifying genotypes for all the plant densities. According to this model, an ideal stable genotype is one which conforms to the following stability parameters: (i) phenotypic index is more than zero, represented by a high genotypic mean (Pi > 0 that is, $g_i > x$), (ii) regression coefficient is equal to unity (b = 1) and (iii) deviation from regression is equal to zero ($S^2d = 0$). Such a genotype would be suitable for general adaptation over all densities (Tables 6 to 9).

Using this criterion, a score chart was prepared for all genotypes for all characters. The scores: ‘m’ for significantly higher (desirable) mean, that is, Pi is more than zero; ‘r’ for ‘b’ value not significantly deviating from unity (that is, b = 1) and‘d’ for S^2d value not significantly deviating from zero, that is, $S^2d = 0$, were used. A combined score chart was computed for all genotypes for all characters (Table 10). The combined score chart indicated that 'Annapurna' and 'GA 2' were stable genotypes. The only other genotype which was acceptable for the three parameters for grain yield per plot was 'SKNA 601'. 'Annapurna' was also identified as the best genotype for plant densities based on its mean performance. Responses of ‘Annapurna’ to density are well known (Sharma et al., 1998, 2001) and are used to compare the fitness of other genotypes.

Genotype GA 2 was not stable for grain yield even though it had stable performance on weight of the inflorescence and number of rachis per inflorescence. It was also unstable across plant densities. Length of rachis per inflorescence was stable in seven genotypes (RMA 3, Annapurna, SKNA 601, GA 2, RMA 4, I C 415290, PRA 2004 - 2). Total carbohydrates (BGA 2, E C 519554, GA 2, I C 415290) and protein content (BGA 2, Annapurna, GA 2, I C 415290) had a stable performance in the four genotypes shown. Grain yield per plant and per plot yield were stable in one (Annapurna) and two genotypes (Annapurna and SKNA 601), respectively.

Genotype “Annapurna” was stable for grain yield per plot, grain yield per plant, plant height, length of the rachis per inflorescence and protein content. No other genotype was stable for grain yield per plot except 'SKNA 601'. For total carbohydrates and protein content, genotypes BGA 2, GA 2 and IC 415290 could be exploited based on their stability.

Stable performance occurred in genotypes: RMA 3, Annapurna, SKNA 601, GA 2, RMA 4, IC 415290 and PRA 2004-2, for length of the rachis per inflorescence. This trait was an important yield

Table 6. Estimates of stability parameters for plant height, leaf area at 50% flowering and number of rachis per inflorescence.

Genotype	Plant height			Leaf area at 50% flowering			Number of rachis per inflorescence		
	Mean (*Pi*)[a]	*b*	$\overline{S^2d}$	Mean (P_i)	*b*	$\overline{S^2d}$	Mean (*Pi*)	*b*	$\overline{S^2d}$
RMA 3	85.90 (8.97)**	1.56	48.04	1034.84 (-249.730)	1.60	-369.67	36.11 (15.07)	2.69	6.77
BGA 2	74.49 (-2.44)	1.35	-12.94	826.35 (-458.220)	1.00	-1159.88	45.49 (-5.69)	0.36	-2.79
E C 519554	96.21 (19.28)**	-0.69	142.87**	2246.07 (961.50)**	-2.24	26399.18**	54.65 (3.47)**	-1.81	20.23
SKNA 21	84.54 (7.61)**	3.57	187.31**	1397.42 (112.55)**	2.90*	-1510.55	52.91 (1.73)**	0.64	82.57**
Annapurna	89.78 (12.85)**	1.48	37.60	908.11 (-376.46)	0.88	-1307.66	51.16 (-0.02)	-0.16	24.15
SKNA 601	80.76 (3.83)**	0.22	118.95**	958.70 (-325.870)	-0.10	-2402.12	60.5 1(9.33)**	5.22	41.03
GA 2	69.84 (-7.09)	0.92	-24.70	1915.58 (631.01)**	2.86**	-1390.07	59.20 (8.02)**	1.98	13.52
RMA 4	69.01 (-7.92)	0.88	-32.27	893.91 (390.66)	1.00	-1131.55	50.34 (-0.84)	-0.15	10.78
I C 415290	58.08 (-18.95)	0.03	16.94	1800.51 (515.940)**	2.20	-17522.74**	52.64 (1.46)	-0.58	67.64**
PRA 2004-2	60.72 (-16.21)	0.65	33.27	864.179 (-420.40)	-0.12	-1035.32	48.82 (-2.36)**	1.78	46.69**
Grand mean	76.93	-	-	1284.57	-	-	51.18	-	-

** Mean significantly above the grand mean in desirable direction at 1% level; [a]Values in parenthesis indicate phenotypic index (*Pi*).

Table 7. Estimates of stability parameters for length of the rachis per inflorescence, number of secondary branches per inflorescence and fresh weight of the inflorescence.

Genotype	Length of the rachis per inflorescence			Number of secondary branches per inflorescence			Fresh weight of the inflorescence		
	Mean (P_i)[a]	*b*	$\overline{S^2d}$	Mean (*Pi*)	*b*	$\overline{S^2d}$	Mean (P_i)	*b*	$\overline{S^2d}$
RMA 3	47.51 (3.28)**	1.48	3.31	4.82 (-0.16)	1.17	-0.03	81.09 (-12.67)	0.22	-68.54
BGA 2	45.37 (1.14)**	2.58	14.29**	4.64 (-0.34)	-0.45	0.69**	82.04 (-11.72)	2.19	1401.24**
E C 519554	34.97 (-9.26)	0.85	12.97**	6.03 (1.05)**	3.26*	-0.07	135.37 (41.61)**	-0.76*	487.95**
SKNA 21	36.30 (-7.93)**	3.24*	0.70	3.86 (-1.12)	1.23	-0.01	106.45 (12.69)**	2.19	1002.84**
Annapurna	51.07 (6.77)**	2.17	5.45	9.42 (4.44)	2.77*	0.04	141.06 (47.30)**	2.20*	1049.81**
SKNA 601	51.96 (7.73)**	0.51	-3.08	3.93 (-0.05)	0.82	0.01	81.38 (-120.38)	2.31	345.65**
GA 2	51.95 (7.72)**	-0.13	-1.24	4.48 (-0.5)	-1.28	0.24	99.86 (6.10)**	1.07	-49.74
RMA 4	32.45 (-11.78)**	0.68	-2.46	3.62 (-0.36)	0.51	-0.55**	73.06 (-20.17)	0.78	-8.11
I C 415290	45.98 (1.75)**	-0.30	0.65	4.74 (-0.22)	0.98	0.39	65.21 (-28.77)	-0.10	-74.01
PRA 2004-2	44.79 (0.56)**	-0.07	5.55	4.29 (-0.69)	0.95	0.25	60.50 (-33.26)	-0.11	328.63**
Grand mean	44.23	-	-	4.98	-	-		-	-

*, ** Mean significantly above the grand mean in desirable direction at 5 and 1% levels. [a]Values in parenthesis indicate phenotypic index (*Pi*).

Table 8. Estimates of stability parameters for Grain yield per plant, total carbohydrate content and fresh weight of the protein content.

Genotype	Grain yield per plant			Total carbohydrate content			Protein content		
	Mean (P_i)	*b*	$\overline{S^2d}$	Mean (*Pi*)	*b*	$\overline{S^2d}$	Mean (P_i)	*b*	$\overline{S^2d}$
RMA 3	11.29 (2.83) [a]	0.01	1.11	31.44 (-3.58)	1.64	-0.63	12.36 (-0.05)	1.31	-0.11
BGA 2	8.95 (-5.17)	0.33	4.80**	37.94 (2.92)**	-0.98	-0.84	15.43 (3.02)**	-3.22	-0.03
E C 519554	23.52 (9.40)**	1.08	7.04**	46.28 (11.26)**	0.19	-0.82	11.27 (-1.14)	1.56	-0.07
SKNA 21	12.40 (-1.72)	1.24	-0.08	27.05 (-7.970	0.92	-0.80	10.56 (-1.85)	3.83	-0.15
Annapurna	23.94 (9.82)**	1.26	-1.30	26.83 (-8.19)	0.42	-0.72	14.51(2.10) **	0.28	-0.06
SKNA 601	19.17 (5.05)**	0.85	18.98*	38.03 (3.01)**	1.31*	-0.84	11.51(-0.90)	3.02	-0.09
GA 2	17.34 (3.22)**	1.46	5.37**	46.93 (11.91)**	0.93	-0.82	12.49 (0.08)**	2.04	-0.04
RMA 4	13.54 (-0.580	2.09	6.48**	38.67 (3.65)**	0.54	-0.60	11.68 (-0.73)	0.04	-0.08
I C 415290	8.16 (-5.96)	-0.21	-0.90	26.48 (-8.54)	3.27*	-0.13	13.87 1.46)**	1.23	-0.02
PRA 2004-2	7.61 (6.51)	1.86	0.76	30.09 (-4.93)	1.73	-0.64	10.46 (-1.95)	-0.10	-0.05
Grand mean	14.12	-	-	34.97	-	-	12.41	-	-

, * Mean significantly above the grand mean in desirable direction at 5 and 1% levels; [a]Values in parenthesis indicate phenotypic index (*Pi*).

Table 9. Estimates of stability parameters for grain yield per plot.

Genotype	Grain yield per plot		
	Mean (P_i)[a]	*b*	$\overline{S^2d}$
RMA 3	277.36 9 (-94.84)	0.85	-1639.64
BGA 2	216.17 (-156.03)	0.52	1336.42
E C 519554	608.22 (236.02)**	1.80	7356.89**
SKNA 21	314.48 (-57.72)	0.69	-1068.21
Annapurna	626.85 (254.65)**	1.70	-1757.52
SKNA 601	516.82 (144.62)**	1.14	14742.24**
GA 2	444.61 (72.41)**	1.34	-1010.53
RMA 4	337.89 (-34.31)	0.86	3991.50
I C 415290	219.20 (-15.30)	0.70	-1709.28
PRA 2004-2	160.83 (-211.37)	0.37	-1291.76
Grand mean	372.24	-	-

** Mean significantly above the grand mean in the desirable direction at 1%; [a]Values in parentheses indicate the phenotypic index (*Pi*).

Table 10. Score chart for stability parameters of ten genotypes for thirteen characters.

Genotype	PH[a]	LAF	FWI	NR	LR	NSB	GYP	GYPP	TCC	PC	Combined score for m, r, d
RMA 3	r, d	r, d	r, d	r, d	m, r, d	r, d	r, d	r, d	r, d	r, d	1
BGA 2	r, d	r, d	r	r, d	m, r	r	r	r, d	m, r, d	m, r, d	2
E C 519554	m, r	m, r	m	m, r, d	r	m, d	m, r	m, r	m, r, d	r, d	2
SKNA 21	r	m, r, d	m, r	m, r	m, d	r, d	r, d	r, d	r, d	r, d	1
Annapurna	m, r, d	r, d	m	r, d	m, r, d	d	m, r, d	m,r,d,	r, d	m, r, d	5
SKNA 601	m, r	r, d	r	m, r, d	m, r, d	r, d	m, r	m, r,d	m, d	r, d	3
GA 2	r, d	d	m, r, d	m, r, d	m, r, d	r, d	m, r	m, r	m, r, d	m, r, d	5
RMA 4	r, d	m, r	r, d	r, d	m, r, d	r	r	r , d	m, r, d	r, d	2
I C 415290	r, d	R	r, d	r	m, r, d	r, d	r, d	r, d	m, d	m, r, d	2
PRA 2004-2	r, d	r, d	r	r	m, r, d	r, d	r, d	r, d	r, d	r, d	1
Combined score for m,r,d	1	1	1	3	7	-	1	2	4	4	7,4,4

'm' = High (desirable) mean; r = 'b' around unity; d = S^2d around zero; (not significant 'b' value); (not significant S^2d value). [a] PH = plant height; DFF = days to 50% flowering; LAF = Leaf area at 50% flowering; LI = Length of the primary inflorescence; DI = Diameter of the inflorescence; FWI = Fresh weight of the inflorescence; NR = Number of rachis per inflorescence; LR = Length of the rachis per inflorescence; NSB = Number of secondary branches per inflorescence; GYP = Grain yield per plant; GYPP = Grain yield per plot; TCC = Total carbohydrates content; PC; Protein content.

contributing character at all plant densities except very high density. These genotypes may be used to obtain stable yields. The genotype SKNA 21 was stable for leaf area at 50% flowering which again may be used for improvement of yield.

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