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GENETIC DIVERGENCE IN GRAIN AMARANTH (*AMARANTHUS HYPOCHONDRIACUS* L.)

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Extent and magnitude of genetic divergence for 14 characters among 98 genotypes of grain amaranth (*Amaranthus hypochondriacus* L.) were determined for the purpose of identifying more diverse parents which are expected to engender maximum variability. Based on genetic divergence D^2 statistics, genotypes were grouped into 18 clusters in which cluster I contained maximum number of genotypes (42), Cluster II (11), Cluster III (7), Cluster IV and V (5 in each case) and Cluster VI has 4 genotypes. Cluster VII, VIII, IX, X have (3 in each), cluster XI, XII, XIII, XIV (2 in each) and clusters XV, XVI, XVII and XVIII (1in each case).

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The clustering pattern revealed that there was no relationship between genetic divergence and eco-geographical region. Intra cluster values ranged from 0.00 to 141.86 and cluster XI is most diverse group. The inter cluster values ranged from 133.08 to 1214.59. Maximum divergence was noticed between clusters VIII and XI (1214.59) followed by clusters XI and XV (982.16) and clusters II and XI (938.89). The diverse clusters derived could be used in hybridization programme to generate wide range of transgressive segregants in population to develop high yielding grain amaranth varieties.

Key words: *Amaranthus hypochondriacus*, dendrogram, D^2 statistics, genetic diversity

INTRODUCTION

Grain amaranths of the genus *Amaranthus* is the most important subsidiary food crop of the people inhabiting to the tropical and subtropical highlands of Central and South Americas (SAUER, 1967). The genus contains more than 60 species (KALAC and MOUDRY, 2000) of which *Amaranthus hypochondriacus* and its hybrids are widely cultivated as ornamental, pseudo-cereal, and fodder crops in many tropical to 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 protein is of an unusually high quality (high in the amino acid lysine 5.0 to 6.0 % and also rich in the sulphur-containing amino acids) confirms its high potential for use in both human and animal nutrition and also shows high promise for supplementing nutritive food and amelioration of protein deficiency strictly in the vegetarian diet people (DOWTON, 1973; SENFT, 1980; VIETMEYER, 1980; BRESSANI *et. al.* 1987a; BRESSANI *et. al.*1987b; DODOK *et.al.* 1997; 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) as grain amaranth (*A. hypochondriacus*) is outbred /inbred crop (WALTON, 1968; KULOKOW and JAIN 1987). Considering the amaranth as more variable crop the choice of parents is very important because it provides promising segregant populations (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, yet 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 nature and extent of genetic diversity present in 98 genotypes of grain amaranth for genetic improvement of grain amaranth through hybridization.

MATERIAL AND METHODS

The present investigations were undertaken during 2007-08 in 98 accessions of *A. hypochondriacus* namely, AG-15, AG-17, AG-22, AG-27, AG-32, AG-39, AG-45, AG-55, AG-63, AG-69, AG-70, AG-72, AG-73, AG-74, AG-76, AG-79, AG-80, AG-85, AG-86, AG-87, AG-88, AG-89, AG-90, AG-92, AG-94, AG-95, AG-96,

AG-97, AG-98, AG-99, AG-106, AG-108, AG-109, AG-112, AG-116, AG-118, AG-119, AG-120, AG-122, AG-123, AG-124, AG-125, AG-128, AG-130, AG-131, AG-132, AG-140, AG-144, AG-145, AG-146, AG-149, AG-150, AG-151, AG-156, AG-157, AG-158, AG-159, AG-160, AG-161, AG-172, AG-174, AG-175, AG-177, AG-180, AG-181, AG-182, AG-184, AG-186, AG-190, AG-195, AG-196, AG-197, AG-200, AG-201, AG-202, AG-203, AG-205, AG-207, AG-210, AG-211, AG-213, AG-214, AG-215, AG-216, AG-220, AG-221, AG-225, AG-226, AG-230, AG-231, AG-234, AG-235, AG-240, AG-246, AG-251, AG-275, AG-300 and AG-308. These were grown in Completely Randomised Design with three replications in the experimental field of National Botanical Research Institute, Lucknow (India). Spacing between rows were 45 cm and plant-to-plant distance was 15 cm. Fifteen plants of each genotype of each replication were selected randomly for gathering observations on 14 characters i.e. plant height, no. of branches/plant, no. of branches near stem base, length of basal lateral branches/plant , length of top lateral branches/plant, stem diameter, leaf size, petiole length, terminal inflorescence stalk length, terminal inflorescence lateral length, panicles/plant, plant weight, grain yield/plant and harvest index. Genetic divergence between genotypes was worked out using Mahalanobis (1936) D^2 statistics and the clustering of genotypes were done following Tocher's method as described by RAO (1952). Ward's hierarchical clustering (Indostat cluster package, 1994) was used for grouping of the genotypes in clusters.

RESULTS

The distribution pattern of 98 genotypes revealed that there were 18 clusters and the distribution of genotypes from different eco-geographical region was apparently random (Table 1). This grouping reflects the wide genetic divergence among the genotypes. Cluster I contains maximum (42), cluster II (11), cluster III (7), cluster IV and V (5 each), cluster VI (4), cluster VII, VIII, IX and X (3 each), cluster XI, XII, XIII and XIV (2 each), cluster XV, XVI, XVII and XVIII have only (1 in each) genotypes.

Clusters VIII and XI were most diverse with maximum (1214.59) followed by clusters XI and XV (982.16), clusters II and XI (938.89) inter-cluster distance (Table 2). Highly divergent genotypes would produce a broad spectrum of variable attributes enabling further selection and improvement. Inter-cluster distance between the cluster I and V was the lowest (133.08) indicating that involved genotypes are closely related. Intra cluster distance ranged from 0.00 to 141.86. Intra-cluster distance was highest for cluster XI (141.86) while the clusters XV, XVI, XVII and XVIII were lowest (0.00).

The genetic contribution towards diversity was made by leaf size (23.964), grain yield/plant (18.935), harvest index (13.570), length of top lateral branches/plant (10.457), length of basal lateral branches/plant (9.005), plant weight (6.480), plant height (5.702) and panicles/plant (5.660) Table 3.

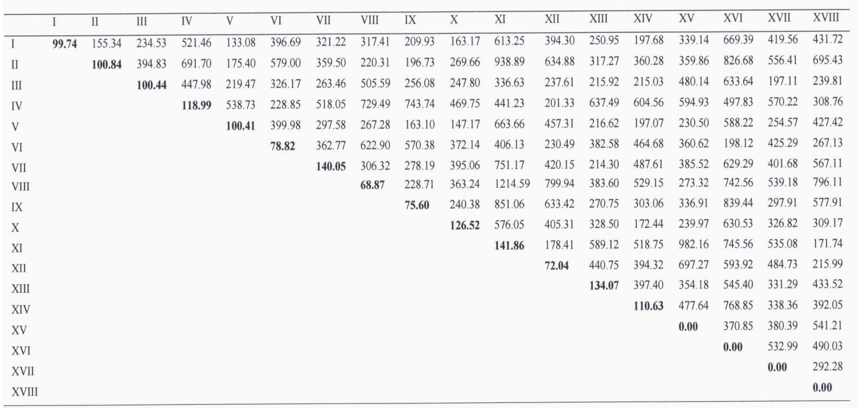
Table 1. Sources and clustering of 98 genotypes in eighteen clusters.

Cluster	No. of genotypes	Genotypes
I	42	AG-70 Delhi, AG-74 Himachal Pradesh, AG-118 NBRI-Lko, AG-158 Madhya Pradesh, AG-214 Tamilnadu, AG-246 America (Maryland), AG-72 America (Maryland), AG-200 NBRI-Lko, AG-196 Mexico, AG-201 Mexico, AG-160 Madhya Pradesh, AG-85 Argentina, AG-231 Madhya Pradesh, AG-125 China, AG-158 Madhya Pradesh, AG-95 Arunachal Pradesh, AG-251 China, AG-235 Banglore, AG-97 Orrisa, AG-215 Tamilnadu, AG-161 Himachal Pradesh, AG-157 Bihar, AG-190 America (Maryland), AG-122 Uttar Pradesh, AG-195 Mexico (Rodale Press), AG-202 Mexico (Rodale Press), AG-172 Uttarakhand, AG-98 Orrisa, AG-197 Mexico, AG-216 Maharastra, AG-175 Uttarakhand, AG-184 Uttar Pradesh (Gorakhpur), AG-131 America (Maryland), AG-275 Orrisa (Bhubneshwar), AG-130 America (Maryland), AG-80 Argentina, AG-182 Uttar Pradesh (Faizabad), AG-99 Himachal Pradesh, AG-123 China, AG-181 Uttar Pradesh (Faizabad), AG-109 Mexico (Rodale Press), AG-177 Uttarakhand
II	11	AG-119 Uttar Pradesh, AG-203 Mexico, AG-210 Kerala, AG-226 Uttarakhand (Almora), AG-207 England, AG-120 Uttar Pradesh, AG-205 England, AG-128 America (Maryland), AG-180 NBRI-Lko, AG-300 Himachal Pradesh, AG-308 Nepal (Kathmandu)
III	7	AG-32 China, AG-89 Gvatemala, AG-88 Gvatemala, AG-112 NBRI-Lko, AG-76 America (Maryland), AG-132 America (Maryland)
IV	5	AG-73 Himachal Pradesh, AG-106 Mexico (Rodale Press), AG-146 Jodhpur, AG-145 Jodhpur, AG-116 NBRI-Lko
V	5	AG-108 Mexico (Rodale Press), AG-234 Banglore, AG-225 Uttarakhand (Almora), AG-124 China, AG-221 West Bengal
VI	4	AG-39 China, AG-45 Mexico, AG-55 Jodhpur, AG-86 Gvatemala
VII	3	AG-22 Jaipur, AG-140 Jaipur, AG-69 Delhi
VIII	3	AG-149 Andhra Pradesh, AG-174 Uttarakhand, AG-150 Andhra Pradesh
IX	3	AG-151 Andhra Pradesh, AG-156 Bihar, AG-213 Tamilnadu
X	3	AG-186 Uttar Pradesh (Azamgarh), AG-230 Madhya Pradesh, AG-211 Kerala
XI	2	AG-15 Orrisa (Bhubneshwar), AG-94 Arunachal Pradesh
XII	2	AG-17 Orrisa (Bhubneshwar), AG-79 America (Maryland)
XIII	2	AG-27 S. Africa, AG-90 Arunachal Pradesh
XIV	2	AG-96 Orrisa, AG-220 West Bengal
XV	1	AG-240 Mexico
XVI	1	AG-63 Jodhpur
XVII	1	AG-92 Arunachal Pradesh
XVIII	1	AG-144 Jaipur

The mean values for plant height 84.989 (cluster VIII) to 278.00 (cluster XV), no. of branches /plant 4.450 (cluster XII) to 163.267 (cluster X), no. of branches near stem base 1.883 (cluster XII) to 12.967 (cluster XV), length of basal lateral branches/plant 4.689 (cluster X) to 51.533 (cluster XVI), length of top lateral branches/plant 7.007 (cluster IV) to 39.633 (cluster XV), stem diameter 1.516 (cluster XIII) to 19.611 (cluster X), leaf size 1.677 (cluster X) to 201.448 (cluster XI), petiole length 5.384 (cluster VIII) to 121.292 (cluster X), terminal inflorescence stalk length 6.540 (cluster XV) to 82.600 (cluster XVIII), terminal inflorescence lateral length 11.800 (cluster VIII) to 67.755 (cluster X), panicles/plant 15.634 (cluster XIII) to 50.933 (cluster XVI), plant weight 29.289 (cluster X) to 379.967 (cluster XVIII), grain yield/plant 39.333 (cluster VIII) to 301.433 (cluster XV) and harvest index 4.810 (cluster XII) to 46.367 (cluster XV).

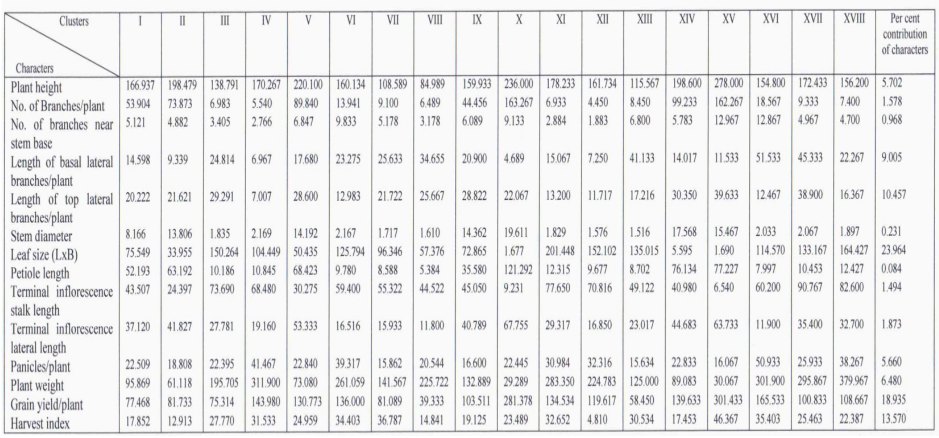
Genotype AG-144 can be utilized in hybridization programme with genotypes AG-211 (488.95), Ag-220 (488.86), AG-240 (487.66) and AG-230 (485.47) as it showed maximum Euclidian values for distance (Fig. 1.) in Ward's clustering analysis.

Table 2. Intra (bold) and inter-cluster D^2 values for 98 amaranth genotypes



	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII
I	**99.74**	155.34	234.53	521.46	133.08	396.69	321.22	317.41	209.93	163.17	613.25	394.30	250.95	197.68	339.14	669.39	419.56	431.72
II		**100.84**	394.83	691.70	175.40	579.00	359.50	220.31	196.73	269.66	938.89	634.88	317.27	360.28	359.86	826.68	556.41	695.43
III			**100.44**	447.98	219.47	326.17	263.46	505.59	256.08	247.80	336.63	237.61	215.92	215.03	480.14	633.64	197.11	239.81
IV				**118.99**	538.73	228.85	518.05	729.49	743.74	469.75	441.23	201.33	637.49	604.56	594.93	497.83	570.22	308.76
V					**100.41**	399.98	297.58	267.28	163.10	147.17	663.66	457.31	216.62	197.07	230.50	588.22	254.57	427.42
VI						**78.82**	362.77	622.90	570.38	372.14	406.13	230.49	382.58	464.68	360.62	198.12	425.29	267.13
VII							**140.05**	306.32	278.19	395.06	751.17	420.15	214.30	487.61	385.52	629.29	401.68	567.11
VIII								**68.87**	228.71	363.24	1214.59	799.94	383.60	529.15	273.32	742.56	539.18	796.11
IX									**75.60**	240.38	851.06	633.42	270.75	303.06	336.91	839.44	297.91	577.91
X										**126.52**	576.05	405.31	328.50	172.44	239.97	630.53	326.82	309.17
XI											**141.86**	178.41	589.12	518.75	982.16	745.56	535.08	171.74
XII												**72.04**	440.75	394.32	697.27	593.92	484.73	215.99
XIII													**134.07**	397.40	354.18	545.40	331.29	433.52
XIV														**110.63**	477.64	768.85	338.36	392.05
XV															**0.00**	370.85	380.39	541.21
XVI																**0.00**	532.99	490.03
XVII																	**0.00**	292.28
XVIII																		**0.00**

Table 3. Cluster means for 14 characters in 98 amaranth genotypes



Clusters / Characters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII	Per cent contribution of characters
Plant height	166.937	198.479	138.791	170.267	220.100	160.134	108.589	84.989	159.933	236.000	178.233	161.734	115.567	198.600	278.000	154.800	172.433	156.200	5.702
No. of Branches/plant	53.904	73.873	6.983	5.540	89.840	13.941	9.100	6.489	44.456	163.267	6.933	4.450	8.450	99.233	162.267	18.567	9.333	7.400	1.578
No. of branches near stem base	5.121	4.882	3.405	2.766	6.847	9.833	5.178	3.178	6.089	9.133	2.884	1.883	6.800	5.783	12.967	12.867	4.967	4.700	0.968
Length of basal lateral branches/plant	14.598	9.339	24.814	6.967	17.680	23.275	25.633	34.655	20.900	4.689	15.067	7.250	41.133	14.017	11.533	51.533	45.333	22.267	9.005
Length of top lateral branches/plant	20.222	21.621	29.291	7.007	28.600	12.983	21.722	25.667	28.822	22.067	13.200	11.717	17.216	30.350	39.633	12.467	38.900	16.367	10.457
Stem diameter	8.166	13.806	1.835	2.169	14.192	2.167	1.717	1.610	14.362	19.611	1.829	1.576	1.516	17.568	15.467	2.033	2.067	1.897	0.231
Leaf size (LxB)	75.549	33.955	150.264	104.449	50.435	125.794	96.346	57.376	72.865	1.677	201.448	152.102	135.015	5.595	1.690	114.570	133.167	164.427	23.964
Petiole length	52.193	63.192	10.186	10.845	68.423	9.780	8.588	5.384	35.580	121.292	12.315	9.677	8.702	76.134	77.227	7.997	10.453	12.427	0.084
Terminal inflorescence stalk length	43.507	24.397	73.690	68.480	30.275	59.400	55.322	44.522	45.050	9.231	77.650	70.816	49.122	40.980	6.540	60.200	90.767	82.600	1.494
Terminal inflorescence lateral length	37.120	41.827	27.781	19.160	53.333	16.516	15.933	11.800	40.789	67.755	29.317	16.850	23.017	44.683	63.733	11.900	35.400	32.700	1.873
Panicles/plant	22.509	18.808	22.395	41.467	22.840	39.317	15.862	20.544	16.600	22.445	30.984	32.316	15.634	22.833	16.067	50.933	25.933	38.267	5.660
Plant weight	95.869	61.118	195.705	311.900	73.080	261.059	141.567	225.722	132.889	29.289	283.350	224.783	125.000	89.083	30.067	301.900	295.867	379.967	6.480
Grain yield/plant	77.468	81.733	75.314	143.980	130.773	136.000	81.089	39.333	103.511	281.378	134.534	119.617	58.450	139.633	301.433	165.533	100.833	108.667	18.935
Harvest index	17.852	12.913	27.770	31.533	24.959	34.403	36.787	14.841	19.125	23.489	32.652	4.810	30.534	17.453	46.367	35.403	25.463	22.387	13.570

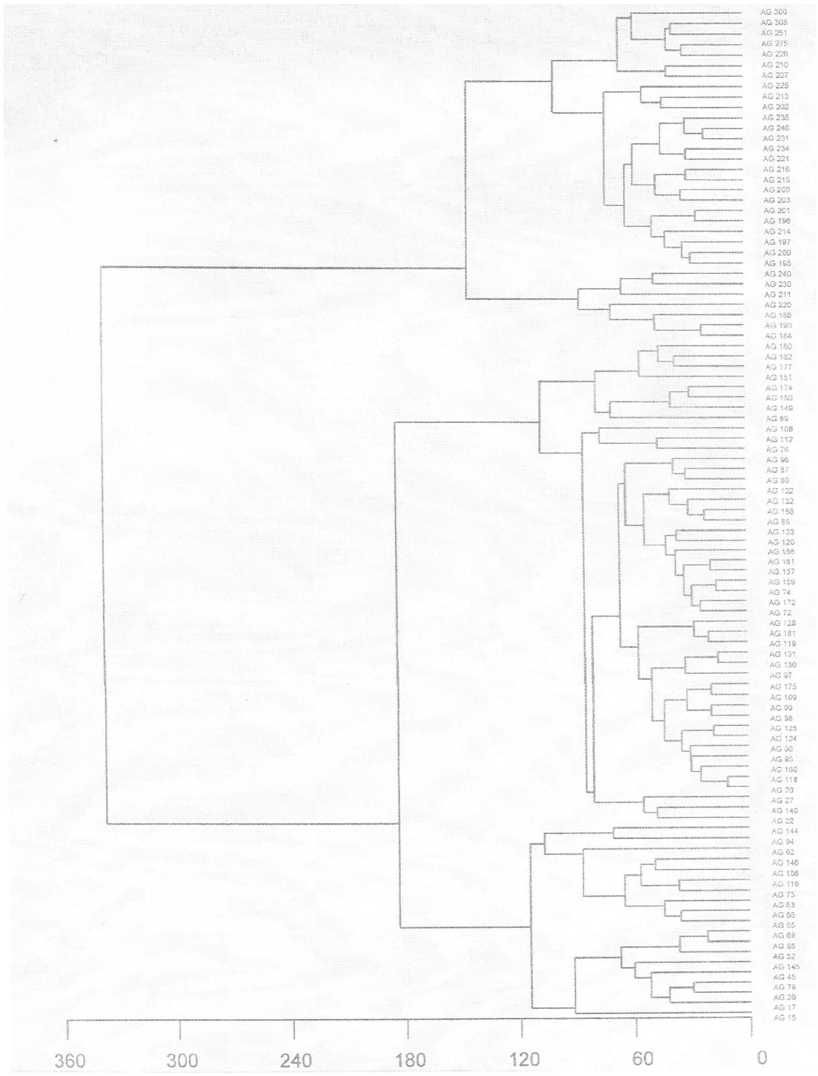


Fig.1 Euclidean dendrogram of 98 genotypes of grain amaranths

DISCUSSION

In present study 98 genotypes were evaluated at same location and were grouped into 18 different clusters. Cluster I was the largest cluster having genotypes from different geographical sources shows 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 perhaps responsible for genetic diversity (NAGARAJAN and PRASAD, 1980). Cluster VIII (AG-149, AG-174 and AG-150) and XI (AG-15, AG-94) has maximum inter-cluster distance which may be used for hybridization programme for obtaining a broad spectrum of variability for transgressive segregants for the genetic improvement of grain amaranth (*Amaranthus hypochondriacus* L.). Percent contribution of characters towards genetic divergence may be beneficial for selection in crop improvement. Leaf size, grain yield/plant, harvest index, length of top lateral branches/plant were contributed more than other characters and may be considered in selection programme.

The characters such as Leaf size (23.964%, 201.448 for cluster XI), grain yield/plant (18.935%, 301.443 for cluster XV), harvest index (13.570%, 46.367 for cluster XV) and length of top lateral branches/plant (10.457%, 39.633 for cluster XV) contributed more towards genetic divergence suggesting thereby that diverse genotypes can be utilized for improvement of yield productivity. In general, Ward's cluster analysis did not show similarity with D^2 analysis but AG-144, AG-211, AG-220, AG-240 and AG-230 may be involved in hybridization.

From the foregoing it is evident that the genotypes from clusters VIII, XI and XV may be used for hybridization programme to generate wide range of variability and provide transgressive segregants for increased yield.

AG-144, AG-211, AG-220, AG-240 and AG-230 being genetically diverse from rest of the genotypes could be used in hybridization with all the clusters.

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GENETIČKA DIVERGENTNOST *Amaranthus hypochondriacus* L.

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Izvod

Obim i magnitude genetičke divergentnosti 14 osobina među 98 genotipova zrna amarantusa (*Amaranthus hypochondriacus* L.) je utvrđen za potrebe identifikacije više divergentnih roditelja kod koji se očekuje maksimalna varijabilnost. Bazirano na statističkoj genetičkoj divergentnosti D^2 genotipovi su grupisani u 18 klastera u kojima klaster I sadrži maksimalni broj genotipova (42), klaster II (11), klaster III (7), klaster IV I V (5 u svakom slučaju) i klaster VI koji je imao 4 genotipa. Klasteri VII, VIII, IX i X su imali po 3 genotipa, klasteri XI, XII, XIII, XIV (po dva genotipa i klasteri XV, XVI, XVII I XVIII (po jedan genotip). Izgled klastera potvrđuje da nije bilo zavisnosti između genetičke divergentnosti i eko-geografskih regiona.

Vrednosti unutar klastera variraju od 0.00 do 141.86 a klaster IX je najrazličitija grupa.. međuklasterske vrednosti variraju od 133.08 do 1214.59. Maksimalna divergentnost je utvrđena između klastera VIII i XI, slede klasteri XI i XV (982.16) i klasteri II i XI (938.89). Dobijeni klasteri divergentnosti mogu da se koriste u programima oplemenjivanja radi generisanja transgresivnih segreganata u populacijama u cilju dobijanja visokoprinosnih varieteta amarantusa.

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