



Intra-and Inter-specific Genetic Diversity in Grain Amaranth (*Amaranthus hypochondriacus* L.)

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Extent and magnitude of genetic divergence for seven characters among thirty-three genotypes of grain amaranth (*Amaranthus hypochondriacus* L.) were determined for the purpose of identifying more diverse parents, which are expected to create maximum variability. The highest genetic contribution towards diversity was made by number of branches (21.9697). Contribution of canonical roots in per cent in first four vectors was 46.611, 24.320, 12.077, 6.771 and total 89.779, respectively. Based on genetic divergence D^2 statistics, genotypes were grouped into 16 clusters in which cluster I (BGA 9, BGA 20, BGA 14 and BGA 11) and cluster XI (RMA 42, RMA 43, BGA 4 and SKNA 809) contained maximum number of four genotypes, Cluster II, III, IV, V, VIII, IX, XIII, XIV and XVI (2 in each case), 3 genotypes in cluster VII (RMA 45, BGA 21 and IC 35482) and Cluster VI (SKNA 403), X (Suvarna), XII (SKNA 401) and XV (GA 2) have one genotypes. The clustering pattern revealed that there was no relationship between genetic divergence and eco-geographical region. Intra cluster values ranged from 0.00 to 23.196 and cluster XIII was the most diverse group. The inter cluster values ranged from 20.3 to 26809. Maximum divergence was noticed between clusters III (AmbikaGA12-1 and KBJ3) and XII (SKNA401) (26809) followed by clusters X (Suvarna) and XVI (AmbikaGA12-2 and BGA 2) (20017) and clusters III (AmbikaGA12-1 and KBJ3) and X (Suvarna) (15031). The diverse clusters derived could be used in hybridization programmes to generate wide range of transgressive segregants to develop high yielding grain amaranth varieties.

Key words: *Amaranthus hypochondriacus*, D^2 statistics, Genetic diversity, Canonical roots.

Grain amaranth (*Amaranthus hypochondriacus* L.) of the genus *Amaranthus* is the most important subsidiary food crop of the people inhabiting the tropical and subtropical highlands of the Central and South America (Sauer, 1967). The genus contains more than 60 species of which *Amaranthus hypochondriacus* and its hybrids are widely cultivated as ornamental, pseudo-cereal and fodder crops in many tropical and warm-temperate regions of the world. In India the species is extensively cultivated as subsidiary food crop from Kashmir to Arunachal Pradesh (Sauer, 1950, 1967). It is closely linked with the life and culture of rural people as the seeds are used in various forms of preparations. Amaranth grain has unusually high quality protein, rich in lysine and sulphur-containing amino acids and thus confirms, its high potential for use in both human and animal nutrition. It also shows high promise for supplementing nutritive food and amelioration of protein deficiency in the vegetarian diet (Dowton, 1973; Senft, 1980; Vietmeyer, 1980; Bressani *et. al.* 1987a; Bressani *et. al.* 1987b; Dodok *et.al.* 1997 and Andrasofszky *et. al.* 1998). A range of plant breeding methods can be used for the improvement of this classical selfed and outcrossed crop (Jain *et. al.* 1986); (Walton 1968; Kulokow and Jain 1987). Considering the amaranth as a highly

variable crop, the choice of parents for breeding programmes is very important (Cruz and Carneiro, 2003). There are many methods like Mahalanobis D^2 statistics described by Rao (1952) to represent variation. Although D^2 statistics is a quantitative measure of genetic divergence, the clustering pattern of the genotypes is arbitrary (Singh and Gupta, 1979). In the present investigation, therefore, the genotypes were subjected to D^2 analysis to find out the nature and extent of genetic diversity present in 33 genotypes of grain amaranth for genetic improvement through hybridization.

Materials and Methods

The present investigations were undertaken during 2012-13 with 33 genotypes of *A. hypochondriacus* (Table 3). The genotypes were raised in Completely Randomised Block Design with three replications in the experimental field of Birsa Agricultural University, Ranchi, Jharkhand (India). Spacing between rows was 45 cm and plant-to-plant distance was 15 cm. Ten plants of each genotype in each replication were selected randomly for recording observations on seven characters *i.e.* plant height (cm), number of branches/plant, inflorescence length (cm), days to 50% flowering, days to maturity, 10ml volume weight (g) and grain yield (kg/ha). Genetic divergence between genotypes was worked out using Mahalanobis (1936) D^2

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statistics and the clustering of genotypes was done following Tocher's method as described by Rao (1952).

Results and Discussion

Analysis of variance showed significant differences among the genotypes for all the seven

Table 1. Contribution of different characters in grain amaranth

Characters	Ranked first	% Contribution
Seed yield kg/ha	58	10.9848
Days to maturity	65	12.3106
Days to 50% flowering	90	17.0455
Plant height (cm)	67	12.6894
Number of branches	116	21.9697
Inflorescence length (cm)	83	15.7197
10ml vol. weight (g)	49	9.2803
TOTAL	528	100.0000

characters indicating the existence of genetic variability. The simultaneous test of significance based on Wilk's criteria for the pooled effect of all

Table 2. Canonical vectors for different characters in grain amaranth

Characters	1 Vector	2 Vector	3 Vector	4 Vector	5 Vector	6 Vector	7 Vector
Seed yield kg/ha	0.1905	0.5226	0.7594	0.1215	-0.2694	-0.0493	0.1544
Days to maturity	0.2525	0.1367	0.1658	0.0502	0.8390	-0.3307	-0.2732
Days to 50% flowering	0.3205	0.2100	-0.1519	0.3245	0.2084	0.8252	0.0110
Plant height (cm)	0.4216	0.3783	-0.5456	0.1716	-0.1145	-0.4050	0.4187
Number of branches	0.5291	0.0993	-0.0793	-0.6814	-0.2239	0.0854	-0.4265
Inflorescence length (cm)	0.4129	-0.5599	0.2517	-0.2179	0.1559	0.0656	0.6138
10ml vol. weight (g)	0.4111	-0.4445	0.0736	0.5798	-0.3040	-0.1780	-0.4093

(0.5798) in 7th vector. Seed yield had the highest positive values for third vector 0.7594 followed by vector 2, 3, 7 and 4, and negative for vectors 5 and 6. Days to maturity had highest positive value in 5th vector (0.8390) followed by 1st vector (0.2525), 3rd vector (0.1658), 2nd vector (0.1367) and 4th vector (0.0502) and negative for 6 and 7 vectors. The mean value of the first four vectors for different genotypes are presented in Table 3, which showed that the genotypes having the highest positive values were BGA 11 (216.5438) in 1st vector, RGA 6 (9.0606) in 2nd vector and (84.1629) in 3rd vector and BGA 2 (60.5666) in 4th vector. Contribution of canonical roots in per cent in the first four vectors was 46.611, 24.32, 12.077, 6.771 and the total 89.779, respectively. Similar results were reported by Mahto (1994) in soybean for 100 seed weight, number of branches and seed yield. Cluster I (BGA 9, BGA 20, BGA 14 and BGA 11) and cluster XI (RMA 42, RMA 43, BGA 4 and SKNA 809) contained maximum number of genotypes (4), Cluster II, III, IV, V, VIII, IX, XIII, XIV and XVI (2 in each case) and in cluster VII (RMA45, BGA 21 and IC35482) 3 genotypes. Cluster VI (SKNA 403), X (Suvarna), XII (SKNA 401) and XV (GA 2) had one genotype each (Table 4). The clustering pattern revealed that there was no relationship between genetic divergence and eco-geographical region. Intra-cluster values ranged from 0.00 to 23.194 and

the characters also showed highly significant differences among the genotypes ($V_{stata}=1847.44$ at df 224). The distribution pattern of the 33 genotypes revealed that there were 16 clusters and the distribution of genotypes in different eco-geographical regions was apparently random. This grouping reflects the wide genetic divergence among the genotypes. The genetic contribution towards diversity was made by number of branches (21.9697), days to 50% flowering (17.0455), inflorescence length (15.7197), plant height (12.6894), days to maturity (12.3106), seed yield kg/ha (10.9848) and 10 ml volume weight (9.2803) Table 1.

Canonical vectors for different characters (Table 2) showed the highest positive values for seed yield (0.7594) in 3rd vector, days to maturity (0.8390) in 5th vector, days to 50% flowering (0.8252) in 6th vector, plant height (0.4216) in 1st vector, number of branches (0.5291) in 1st vector, inflorescence length (0.6138) in 7th vector and 10ml volume weight

cluster XIII is the most diverse group. The inter-cluster values ranged from 20.3 to 26809. Maximum divergence was noticed between clusters III (AmbikaGA12-1 and KBJ3) and XII (SKNA401) (26809) followed by clusters X (Suvarna) and XVI (AmbikaGA12-2 and BGA 2) (20017) and clusters III (AmbikaGA12-1 and KBJ3) and X (Suvarna) (15031). Highly divergent genotypes would produce a broad spectrum of variable attributes enabling further selection and improvement. Inter-cluster distance between the cluster IV and XV was the lowest (20.3) indicating that the genotypes are closely related. Intra-cluster distance ranged from 0.00 to 23.194 and it was the highest for cluster XIII (23.194), while the clusters VI, X, XII and XV were found to be the lowest (0.00) (Table 5).

The mean values for seed yield varied from 426.5 (Cluster IX) to 1191.667 (Cluster III). Days to maturity ranged from 148.17 (Cluster II) to 173.333 (Cluster XII and Cluster XV). Days to 50% flowering varied from 58.83 (Cluster II) to 94.5 (Cluster IX). Plant height ranged from 74.817 (Cluster VIII) to 104.525 (Cluster IX). Number of branches varied from 1.667 (Cluster X) to 3.2 (Cluster VI). Inflorescence length ranged from 20.167 (Cluster X) to 29.067 (Cluster XIII) and 10 ml vol. weight varied from 7.367 (Cluster IV) to 10.233 (Cluster X) (Table 6).

Table 3. Mean values of the first four canonical vector in grain amaranth

Genotypes	1 vector	2 vector	3 vector	4 vector
MGA507	69.9339	20.2645	32.8144	2.8482
BGA9	43.4008	12.0525	4.7887	18.4014
BGA20	102.3238	-15.3142	9.2170	4.4610
BGA14	146.6409	-49.9178	50.0486	-4.0270
BGA3	71.2189	54.7772	64.9738	53.6845
RMA45	56.5568	27.5025	32.9947	4.4173
RMA43	127.0294	-25.8162	31.1970	29.9470
RMA42	201.6246	88.3869	-15.8702	43.1319
BGA21	165.7958	78.8964	-10.5150	-27.5696
BGA12	57.3890	2.4527	1.8242	13.7349
BGA4	81.0009	0.6196	0.2487	19.0248
BGA11	216.5438	-17.7686	61.3615	-2.3024
SKNA808	167.6798	-46.0717	10.1462	50.6111
SKNA809	58.2759	19.6738	-6.0090	18.9371
IC35482	65.9209	-5.8344	3.2537	1.4336
IC35370	151.3316	-37.6584	18.4227	41.0569
RMA51	135.1333	-1.3252	41.0258	35.8851
GA2	68.6837	47.7066	60.3878	8.9099
MGA15	54.3497	30.9092	19.9874	11.9224
MGA16	135.2220	32.7672	37.6486	8.0168
BGA5-1	174.6261	28.0631	16.7974	-6.2532
BGA7-1	82.3946	23.2862	21.0927	18.5625
BGA2	106.4630	4.7534	5.5941	60.5666
BGA11-1	146.4334	23.9905	21.2275	59.6545
AmbikaGA12-1	172.7752	50.3112	-19.4813	13.8848
AmbikaGA12-2	48.4414	39.1878	58.6524	8.3759
Suvarna	86.9791	-28.2338	14.8145	23.2269
SKNA401	174.5346	71.2948	2.7426	30.7555
SKNA403	174.4336	83.5731	16.0083	4.4813
KBJ3	35.4254	4.8957	1.6816	3.7124
KBJ3-1	171.5600	-30.6115	-8.3261	11.8426
RGA5	209.5949	-15.2797	80.7458	-2.2029
RGA6	99.3535	94.0606	84.1629	39.7791
Lambda	1=94930.18	2=49532.23	3=24596.60	4=13790.81

Sum of other canonical roots = 20817.030
Sum of all canonical roots = 203666.900
Contribution of canonical roots in percent (1) = 46.611
Contribution of canonical roots in percent (2) = 24.320
Contribution of canonical roots in percent (3) = 12.077
Contribution of canonical roots in percent (4) = 6.771
Total contribution of canonical roots in percent = 89.779

In the present study 33 genotypes were evaluated at the same location and grouped into 16

Table 4. Genotypes groups into 16 clusters in grain amaranth

Cluster number	Genotype(s)
Cluster I	BGA9, BGA20, BGA14, BGA11 (Bhubaneswar)
Cluster II	BGA7-1 (Bhubaneswar), RGA6 (Ranchi)
Cluster III	AmbikaGA12-1 (Ambikapur), KBJ3 (Bangalore)
Cluster IV	MGA16 (Mettupalayam), BGA 5-1 (Bhubaneswar)
Cluster V	BGA3 (Bhubaneswar), IC35370 (Akola)
Cluster VI	SKNA403 (S. K. Nagar)
Cluster VII	RMA45 (Mandor), BGA 21 (Bhubaneswar), IC35482 (Akola)
Cluster VIII	BGA11-1 (Bhubaneswar), RGA5 (Ranchi)
Cluster IX	MGA507 (Rahuri), SKNA808 (S. K. Nagar)
Cluster X	Suvarna (Bangalore)
Cluster XI	RMA43, RMA42 (Mandor), BGA4 (Bhubaneswar), SKNA809 (S. K. Nagar)
Cluster XII	SKNA401 (S. K. Nagar)
Cluster XIII	BGA12 (Bhubaneswar), KBJ3-1 (Bangalore)
Cluster XIV	RMA51 (Mandor), MGA15 (Mettupalayam)
Cluster XV	GA2 (S. K. Nagar)
Cluster XVI	BGA 2 (Bhubaneswar), AmbikaGA12-2 (Ambikapur)

different clusters. Cluster I was the largest one having genotypes from different geographical sources showing that genetic divergence has no relationship with geographical divergence. The absence of relationship between genetic diversity and geographical diversity indicates that forces other than geographical origin, such as exchange of genetic stocks, genetic drift, spontaneous variation, natural and artificial selection, are responsible for genetic diversity (Nagarajan and Prasad, 1980). Genotype SKNA 401 (cluster XII) can be utilized in hybridization programme with genotypes AmbikaGA12-1 and KBJ3 (cluster III) as it showed the maximum divergence values for distance (26809). Hybridization programme between genotype Suvarna (Cluster X) and genotypes RMA51 and MGA15 (Cluster XIV) would be utilized for better improvement as it showed 2nd highest divergence values for distance (20017). Genotype Suvarna (Cluster X) can be utilized in hybridization programme with genotypes AmbikaGA12-1 and KBJ3 (cluster III), as it showed the maximum divergence values for distance (15031). Cluster III (AmbikaGA12-1 and KBJ3) and XII (SKNA401) showed maximum inter-cluster distance, which may be used for hybridization programme for obtaining a broad spectrum of variability for transgressive segregants. Per cent contribution of characters towards genetic divergence may be beneficial for selection in crop improvement. Number of branches, days to 50% flowering, inflorescence length, plant height, days to maturity and seed yield (kg/ha) have contributed more than other characters and may be considered in selection programme. The characters such as number of branches (21.97%, 3.2 for cluster VI), days to 50% flowering (17.05%, 58.83 for cluster II for earliness 91.167 for cluster V for late), inflorescence length (15.72%, 29.067 for cluster XIII), plant height (12.69%, 74.817 for short stature and cluster VIII and 104.525 for long stature), days to maturity (12.31%, 148.17 for short duration Cluster II and 173.333 for long duration Cluster XII and Cluster XV), seed yield (kg/ha) (10.98%, 1191.667 for cluster III), 10 ml vol. weight (9.28%, 10.233 for Cluster X) contributed more towards genetic divergence suggesting that thereby diverse genotypes can be utilized for improvement of yield. It is assumed that maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to the most divergent clusters. But, for a plant breeder, the objective is not only high heterosis, but also reduction of duration. The greater the distance between two clusters, the wider is the genetic diversity between the genotypes. Keeping this in view, the clusters III, X, XII and XVI were among the most divergent clusters having high seed yield performance along with contributing traits, which can be utilized in hybridization programmes for getting desirable transgressive segregants and high

Table 5. Inter- and intra- cluster (diagonal) distance of different genotypes in grain amaranth

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI	Cluster XII	Cluster XIII	Cluster XIV	Cluster XV	Cluster XVI
Cluster I	6.527	76.897	53.535	52.960	40.111	49.836	37.088	63.908	39.088	50.84	24.685	44.719	60.436	53.441	55.59	82.81
Cluster II		5.924	926.1	87.006	34.503	5090.3	70.743	2156.9	59.76	976.3	55.737	2565.7	137.12	39.635	54.111	6677.5
Cluster III			4.959	75.365	39.21	5045.8	78.41	7937	58.85	15031	71.59	12786	26809	50.3	40.89	975.1
Cluster IV				8.03	47.564	37.596	58.626	50.332	75.679	88.254	66.64	99.95	54.713	47.775	20.301	76.830
Cluster V					14.39	53.207	34.304	47.009	32.036	80.267	28.341	83.366	43.265	63.636	67.848	37.898
Cluster VI						0.0	48.958	1504.4	70.866	6607	79.086	24612	1574.8	54.033	31.093	2815.1
Cluster VII							12.916	109.43	32.067	41.496	27.109	75.656	58.285	93.558	68.106	55.335
Cluster VIII								9.861	47.953	4303.9	56.391	2034	8853.4	77.10	114.7	345.5
Cluster IX									7.980	71.461	23.215	83.981	34.148	51.986	38.859	38.615
Cluster X										0.0	79.857	6236	15338	89.794	59.191	20017
Cluster XI											13.593	95.488	42.072	64.749	71.216	78.037
Cluster XII												0.0	891.35	79.831	77.995	61.239
Cluster XIII													23.194	82.543	108.63	5131
Cluster XIV														18.411	48.349	52.362
Cluster XV															0.0	43.318
Cluster XVI																1.807

heterotic response. Thus, it is evident that the genotypes from clusters III, X, XII and XVI may be

used for hybridization programmes to generate wide range of variability and provide transgressive

Table 6. Cluster mean of different characters in grain amaranth

Clusters	Characters						
	Seed yield kg/ha	Days to maturity	Days to 50% flowering	Plant height (cm)	Number of branches	Inflorescence length (cm)	10ml vol. weight (g)
Cluster I	726.750	152.084	74.750	92.350	2.733	27.583	9.008
Cluster II	1013.83	148.17	58.83	76.92	2.73	22.20	9.40
Cluster III	1191.667	160.167	66.167	77.384	2.700	21.567	9.784
Cluster IV	515.500	172.500	82.500	100.884	2.700	21.567	7.367
Cluster V	468.834	157.500	91.167	95.183	2.800	25.500	9.084
Cluster VI	861.000	157.000	70.333	80.967	3.200	23.567	9.700
Cluster VII	474.556	158.889	82.000	88.600	2.133	26.800	8.500
Cluster VIII	895.334	154.000	60.000	74.817	2.984	26.684	8.167
Cluster IX	426.500	159.833	94.500	100.717	2.734	23.167	8.534
Cluster X	1156.333	168.000	69.000	75.767	1.667	20.167	10.233
Cluster XI	530.583	153.750	93.334	104.525	2.300	26.600	9.234
Cluster XII	377.000	173.333	86.000	102.433	2.033	22.567	7.567
Cluster XIII	573.334	162.667	75.167	89.933	2.967	29.067	8.350
Cluster XIV	770.667	162.500	74.167	99.517	2.967	24.767	8.700
Cluster XV	850.667	173.333	70.000	98.900	2.467	23.800	7.600
Cluster XVI	854.834	164.000	80.167	89.500	2.500	22.700	8.833

segregants for increased yield. The genotypes SKNA401, AmbikaGA12-1, KBJ3, Suvarna RMA51 and MGA15, being genetically diverse from the rest of the genotypes can be used in hybridization with all the clusters.

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