



Genetic divergence in amaranth (*Amaranthus hypochondriacus* L.)

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(Received: March 2002; Revised: November 2002; Accepted: November 2002)

Amaranth has been a pseudo-cereal with high nutritive value along with wide range of uses as human food on one hand and as a potherb on the other hand since centuries. Besides having high nutritional quality, their high tolerance to arid conditions and sub soils, are also other attributes to be looked for its future cultivation prospects. To breed adaptable cultivars for Wide agro-climatic zones, selection of suitable parents is important. D^2 statistics is a powerful tool for determining the degree of divergence between populations and relative contribution of different components to the total divergence in isolating suitable parents. Such studies are very meager in grain amaranth [1]. Hence, an effort has been made to assess (i) the genetic diversity among parents for hybridization and (ii) to attain the meaningful classification or grouping of germplasm in relation to contribution of each character towards the divergence in a set of 66 genetically diverse genotypes of grain amaranth.

In the present study 66 strains of amaranth (*Amaranthus hypochondriacus* L.) were grown in RBD with 3 replications at National Botanical Research Institute, Lucknow, located at 26°N, 80.5°E and 120 meter above mean sea level. The rows were 3 meter long and 45 cm apart. In each row plant to plant distance was maintained at 15 cm by thinning. Observations were recorded on 5 plants of each treatment in each replication for 10 economic traits i.e. days to flower, days to maturity, plant height (cm), stem diameter (cm), number of branches/plant, number of inflorescence/plant, inflorescence length (cm), leaf size (cm²), number of spikelets/spike and grain yield/plant (g). The statistical analysis was computed on the mean basis across the genotypes following Mahalanobis' D^2 generalized group distance to determine the degree of difference among $n(n-1)/2$ pairs of 'n' populations and grouping of strains was done according to Tochar's method [2].

Analysis of variance indicated significant variation among the 66 populations for each of the ten characters, suggesting adequate variability among the genotypes. A wide range of variability was noticed for different

agronomic and economic traits (Table 2). The range of variation was from 44.33 to 75.33 for days to flower, 123.5 to 160.0 for days to maturity, 31.67 to 125.33 cm for plant height, 4.33 to 19.67 for number of branches/plant, 15.5 to 213.00 for number of inflorescence/plant, 10.00 to 39.00 cm for inflorescence length, 1.00 to 5.00 for number of spikelets/spike, 4.83 to 32.10 for number of nodes/plant, 11.20 to 144.79 cm² for leaf size and 6.17 to 27.73 g/plant for grain yield. The maximum coefficient of variability was noticed for number of inflorescence/plant (39.76) followed by leaf size (34.68 cm²). The multivariate analysis of variance for the simultaneous testing of significance of differences in the mean values based on Wilk's lambda criterion revealed significant difference among the genotypes for aggregate ten traits (650 df, $X = 2904.05^{**}$). Days to flower contributed maximum towards genetic divergence followed by plant height and number of nodes/plant. This was also confirmed by first and second canonical vectors. In first vector maximum contribution of divergence was shown by days to flower (0.7815) followed by number of nodes/plant (0.3589) while in vector second maximum contribution towards genetic divergence was noticed through plant height (0.8524).

The 66 strains could be grouped in nine clusters depending upon the genetic constitution of strains (Table 1). The cluster I contain 22 strains followed by cluster VII with 12 strains. The cluster VIII was quite unique, having single strain (AG-198). In present investigation, lines selected showed greater diversity despite common parentage. This genetic diversity among the genotypes may be due to factors like history of selection, heterogeneity, selection under diverse environments and genetic drift. So, for hybridization, the selection of parents should be based on genetic diversity besides per-se performance and geographical origin. The intra cluster values varied from 0.00 to 2.253. The maximum was found in VI followed by III and I. The genotypes in clusters II (1.498), IV (1.498) and IX (1.496) were very close to each other and clusters VII and V were

Table 1. Intra and inter cluster distances (\sqrt{d}) between 66 lines of amaranth.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	1.77	9.58	15.15	05.97	12.17	19.79	14.62	40.51	19.14
II		1.50	25.23	07.79	17.83	29.41	21.68	49.80	19.25
III			01.77	19.72	29.54	36.10	29.39	47.84	41.10
IV				01.50	16.02	29.81	12.55	43.85	19.92
V					01.31	13.05	10.46	31.47	12.24
VI						02.25	34.42	37.99	41.31
VII							01.43	45.91	07.67
VIII								00.00	65.16
IX									01.50

*Each cluster involves the following strains; Cluster I: AOS005, AOS008, AOS009, AOS010, AOS011, AOS012, AOS013, AOS016, AOS017, AOS018, AOS019, AOS020, AOS021, AOS022, AOS025, AOS026, AOS027, AOS029, AOS036, AOS038, AOS039, AOS042; II: AOS040, AOS041, AOS043; III: AOS001, AOS003, AOS004; IV: AOS014, AOS031, AOS037, AOS054, AOS055, AOS056, AOS057, AOS058, AOS059, AOS060; V: AOS035, AG-21, AG-TSL; VI: AG-67, AG-198-2, AG-114; VII: AOS002, AOS006, AOS007, AOS015, AOS028, AOS030, AOS032, AOS033, AOS034, AOS041, AOS051, AOS052; VIII: AG-198; IX: AOS023, AOS024, AOS045, AOS046, AOS047, AOS048, AOS049, AOS050, AOS053.

Table 2. Cluster means of different agronomic traits in grain amaranth.

Cluster	Days to flower	Days to maturity	Plant height (cm)	No. of primary branches/ plant	No. of inflorescence/ plant	Inflorescence length (cm)	No. of spikelets/ spike	No. of nodes/ plant	Leaf size (cm ²)	Grain yield /plant(g)
I	56.43±0.43	128.86±0.17	100.67±2.08	10.37±0.20	58.75±1.67	15.49±0.47	3.52±0.08	19.42±0.46	74.76±2.93	14.67±0.42
II	71.11±0.49	130.11±0.02	96.17±0.59	11.11±0.47	53.06±2.53	19.06±0.76	2.89±0.09	17.67±0.16	48.79±1.52	9.61±0.17
III	54.83±0.25	128.00±0.06	106.89±3.74	12.11±0.06	180.89±3.46	22.31±0.42	3.17±0.06	19.11±0.89	57.22±1.05	15.94±0.69
IV	57.75±0.16	127.90±0.21	102.67±1.65	16.22±0.33	40.33±1.27	22.60±0.52	2.55±0.05	18.28±0.43	59.22±1.94	11.52±0.36
V	52.81±0.24	149.11±0.57	67.86±1.58	7.82±0.19	41.61±1.17	20.11±0.74	3.11±0.01	15.60±0.43	48.99±2.18	11.03±0.45
VI	54.58±0.52	154.50±0.65	99.20±1.09	6.53±0.16	58.97±0.78	17.86±0.79	4.30±0.08	37.60±1.55	62.87±2.40	11.77±0.71
VII	47.62±0.38	129.17±0.25	84.31±2.64	7.07±0.17	30.85±1.39	25.39±0.39	2.17±0.07	11.24±0.21	24.77±1.54	10.40±0.30
VIII	57.50±0.00	158.00±0.00	110.00±0.00	9.00±0.00	47.80±0.00	39.00±0.00	4.10±0.00	13.80±0.00	64.20±0.00	27.73±0.00
IX	54.83±0.56	131.06±0.18	47.65±1.14	5.67±0.10	22.50±0.59	15.41±0.35	1.37±0.09	8.48±0.56	29.77±1.52	8.72±0.33
Mean	56.38	137.41	90.60	9.54	59.42	21.91	3.02	17.91	52.29	13.49
±SE	±2.38	±4.19	±6.87	±1.10	±15.72	±2.40	±0.31	±2.75	±5.42	±1.94
Range	44.33-75.33	123.5-160.00	31.67-125.33	4.33-19.67	15.50-213.00	10.00-39.00	1.00-5.00	4.83-32.10	11.20-144.79	6.17-27.73

also shifting towards these clusters. The inter cluster distance was maximum between VIII and IX (65.157) followed by II and VIII (49.801) and III and VIII (47.845) and diverse much to each other. Genetic diversity is the most important tool to select prospective parents for crop improvement program. The genotypes belonging to the clusters separated by high estimated distance could be utilized in hybridization program for obtaining wide variation among the segregates [3-5].

The cluster means for each character are presented in Table 2. The cluster VIII had maximum grain yield, days to maturity, plant height, inflorescence/ plant and next to the highest leaf size. The cluster III had the highest number of inflorescence/ plant and next to the highest grain yield (15.94 g/plant). It is interesting to note that the grain yield in different clusters are greatly influenced by the different component traits mainly by the plant height, number of inflorescence/ plant, number of spikelets/spike, number of nodes/plant and leaf size. Among different component traits, studied in present investigation, the days to flower contributed the maximum towards divergence followed by plant height, nodes/plant and leaf size. This indicates the utility of multivariate analysis in identifying useful parents with high yield and other desirable traits. In a breeding program aimed at crop improvement, the choice of parents is quite important and only component characters of yield should be taken into account for selecting

genetically divergent parents. The hybridization among genetically diverse parental genotypes for specific trait may be helpful in bringing the new gene pool in population and expanding the range of adaptation. For example the genotypes of the cluster III for inflorescence number and cluster VIII for long plant height can be utilized as donor parents for enhancing the yield of other genotypes grouped in a cluster in F₁s and can be fixed by selecting transgressive segregants followed by continued selection in advance generations which may lead to development of a high yielding varieties with desired component characters.

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