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Correction: power of tests for QTL detection using replicated progenies derived from a diallel cross

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It has been drawn to our attention that Table 1 in Rebaï and Goffinet (1993) contains some mistakes. These errors arose as a consequence of a misspecification of the matrices used to obtain the analytical expressions of the decentrality coefficients of the test distributions. We used a constrained model for F_3 progenies by imposing constraints on dominance parameters that are necessary for topcross (TC) progenies but not for those of the F_3. In F_3 the six dominance parameters d_{ij} are estimable but only two d_{ij} are in TC. The constraint $\sum a_i = 0$ on additive effects is necessary for both F_3 and TC. It follows that the test statistics are distributed, under the null hypothesis, as (n and N are the number of individuals observed):
$T_1 \sim F(9,n-15)$ in F_3 and $T_1 \sim F(5,N-17)$ in TC; and
$T_2 \sim F(3,n-15)$ in F_3 and $T_2 \sim F(3,N-17)$ in TC;

The expressions of the decentrality parameters are given in Table 1. T_3 considers independently the six F_3 populations and tests the six contrasts between homozygous marker class means. Powers of test T_1, T_2, and T_3 (to be read $\Pi_3 = 1 - \Pi_{k=1}^{6} \beta_k$) are calculated as described in Rebaï and Goffinet (1993). The percentage of variance explained by the quantitative trait loci (QTL) could be calculated as the ratio between the model mean squares of QTL (MSQ) parameters (a_i and d_{ij}) and the total mean square (MST) adjusted to the means ($\mu_{ij(t)}$):

$$r^2 = \frac{\mathrm{MSQ}}{\mathrm{MST}} = \frac{Y'(XX^- - X_0X_0^-)Y}{Y'(I - X_0X_0^-)Y} \text{ or } r^2 = \frac{\sigma_a^2 + \sigma_d^2}{\sigma_a^2 + \sigma_d^2 + \sigma^2}.$$

The right-hand expression is the expectation of the left-hand expression. $\sigma_a^2 = c_a \sum_{i=1}^{4} a_i^2$ and $\sigma_d^2 = c_d \sum_{i,j>i} d_{ij}^2$ are, respectively, the additive and dominance variances due to the QTL, and σ^2 is the residual variance of the model. c_a and c_d are specific constants with $c_a = \frac{1}{3}$ for F_3 and $\frac{1}{6}$ for TC and $c_d = \frac{1}{24}$ for F_3 and $\frac{1}{8}$ for TC.

Most of our previous conclusions remain valid. T_2 is always more powerful than T_3. For additive QTL, T_2 is more powerful than T_1 for both F_3 and TC, but its advantage is greater in F_3 because of the larger difference between the degrees of freedom used by the tests. When dominance increases, the difference in power is reduced and T_1 becomes better than T_2 for relatively large dominance effects ($\sigma_d^2 > \sigma_a^2/2$). The main practical conclusions of these comparisons are:
– the simultaneous analysis of several connected populations derived from a diallel is more powerful than the approach considering them to be independant.

Table 1 Expressions of decentrality coefficients for tests T_1 and T_2 calculated for both F_3 and TC progenies

For test T_1[a]

TC

$$\lambda_1^t = \frac{n}{6\sigma_t^2}\left[\sum_{i=1}^{4} a_i^2 + \frac{3}{4}\sum_{i,j>i}^{4} d_{ij}^2\right]$$

F_3

$$\lambda_1^f = \frac{n}{6\sigma_f^2}\left[2\sum_{i=1}^{4} a_i^2 + \frac{1}{4}\sum_{i,j>i}^{4} d_{ij}^2\right]$$

For test T_2

TC

$$\lambda_2^t = \frac{n}{6\sigma_t^2}\left[\sum_{i=1}^{4} a_i^2\right] \quad C = \frac{\sigma_t^2}{\sigma_t^2 + \frac{3}{24}\sum_{i,j>i}^{4} d_{ij}^2}$$

F_3

$$\lambda_2^f = \frac{n}{6\sigma_f^2}\left[2\sum_{i=1}^{4} a_i^2\right] \quad C = \frac{\sigma_f^2}{\sigma_f^2 + \frac{1}{24}\sum_{i,j>i}^{4} d_{ij}^2}$$

[a] n is the number of F_2 individuals (F_3 families). In TC the number of individuals is $2n$ because each F_3 family derived from each F_2 individual is crossed with two testers

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– both tests T_1 and T_2 should be used when searching for QTL because T_2 would detect additive QTL with small effects that are undetectable by T_1.

An interval mapping version of the method described in Rebaï and Goffinet (1993) is now available (Rebaï et al. 1994; Rebaï 1995). It allows QTL mapping in diallel and related schemes using flanking markers, even those that are not polymorphic in all the populations. Its application to experimental data from a diallel between four inbreds of maize gave interesting results, to be published in another issue.

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