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Genetic studies of yield contributing traits in *Amaranthus*

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Summary. Genetical studies on grain yield and its contributing traits were made in a six parent complete diallel in the F_1 and F_2 generations of one of the most widely grown grain species of grain amaranths (*Amaranthus hypochondriacus* L.). Graphical analysis indicated that epistasis exists for 1,000-grain weight in the F_1. Grain weight/panicle, yield/plant and harvest index indicated absence of non-allelic gene interaction. The harvest index in the F_1 and F_2 and grain weight/panicle, 1,000-grain weight, yield/plant in the F_2 appeared to be controlled by overdominance effects. Higher grain yield appeared to be associated with dominant genes. Both additive and non-additive gene effects were responsible for the genetic variation in the diallel population. However, dominance variance was more important than additive variance in grain yield/plant and harvest index in the F_1 and F_2. For 1,000-grain weight additive genetic variance was more important in the F_1 and non-additive in F_2. There was overdominance of a consistent nature in the two analyses for harvest index in the F_1 and F_2, grain weight/panicle, 1,000-grain weight and yield/plant in the F_2 and partial dominance for 1,000-grain weight in the F_1.

Key words: *Amaranthus hypochondriacus* – Grain amaranths – Yield components – Harvest index – Diallel

Introduction

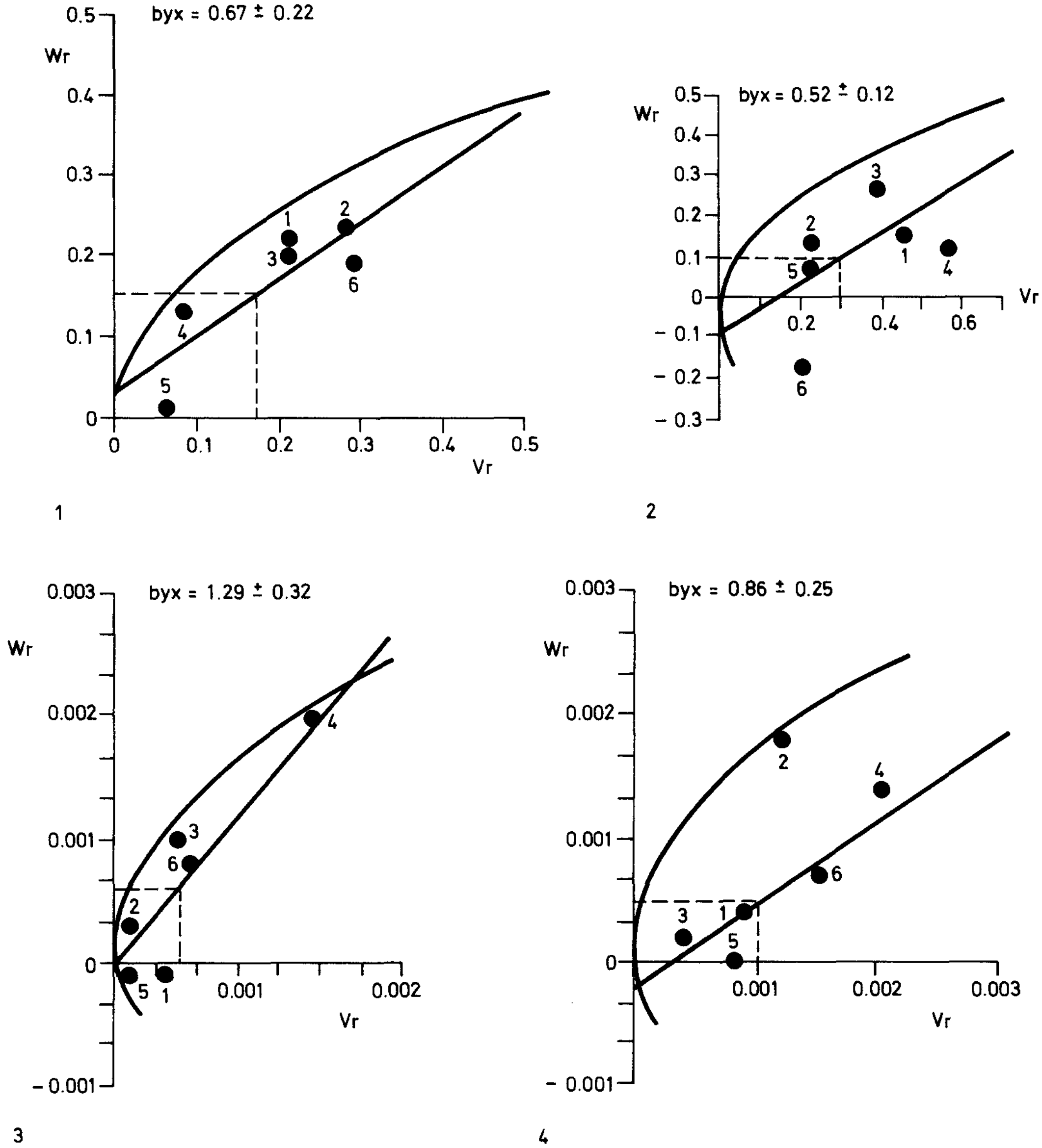
The grain amaranths (Genus *Amaranthus*) is an ancient crop plant which at the time of the Spanish conquest was the major grain source in the tropical highlands of the Americas (Agogino 1957). After being introduced from America the grain Amaranths have done exceptionally well in some parts of China and its use is spreading into the North Indian hills as a subsidiary food (Singh and Thomas 1978). Its important features include fast maturation and adaptability to marginal soils (Anonymous 1975). Since no precise information is available on the grain yield, and the genetics of the nature of yield contributing characters, six cultivars of one of the most widely grown grain amaranths (*Amaranthus hypochondriacus* L.) were chosen in order to gather desired information through diallel analysis.

Materials and methods

The material consisted of 30 F_1s and 30 F_2s derived from six phenotypically distinct lines, viz. AG-16 (Calicut, Kerala), AG-26 (Mahabaleswar, Maharastra), AG-19/2 (NBRI, Lucknow), AG-24 (Garhwal, Uttar Pradesh), AG-21 (Barabanki) and AG-19/1 (NBRI, Lucknow). The F_1s, F_2s and parental lines were grown in a randomized complete block design with four replications: a single row of parents and F_1s and two rows of F_2s, the row length being 5.80 metre. The spacing was 47 cm between rows and 30 cm within rows. Organic and inorganic fertilizers were not applied. Ten plants from the parents and F_1s and 20 plants from F_2s were taken at random from each replication in order to record observations on grain weight/panicle (g), test weight (1,000 grains, g), yield/plant (g) and harvest index (%). The graphical and components analyses were made according to Jinks and Hayman (1953); Jinks (1954) and Hayman (1954). Heritability in the narrow sense was worked out in the F_1 and F_2 following Crumpacker and Allard (1962) and Verhalen and Murray (1969), respectively.

Results and discussion

The analysis of variance for the experiment is presented in Table 1. Significant differences were observed for all characters in both generations, suggesting substantial



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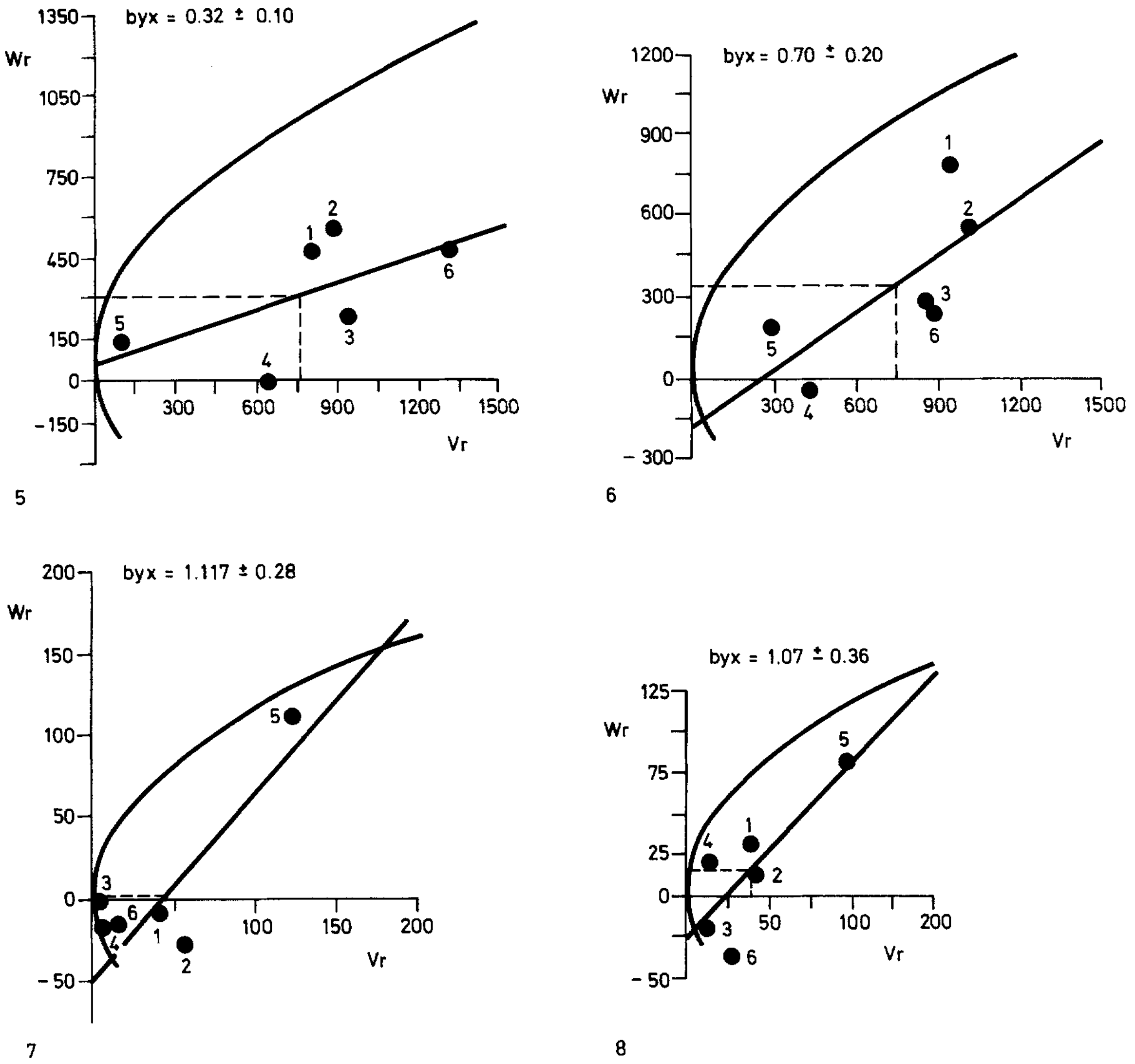
Figs. 1–4. Wr-Vr graphs for grain weight/panicle and 1,000-grain weight in the F_1 and F_2, respectively

Table 1. Analysis of variance for yield and its contributing traits in *Amaranthus*

Source of variation	d.f.	Mean sum of squares			
		Grain wt/ panicle	1,000-grain wt	Grain yield/ plant	Harvest index
Replications	3	14.468	0.034	5,023.666	128.600
Treatments	65	2.366*	0.007*	3,292.492*	229.518*
Parents	5	1.230	0.012*	5,056.600	490.200*
F_1s	29	2.432*	0.006*	2,583.265*	248.855*
F_2s	29	2.098*	0.008*	1,482.079*	144.306*
Parents vs. hybrids	1	1.090	0.001	49,431.600*	483.360*
F_1s vs. F_2s	1	7.300*	0.003	23,603.000*	584.520*
Error	195	1.063	0.005	456.712	25.409

* Significant at 1% level of probability



Figs. 5–8. Wr-Vr graphs for yield/plant and harvest index in the F_1 and F_2, respectively

amounts of variability among lines. Assumptions for the diallel set was tested using the variance table of Hayman (1954): the t^2 was not significant in the F_1 and F_2. The assumption of diploid segregation was fulfilled since the parents used in the present investigation revealed 16 bivalents at meiotic metaphase I (2n = 32, diploid). The selfing and selection year after year was done for attaining homozygosity.

The Wr and Vr statistics obtained for each array for the yield and its contributing traits in the diallel cross population were plotted in the form of a variance – covariance diagram (Figs. 1–8).

The slope of the regression line was not significantly different from zero or unity for 1,000-grain weight in the F_1, suggesting the existence of epistasis for this trait (Fig. 3). Allard (1956) reported that complementary gene interaction increases Vr and decreases Wr. A significant deviation of the regression line from unity was observed for grain weight/panicle, yield/plant and harvest index in both the generations and test weight (1,000 grains) in the F_2, indicating the absence of non-allelic gene interaction for these traits.

The regression line intersected the Wr axis above the origin in the F_1s for grain weight/panicle, test weight and yield/plant, suggesting partial dominance (Figs. 1, 3, 5). The regression line cut the Wr axis below the origin for harvest index in both F_1 and F_2, indicating overdominance (Figs. 7–8). For grain weight/panicle, test weight and yield/plant in the F_2 overdominance was apparent since the regression line intersected the Wr axis below the origin (Figs. 2, 4, 6).

Wr and Vr statistics indicated that parent 6 in the F_1 and F_2 and parent 5 in the F_2 contained the maximum number of dominant genes, whereas parents 2 in the F_1

and 3 in the F_2 contained the greatest number of recessive genes for grain weight/panicle. For 1,000-grain weight, parent 1 in the F_1 and 5 in the F_1 and F_2 carried a higher number of dominant genes, whereas parent 4 in both the F_1 and F_2 generations carried the maximum number of recessive genes. For yield/plant, parents 5 in the F_1 and 4 in the F_1 and F_2 contained a higher proportion of dominant genes, whereas parents 6 in the F_1 and 1 in the F_2 contained a higher proportion of recessive ones. For harvest index parents 1, 2, 4 in the F_1 and 3, 6 in the F_1 and F_2 contained a maximum number of dominant genes, whereas patent 5 in both F_1 and F_2 contained a higher number of recessive ones.

Among the estimates of variance components in the diallel using Hayman's method (1954), both $\hat{D}$ and $\hat{H}$ were significant in grain yield/plant and harvest index in the F_1 and F_2, suggesting that both additive and dominance effects were responsible for the variation observed in the diallel cross population. For the grain weight/panicle and 1,000-grain weight, the variation was mainly due to dominant gene action and $\hat{D}$ was non-significant in both generations. Grain yield/plant revealed positive and significant values of $\hat{h}^2$ in the F_1 and F_2, indicating a high proportion of additive, and additive × additive interaction components. Sharma et al. (1978) have also reported similar findings in wheat.

The average degree of dominance over all the loci was estimated by the value $(\hat{H}_1/\hat{D})^{1/2}$. Overdominance was apparent for grain weight/panicle, grain yield/plant and harvest index in both F_1 and F_2 as the value of $(\hat{H}_1/\hat{D})^{1/2}$ was greater than unity (Table 2). Complete dominance or overdominance was found for 1,000-grain weight in the F_2 since the value of $(\hat{H}_1/\hat{D})^{1/2}$ was slightly higher than unity whereas in the F_1 the dominance was incomplete for this trait.

An excess of dominant genes was found for 1,000-grain weight, grain yield/plant and harvest index in both F_1 and F_2 since the values of $\hat{K}_D/\hat{K}_R$ were greater than unity and the $\hat{F}$ values were positive (Table 2). The values of $\hat{K}_D/\hat{K}_R$ were less than unity for grain weight/panicle in the F_1 and F_2, indicating that the parents carried more recessive genes than dominant ones for this trait. The negative $\hat{F}$ values found for this trait also confirms the finding. According to the theory of diallel analysis, when positive (dominant) and negative (recessive) genes are equally distributed in the parents, the value of $\hat{H}_2/4\hat{H}_1$ is 0.25. This value was not found for any trait except 1,000-grain weight, indicating that positive and negative genes were not equally distributed in the parents.

The quantity $\hat{h}^2/\hat{H}_2$ estimates to some degree, the number of effective factors or groups of genes exhibiting dominance, but greater reliance can not be placed on it as it underestimates the number of genes

Table 2. Estimates of genetic components of variation for yield and its contributing traits

Various components and allied parameters	Grain wt/panicle		1,000-grain wt		Grain yield/plant		Harvest index	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
$\hat{D}$	0.041 ±0.04	−0.069 ±0.10	0.001 ±0.00	0.001 ±0.00	1,122.00 ± 247.31	1,168.00 ± 168.16	133.300 ± 19.02	135.60 ± 17.80
$\hat{H}_1$	−0.329 ±0.10	1.120 ±1.09	−0.000 ±0.00	0.002 ±0.00	2,687.00 ± 627.83	10,340.00 ±1,707.60	287.80 ±148.28	886.100 ±180.83
$\hat{H}_2$	−0.187 ±0.09	1.745 ±0.97	−0.000 ±0.00	0.002 ±0.00	23,329.00 ± 560.85	9,486.00 ±1,525.44	153.80 ± 43.13	512.100 ±161.54
$\hat{h}^2$	−0.000 ±0.00	−0.008 ±0.16	−0.001 ±0.00	−0.001 ±0.00	7,756.678 ± 377.49	7,390.00 ± 256.68	−3.633 ± 29.03	21.969 ± 27.18
$\hat{F}$	−0.337 ±0.10	−0.515 ±0.52	0.001 ±0.00	0.001 ±0.00	1,057.00 ± 604.19	2,089.00 ± 821.65	260.70 ± 46.46	433.60 ± 87.01
$\hat{E}$	0.284 ±0.01	0.395 ±0.04	0.001 ±0.00	0.001 ±0.00	142.100 ± 13.47	96.280 ± 63.56	7.191 ± 7.18	4.877 ± 6.73
$(\hat{H}_1/\hat{D})^{1/2}$	2.823	4.149	0.586	1.056	1.547	2.975	1.469	2.556
$\hat{H}_2/4\hat{H}_1$	0.142	0.201	0.325	0.265	0.216	0.229	0.133	0.144
$\hat{K}_D/\hat{K}_R$	0.182	0.058	8.456	2.191	1.868	1.859	4.979	4.339
$\hat{h}^2/\hat{H}_2$	0.001	−0.004	0.874	−0.277	3.330	0.779	−0.023	0.042
Heritability (%)	3.485	−2.160	39.090	17.321	33.728	11.909	70.462	22.316
r	0.578 ±0.31	0.007 ±0.00	0.719 ±0.23	0.367 ±0.42	−0.855 ± 0.12	−0.621 ± 29	0.799 ± 0.18	0.642 ± 0.23

exhibiting little or no dominance (Gilbert 1958). Complementary gene interaction also depresses the ratio. It appeared that at least one group of genes was involved in grain weight/panicle, 1,000-grain weight and harvest index and at least three for grain yield/plant. The narrow sense heritability was high for harvest index (70.462%) and intermediate for 1,000-grain weight (39.09%) and yield/plant (33.728%) in the F_1. In general, the heritability estimate was relatively low in the F_2 generation. Grain weight/panicle showed very low heritability values in both generations (Table 2).

Partial dominance of a consistent nature in the two analyses (Wr and Vr statistics and component of variation) was observed for 1,000-grain weight in the F_1, whereas overdominance was observed for harvest index in the F_1 and F_2. Inconsistency in the estimated ratio was found for grain weight/panicle and yield/plant.

In the present study, both the additive and non-additive genetic variances were found to be important for most of the characters. Under such circumstances, the maintenance of a certain degree of heterozygosity would be desirable in exploiting the additive genetic effect. Thus a suitable breeding procedure would be one which mops up the additive genetic variance and at the same time maintains heterozygosity. Therefore, recurrent selection followed by population improvement in the form of intermating (Jensen 1970) among the most desirable segregates would lead to the elevation of the genetic ceiling through accumulation of favourable additive genes in the core material. It will also provide a greater speed of recombination which would break the genetic barriers, if present.

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