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Comparative genetic analyses of metric traits using diallel and factorial mating designs in bread wheat

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Summary. For studying the inheritance of metric traits, diallel cross and factorial mating designs are commonly used. Since factorial mating design is less restrictive in crossing plans, the genetic information drawn from it was compared with that from a diallel cross. The comparison was made using graphical, genetic components and combining ability analyses for grain yield, grain weight and spike length in a field experiment of bread wheat (*Triticum aestivum* L.). Analyses were made on a nine parent diallel cross and a 4 ♀ × 5 ♂ factorial mating design which was sampled from the diallel cross. In general, there was a high degree of agreement between the results obtained from factorial mating design and diallel cross analyses showing thereby that the former provides almost equivalent genetic information to the latter.

Key words: Line × tester analysis – *Triticum aestivum* – Gene action – Combining ability – Mating designs

Introduction

Diallel and factorial mating (FM) designs are most commonly used for investigating the genetical structure of a population of pure-breeding lines. In diallel mating designs, all possible crosses are attempted among 'n' parental lines but in FM designs crosses are made between 'm' males and 'f' females. The FM design is an analogue of the North Caroline Design II of Comstock and Robinson (1948) and is also known as the line × tester design (Murty et al. 1967; Arunachalam 1976). Kempthorne (1957) and Simmonds (1979) illustrated the use of FM design. While various kinds of approaches are available to analyse the data from diallel crosses, the analysis of FM data is usually restricted to combining ability evaluation. In the present paper we attempt to show that (a) the data from the FM design can be analysed by computing variance (Vr) and covariance (Wr) statistics hitherto restricted for diallel crosses only (Jinks 1954; Hayman 1954), (b) the FM design provides a test for the adequacy of the additive-dominance model and (c) the FM design with fewer number of crosses provides similar genetic information as obtainable from diallel cross. The two designs have been compared by using data from a bread wheat experiment.

Materials and methods

The experimental material comprised nine diverse parents and 36 direct crosses among them. The nine parental lines were (1) 'C 306', and (2) 'C 273' from Punjab, India; (3) 'USA 352' from USA; (4) 'NP 876' and (5) 'NP 839' from New Delhi, India; (6) 'E 368' from USSR; (7) 'E 173' from Australia; (8) 'Turkey 1316' from USA and (9) 'Sonora 64' from Mexico. The material was evaluated at Ludhiana, Gurdaspur, Abohar and Jullundur substations of the Punjab Agricultural University in a randomized complete block design with four replications. There were 15 plants in a single row plot for each of the parents and F_1's. The plants were kept at 15 cm, within rows spaced 30 cm apart. Observations were recorded on ten random plants in a single row plot. Grain yield (g) was measured at all the four locations but data on 1,000-grain weight (g) and average spike length (cm) were recorded at Ludhiana only. Mean grain yield over all the four locations was used in the analyses.

A set of 20 crosses (4 females × 5 males) was extracted from the diallel crosses to form the factorial design. The parents, 'C 306', 'C 273', 'USA 352', 'NP 876' were taken as females and the rest of the five parents as males. No special criterion was fixed to extract either males females.

The variances and covariances calculated from the diallel table of means are V_p (the variance among parents), $\bar{V}_r$ (the mean variance of arrays), $V_{\bar{r}}$ (the variance of array means), and $\bar{W}_r$ (the mean covariance of array values with parental values) as described by Mather and Jinks (1971). All these four statistics can also be generated in the similar way for the FM de-

Table 1. Coefficients of genetical and environmental expectations of various statistics for diallel and factorial mating (FM) designs

Parameter[a]	Diallel cross statistic					FM design statistic				
	V_p	$\bar{V}_r$	$V_{\bar{r}}$	$\bar{W}_r$	E	V_p	$\bar{V}_r$	$V_{\bar{r}}$	$\bar{W}_r$	E′
$D=D_p$	1	0	0	0	–1	1	0	0	0	–1
H_1	1	4	0	–4	–(5n–4)/n	1	4	0	–4	–5
$H_2=H_R$	0	4	–4	0	–4 (n–1)/n	0	4	–4	0	–4 (n–1)/n
F	2	0	0	–4	–2 (n–2)/n	2	0	0	–4	–2
D_R	0	0	4	0	–4/n	0	0	4	0	–4/n
D_W	0	0	0	2	–2/n	0	0	0	2	0

[a] For definition of parameters see Mather and Jinks (1977)

sign, however, there would be two sets of statistics, one from the females and the other from the males. The expectations are the same for the FM design based on either females or males. If lines and testers are from different populations, analysis of rows and columns would yield different estimates depending upon the distribution of alleles in lines and testers (Jinks 1955). Under these circumstances, it would be desirable to carry out analysis for female lines only, that would again potentially yield the same amount of information as that of diallel. However, these statistics can be pooled over males and females to draw inferences about the population from which the male and female parents have been taken. The statistics so generated can be used to estimate the components of genetic variation only after these have been corrected for their non-genetic component. The non-genetic component associated with each of the statistics for a half-diallel cross and FM design would be as follows. The V_p, $\bar{V}_r$, $V_{\bar{r}}$ and $\bar{W}_r$ carry E, E, E/n and E/n, respectively, for the diallel cross and E′, E′, E′/m or f and zero, respectively, for the FM design (n, m and f are the number of parents, males and females, respectively and E and E′ are the non-heritable variations associated with individual means of diallel and FM design). The estimates of various parameters from various statistics using a perfect fit solution will be as presented in Table 1. Although Hayman (1954) has given approximate standard errors for some of the components presented in Table 3, no worthwhile estimate of the errors of variance components is available (Mather and Jinks 1971). Hence, the variance components from the two analyses can be compared on the basis of their magnitudes.

A general test of the assumptions is provided by the analysis of (V_r, W_r) regression. The regression coefficient is expected to be significantly different from zero but not from unity. This test is valid both for diallel and FM designs.

The V_r and W_r quantities can be plotted in the form of a graph not only for diallel crosses, as has been done by a large majority of workers, but also for the FM design. The graphs could be drawn considering all the parents together, or separately for females and males, depending upon the objective. We shall, however, consider females and males together for comparing the inferences from the FM design to diallel cross. The V_{ri} and W_{ri} quantities contain an environmental component which results in a biased intercept, inferences about the degree of dominance, and the placing of array points along the regression line. Therefore, V_{ri} and W_{ri} quantities were corrected for their environmental components as suggested by Mather and Jinks (1971, 1977). The non-genetic components associated with V_{ri} and W_{ri} values for diallel cross are E and E/n, respectively, and for FM design they are E′/n and zero, respectively. Different ratios of components of genetic variation were also computed for diallel cross and FM design.

The combining ability analysis was carried out for diallel cross using method II, model I of Griffing (1956) and for FM design using fixed effects model (Kempthorne 1957; Simmonds 1979).

Results and discussion

The analysis of variance revealed highly significant differences among the nine parents and their 36 hybrids for all three traits. Similarly, significant differences among four female and five male parents and their 20 hybrids in FM design were observed.

The regression coefficients of W_{ri} on to V_{ri} (Table 2) showed that the additive-dominance model was adequate for grain weight (GW) and spike length (SL) but not for grain yield (GY). Therefore, the components of genetic variation and their ratios are presented for GW and SL only in Table 3. The estimates of D, D_R, D_W and H_1 were consistent over the two analyses, except H_1 for SL. Both analyses indicated partial dominance for GW. For SL, diallel cross indicated overdominance while FM design analysis revealed partial dominance. An estimate of average frequency of negative versus positive alleles at loci exhibiting dominance ($\overline{uv}$) showed an equal distribution of alleles among parents for GW and SL for diallel cross analysis. However, FM design showed unequal distribution of alleles for these characters. The quantity $\frac{1}{2}F/(D(H_1-H_2))^{\frac{1}{2}}$ obtained from both the

Table 2. Regression coefficients of W_r on V_r for grain yield (mean over four locations), grain weight and spike length of a nine parent diallel cross and a 4×5 factorial mating (FM) design in bread wheat

Trait	Regression coefficient	
	Diallel cross	FM Design
Grain yield	0.1949±0.2381	0.4758±0.2261
Grain weight	0.8837±0.1067	1.1551±0.2776
Spike length	0.8747±0.1505	0.8844±0.1913

Table 3. Estimates of genetic parameters for grain weight and spike length of a nine parent diallel cross and a 4×5 factorial mating (FM) design in bread wheat

Component	Grain wt		Spike length	
	Diallel cross	FM Design	Diallel cross	FM Design
$D = D_P$	47.10 ±1.94	37.69 ±3.62	0.65 ±0.07	0.68 ±0.06
H_1	31.63 ±4.28	30.65 ±7.99	0.81 ±0.15	0.37 ±0.14
$H_2 = H_R$	25.01 ±3.68	10.18 ±6.87	0.71 ±0.13	0.05 ±0.12
F	10.34 ±4.53	22.86 ±8.44	0.06 ±0.16	0.29 ±0.14
D_R	45.37	35.29	0.69	0.71
D_W	41.92	26.26	0.62	0.53
$\overline{uv}$	0.19	0.08	0.22	0.04
$(H_1/D)^{1/2}$	0.82	0.90	1.11	0.74
$½F/\{(D(H_1-H_2)\}^{1/2}$	0.29	0.41	0.11	0.31
h^2 (broad sense)	0.98	0.98	0.90	0.93
h^2 (narrow sense)	0.76	0.85	0.61	0.87

analyses is neither zero nor unity showing thereby that h/d is neither constant nor does it vary independently over all loci for both these traits. Heritability is high for both these traits and the magnitude is almost similar from diallel cross and FM design. A correlation of the estimates of components of genetic variation and their ratios from diallel cross with FM design for the 22 pairs of values, irrespective of the character, was 0.94 ($P < 0.01$), showing thereby a general agreement between the two approaches. Further, the differences in the variance components estimated by the two approaches, whenever they exist, could be attributed to sampling in the FM design.

The additive-dominance model failed for GY. No precise estimates could therefore be obtainted but in order to compare diallel and FM designs the genetic components were calculated. The estimates of H_1, H_2 and F differed widely in the analyses. A correlation among the estimates of components of genetic variation and their ratios from diallel cross and FM design between 11 pairs of values was 0.84 ($P < 0.01$), showing thereby a general agreement between the two approaches, even where the additive-dominance model fails.

The corrected values of W_r and V_r statistics were used to draw graphs for GW and SL (Fig. 1). For GW, graphical analysis showed partial dominance in the diallel analysis and complete dominance in the FM design. However, $(H_1/D)^{½}$ showed partial cominance for GW from both the analyses (Table 3). For SL, graphical analysis as well as $(H_1/D)^{½}$ (Table 3) exhibited complete dominance and partial dominance through diallel and FM designs, respectively.

The scatter of the array points in the graphs based on the two analyses was broadly similar which is supported by the significant correlation among W_{ri}, V_{ri} values. The rank correlation coefficients were 0.63 ($P < 0.10$) and 0.69 ($P < 0.05$) for GW and SL, respectively. It follows that the placement of parents in the order of dominance from the two approaches is generally similar though not exactly the same.

Analysis of variance for combining ability for diallel cross and FM design showed both general combining ability (gca) and specific combining ability (sca) mean squares to be significant for all three traits. The gca and sca effects for GY, GW and SL were computed. The gca rank correlation coefficients for GY, GW and SL were 0.90, 0.85 and 0.88 (all with $P < 0.01$), respectively, indicating a general agreement between the two methods for isolating either the best or the poorest general combining parents. Similarly, the sca rank correlation coefficients for GY, GW and SL were 0.76, 0.62 and 0.79 (all with $P < 0.01$), respectively, indicating a general agreement between the two approaches. On the basis of the standard errors it was observed that gca effects were more precise from diallel cross while sca effects were equally precise from both the designs. The loss in precision of gca effects from the FM design could be due to the sub-sampling of the parents.

It is evident from the results presented above that the FM design provided almost similar information as compared to the diallel cross even though it is based on a lesser number of crosses. Compared with the diallel cross the FM design is less restrictive in crossing plan and requires far less resources in the generation and evaluation of the materials and analysis of data.

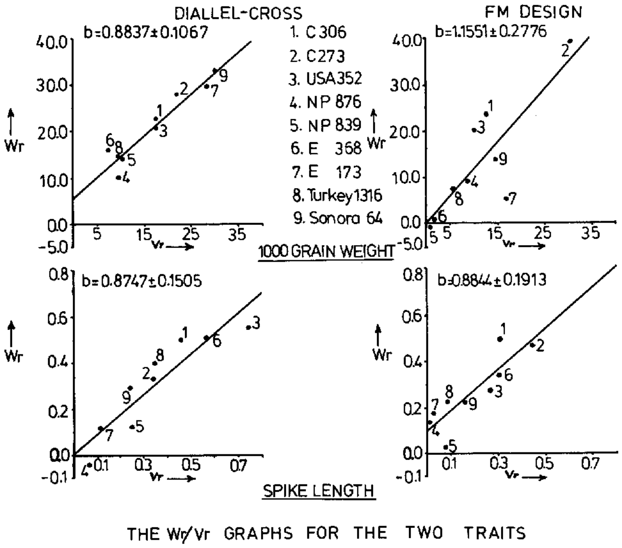

Fig. 1. W_r/V_r graphs for 1,000 grain weight and spike length

Although most of the inferences, except the grain yield, have been drawn on unilocational data, the evidence is sufficient enough for the present purpose which points out the predictive value of the FM design as compared to the diallel cross.

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