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# Relative Efficiency of North Carolina Designs I and II and Standard Design III in Three Wheat Crosses

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**Summary**. The efficiency of three analyses, namely, Designs I and II of Comstock and Robinson (1952) and standard Design III analysis of Kearsey and Jinks (1968), was compared in the $F_2$s of three wheat crosses (Norteno 67 × HD 1982, HD 1982 × Moti and Sonalika × Moti) for plant height, spikelets per spike and yield per plant. The three analyses showed a remarkable agreement in estimating the additive (D) component for all three characters in all three crosses. But, as regards the estimation of dominance (H) component, standard Design III analysis proved to be more efficient than the other two analyses in crosses 2 (HD 1982 × Moti) and 3 (Sonalika × Moti) for all three characters except spikelets per spike in cross 3.

**Key words**: North Carolina design – Standard design – Efficiency – Wheat

## Introduction

Comstock and Robinson (1952) suggested three mating designs (I, II and III) and described their analyses to study gene action affecting metrical traits. Kearsey and Jinks (1968) redefined $\sigma^2$ml of the Design III of Comstock and Robinson (1952). In the new analysis, $\sigma^2$d (differences variance, measuring the dominance component) is equal to $\frac{1}{2}$ $\sigma^2$ml of the original analysis. This modification in the coefficient of dominance component has been done to facilitate comparisons between additive and dominance components. Under such a situation, $\sigma^2 d / \sigma^2 s$ ($\sigma^2$s is the sums variance, measuring the additive component) would be a measure of mean degree of dominance regardless of gene distribution in the population.

Since the three analyses (Designs I and II and standard Design III) have importance of their own in knowing the genetic architecture of heterozygous and genetically heterogeneous populations, it was thought worthwhile to compare their efficiency.

## Materials and Methods

The $F_2$ families investigated in the present investigation were obtained from three spring wheat crosses (Norteno 67 × HD 1982, HD 1982 × Moti and Sonalika × Moti). The number of plants randomly chosen from these $F_2$s and crosses made for three analyses, namely, Designs I and II of Comstock and Robinson (1952) and standard Design III analysis of Kearsey and Jinks (1968), which were used to estimate different components of variation, were as follows:

Design I: 48 plants were randomly chosen from each $F_2$. Of these, 12 plants were used as males and 36 as females. Each male was crossed to three different females but each female was crossed once only.

Design II: In each case, 24 $F_2$ plants were grouped into four sets of 6 plants each. In each set, three plants were taken as males and three as females. Each male was crossed to each of the three females, yielding 9 crosses in each of the four sets in each $F_2$.

Standard Design III: Each of the 18 plants randomly chosen from each $F_2$ was crossed, as the male parent, to $P_1$ (larger parent) and $P_2$ to produce eighteen $L_1$ ($F_2 \times P_1$) and the same number of $L_2$ ($F_2 \times P_2$) families.

In each crossing programme, therefore, 36 crosses were made in each $F_2$.

All 108 families from each of the three $F_2$s along with their parents were raised in completely randomized blocks in three replications. Five competitive plants from each progeny family, in each replication, were scored for final plant height, number of spikelets per spike and kernel yield per plant. Except for the item variance within families, all items in all the three analyses were based on the means of these five plants. The item variance within families was, therefore, divided by five in each analysis to bring it into line with the other items of the analysis.

## Results

The estimates of D, H and $E_1$ (environmental) components obtained by the three analyses, with their standard errors, for all the three characters studied in all three crosses are presented in Table 1. The first two analyses (Designs I and II) showed remarkably good agreement regarding the estimation of all three components (D, H and

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$E_1$) for all characters in the three crosses, indicating that the two analyses were equally efficient for the estimation of these parameters. However, whereas the standard Design III analysis was in a good agreement with the other two analyses in estimating D for all the characters in all three crosses and for estimating H for all the characters in cross 1 and spikelets per spike in cross 3, it gave significantly different estimates of H for all the three characters in cross 2 and for plant height and yield per plant in cross 3. Also, relatively higher estimates of $E_1$ with smaller standard errors were given by the standard Design III analysis for all the characters in all the three crosses. A general feature of the present results was that the estimates of all the three components, D, H and $E_1$, obtained by using Design I analysis were associated with largest standard errors for all the three characters in all three crosses.

Higher estimates of D as compared to those of H for the trait plant height in all three crosses in all the three analyses indicated that the additive effects of the genes were more important for the control of this character. But in case of the other two traits (spikelets per spike and yield per plant), the relative importance of D and H components varied from cross to cross. The H/D ratio ranged from 0.149 for plant height in cross 3 in the Design II analysis to 1.457 for spikelets per spike in cross 2 of the Design III analysis.

## Discussion

A close agreement among the three analyses for the estimation of the D component for all the characters in all three crosses may be attributed to a similar coefficient (1/8) of this component in all the three analyses. A greater efficiency of the standard Design III analysis relative to

**Table 1.** Estimates of D, H and $E_1$ in three analyses, a (North Carolina Design I), b (North Carolina Design II) and C (standard Design III), for three characters in three wheat crosses

| Item | | Plant height | Spikelets per spike | Yield per plant |
|---|---|---|---|---|
| Cross 1 (Norteno 67 X HD 1982): | | | | |
| | D a | 96.5 ± 59.9 | 21.5 ± 15.4 | 43.9 ± 31.5 |
| | b | 83.0 ± 43.3 | 31.2 ± 17.7 | 47.5 ± 30.0 |
| | c | $^{a}$106.3 ± 45.5 | $^{a}$36.7 ± 15.7 | 49.0 ± 25.4 |
| | H a | 33.0 ± 148.6 | 14.7 ± 41.6 | 49.1 ± 84.5 |
| | b | 40.0 ± 27.3 | 25.0 ± 17.0 | 57.0 ± 38.2 |
| | c | $^{a}$42.1 ± 19.2 | $^{a}$23.4 ± 9.4 | $^{a}$53.5 ± 22.9 |
| | $E_1$ a | 12.2 ± 15.1 | 4.6 ± 3.9 | 10.4 ± 7.9 |
| | b | 10.7 ± 8.6 | 2.0 ± 4.5 | 4.1 ± 8.9 |
| | c | $^{b}$19.5 ± 6.2 | $^{b}$6.0 ± 2.3 | $^{c}$14.5 ± 4.3 |
| Cross 2 (HD 1982 X Moti): | | | | |
| | D a | $^{b}$73.0 ± 28.1 | $^{a}$34.6 ± 14.3 | $^{b}$47.6 ± 18.4 |
| | b | $^{b}$80.2 ± 26.2 | $^{b}$30.9 ± 11.9 | $^{a}$36.0 ± 15.5 |
| | c | $^{c}$116.4 ± 27.0 | $^{b}$45.5 ± 14.2 | $^{c}$38.2 ± 9.9 |
| | H a | 11.9 ± 17.7 | 34.1 ± 36.3 | 63.2 ± 41.2 |
| | b | 14.5 ± 7.6 | $^{c}$31.6 ± 9.1 | $^{c}$50.6 ± 15.4 |
| | c | $^{c}$39.8 ± 6.4 | $^{c}$66.4 ± 9.1 | $^{c}$24.3 ± 4.5 |
| | $E_1$ a | 6.3 ± 7.0 | 3.5 ± 3.6 | 8.3 ± 10.6 |
| | b | $^{b}$6.0 ± 2.2 | $^{a}$3.0 ± 1.2 | $^{a}$6.7 ± 3.1 |
| | c | $^{c}$12.6 ± 2.1 | $^{c}$6.7 ± 1.1 | $^{c}$15.4 ± 1.8 |
| Cross 3 (Sonalika X Moti) | | | | |
| | D a | $^{b}$111.3 ± 42.0 | $^{a}$39.8 ± 19.0 | $^{a}$51.6 ± 24.6 |
| | b | $^{b}$109.1 ± 36.6 | $^{b}$42.0 ± 16.2 | $^{b}$55.2 ± 20.6 |
| | c | $^{c}$157.3 ± 36.3 | $^{c}$58.9 ± 17.7 | $^{c}$71.1 ± 20.2 |
| | H a | 20.7 ± 24.1 | 56.2 ± 33.2 | 18.4 ± 22.4 |
| | b | 16.2 ± 9.1 | $^{c}$59.3 ± 15.9 | $^{b}$23.7 ± 8.3 |
| | c | $^{c}$53.4 ± 9.6 | $^{c}$66.9 ± 11.3 | $^{c}$49.3 ± 8.5 |
| | $E_1$ a | 22.2 ± 18.5 | 9.9 ± 8.4 | 17.7 ± 15.7 |
| | b | 15.3 ± 13.0 | 6.8 ± 3.8 | $^{a}$12.3 ± 6.1 |
| | c | $^{c}$32.0 ± 6.6 | $^{c}$15.2 ± 2.2 | $^{c}$25.3 ± 4.5 |

$^{a}p = 0.05 - 0.01$ $^{b}p = 0.01 - 0.001$ $^{c}p = 0.001$

the other two in estimating the H component for all three characters in cross 2 and plant height and yield per plant in cross 3 is probably because the coefficient of H in the standard Design III analysis is higher than its coefficient in other two analyses. Further, the estimates of D and H obtained by standard Design III analysis provided direct estimate of the square of the dominance ratio and were independent of gene correlations since both $\sigma^2$s and $\sigma^2$d were equally affected by excess coupling linkages in $L_1$ and $L_2$.

Design I is more useful than Design II and standard Design III if the number of the two sexes are unequal. Also, it allows a larger number of parents from the population to be tested for the same experimental efforts. If the number of families to be investigated is infinite, with an infinite number of individuals in each family, and if the D, H and $E_1$ model is adequate, Design II is superior to Design I since it provides more information about each of the three parameters D, H and $E_1$ because of the marked reduction in the correlations between these parameters, particularly those involving D. But if the number of families is finite, each of a finite size, as in the present case, this advantage of Design II over design I is reduced and, under such a condition, the estimates of D and H in Design II are no longer independent. Both Design I and Design II analyses, however, provide considerably less information about H than about D or $E_1$.

## Literature

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