NOTES AND COMMENTS

A NOTE ON THE TEST FOR THE DIRECTION OF DOMINANCE IN THE TRIPLE TEST CROSS IN THE PRESENCE OF GENOTYPE X ENVIRONMENT INTERACTION

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SUMMARY

In a triple test cross F_2 males are backcrossed to females from both the parental inbred lines and from an F_1 cross between them. A previously suggested test for the direction of dominance uses the covariance over sires of the sums and differences of the mean scores of the backcrosses to the inbred lines. This test is biased in the presence of some types of genotype $\times$ environment interaction while an alternative test using the covariance over sires of the means of the backcrosses to the F_1 with differences between the backcrosses to the inbred lines is not. A comparison of the two covariances could provide a scaling test for this breeding design.

1. INTRODUCTION

KEARSEY and Jinks (1968) first described the triple test cross (TTC) in which males of an F_2 from two inbred lines are backcrossed to females from both these inbred lines (L_1 and L_2) and from an F_1 cross between them (L_3). Alternatively, a set of inbred lines can be crossed to each of two extreme inbred lines (L_1 and L_2) and the various inbred lines entering into this crossing scheme replace the crosses to L_3 in the full TTC as the third component of the breeding design (Jinks *et al.*, 1969). In either case tests for epistasis, additive and dominance effects are available and the prevailing direction of any dominance can be tested as the correlation across the sires of the sums and differences of the mean scores of the backcrosses to the two inbred lines. In the case of inbred lines crossed to extreme testers the genetic component of the covariance over sires of the sums and differences of the family means, $\bar{L}_{1i}$ and $\bar{L}_{2i}$ for the i th sire backcrossed to L_1 and L_2 , has the expectation:

$$\text{covariance } (\bar{L}_{1i} + \bar{L}_{2i})(\bar{L}_{1i} - \bar{L}_{2i}) = -\frac{1}{4}F$$

and in the case of an F_2 backcross or a TTC with a random mating population crossed to extreme tester lines:

$$\text{covariance } (\bar{L}_{1i} + \bar{L}_{2i})(\bar{L}_{1i} - \bar{L}_{2i}) = -\frac{1}{2}F$$

where $F = \sum dh$ with equal gene frequencies in the absence of epistasis and linkage. The summation is here over all loci and d and h are the additive and dominance deviations defined by Mather and Jinks (1971). Thus the sign of this covariance can be taken to be opposite that of the prevailing direction of dominance although when the tester lines are not extreme, and are hence inadequate, the meaning of F will depend jointly on the degree of association and the distribution of dominant to recessive alleles in the tester lines

(Virk and Jinks, 1977). In this note we shall explore the effects of one type of genotype $\times$ environment interaction on this test in the case of the F_2 triple test cross to adequate testers, discover both that we may be misled in the presence of such interaction but that we can, in the absence of genotype-environment covariance, construct an alternative test which is free of these confounded effects.

2. EXPECTATIONS OF THE COVARIANCE RELATING TO THE DIRECTION OF DOMINANCE

If we let $\bar{L}_{ji}$ be the mean phenotypic score of the offspring of the cross between the i th sire and the j th tester line in a triple test cross then the covariance of $\Sigma_i = \bar{L}_{1i} + \bar{L}_{2i}$ and $\Delta_i = \bar{L}_{1i} - \bar{L}_{2i}$ for s sires is

$$\begin{aligned}\text{COV}_{\Sigma\Delta} &= \text{COV}[(\bar{L}_{1i} + \bar{L}_{2i})(\bar{L}_{1i} - \bar{L}_{2i})] \\ &= \text{variance}_{\bar{L}_{1i}} - \text{variance}_{\bar{L}_{2i}}\end{aligned}$$

Now if there are n offspring in each family then in the terminology of Perkins and Jinks (1970), and considering environmental effects arising only within families,

$$\text{variance}_{\bar{L}_{1i}} - \text{variance}_{\bar{L}_{2i}} = -\frac{1}{2}\left(1 + \frac{1}{n}\right)F + \frac{2}{n}W_{e_j g_d} + \frac{1}{n}W_{g_d g_h}$$

where $W_{e_j g_d}$ is the covariance of individual environmental deviations, e_j , with the genotype $\times$ environmental deviations, g_d , arising from the interaction of additive genetic deviations and the e_j , and $W_{g_d g_h}$ is the covariance between additive genetic $\times$ environmental interaction deviations, g_d , and dominance genetic $\times$ environmental interaction deviations, g_h .

An alternative way of viewing this expectation is to let V_{e_1} and V_{e_2} be the components of variation of L_{1i} and L_{2i} type individuals respectively which are either environmental or genotype $\times$ environmental interactional. Then

$$\text{COV}_{\Sigma\Delta} = -\frac{1}{2}\left(1 + \frac{1}{n}\right)F + \frac{1}{n}V_{e_1} - \frac{1}{n}V_{e_2}$$

Thus providing $V_{e_1} = V_{e_2}$, or n , the number of subjects per sire family, is large, then the covariance of sums and differences of crosses to L_1 and L_2 estimates $-\frac{1}{2}\Sigma dh$. But if $V_{e_1} \neq V_{e_2}$ and n is not large this covariance will be inflated by $1/n (V_{e_1} - V_{e_2})$.

These considerations will be irrelevant if we have a scale of measurement not exhibiting genotype $\times$ environmental interactions, or if n is large. However, for inbred line TTC's where it is possible directly to assess the presence of genotype $\times$ micro-environment interactions they have been found to be present for a large proportion of characters measured in *Nicotiana rustica* (Pooni *et al.*, 1978), and for work with mammals (Hewitt and Fulker, 1980) the n is likely to be relatively small in practice.

3. EXPECTATIONS OF AN ALTERNATIVE TEST

However, if we consider in similar fashion the crosses to the F_1 tester line, L_3 , we have

$$\begin{aligned}\text{COV}_{L_3\Delta} &= \text{COV}[\bar{L}_{3i}(\bar{L}_{1i} - \bar{L}_{2i})] \\ &= \text{COV}_{L_3L_1} - \text{COV}_{L_3L_2}.\end{aligned}$$

In this covariance the kinds of genotype $\times$ environment interaction we have been considering vanish in the constituent covariances and for the simple case of equal gene frequencies, and no epistasis or linkage

$$\text{COV}_{L_3\Delta} = -\frac{1}{4}F \quad \text{and} \quad \text{COV}_{2L_3\Delta} = -\frac{1}{2}F.$$

By considering, then, the correlation of the $\bar{L}_{3i}$ with the $\bar{L}_{1i} - \bar{L}_{2i}$ over the tested sires we have a test of the prevailing direction of dominance which is free of the effects of heterogeneity of environmental variance or genotype $\times$ environment interaction, and a comparison of the covariances of $2\bar{L}_{3i}$ with Δ_i and Σ_i with Δ_i provides a scaling criterion for the full TTC.

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4. REFERENCES

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