POWER AND ROBUSTNESS OF STATISTICAL TESTS FOR MAJOR GENE DETECTION IN DIALLEL PROGENY TEST DATA

Wen Zeng and Bailian Li [1]

Abstract: Three simple statistical tests (Bartlett test, log-ANOVA test, and Fain test) were investigated for detecting the segregation of a major gene that control quantitative trait in half-diallel progeny tests of outbred tree population. Data with different degrees of major and polygenic effects were simulated for 6-parent half-diallel progenies. Consequently, there are 15 full-sib families, and 5 half-sib relationships among those full-sib families. The experiment design was assumed to be a randomized completely block design with 6-tree-row plot in each block, and 6 blocks in each of 4 different locations. The location effect and block effect were assumed to be fixed effects. A single major gene was assumed to be biallelic (A and a), autosomal locus with Mendenlian transmission probabilities. As a result, there are three possible genotypes: AA, Aa, and aa, and the genetic values are a, d, and –a respectively. The total phenotypic variance a_p is equal to 1.0. The parameters for the major gene set up as following: difference between homozygotes 2a (u_p unit) with values 0.0, 1.0, 1.5, or 2.0; frequency of the favorable allele p(A) with values 0.1, 0.5, or 0.9; dominance mode D with values a, a/2, or 0. For the polygenic part, the parameters are the heritability with values 0.0, 0.1, 0.2, or 0.3; the ratio of dominance to additive with values 0.00, 0.25, 0.50, or 0.75; the type-B genetic correlation with values 0.00, 0.60, 0.75, or 0.90. The major gene and the polygene were assumed to be independent. 500 repeats of each of 24 cases of combination were studied.

The power, the probability of rejecting the null hypothesis when it is false, of the statistical tests to detect the segregation of the major gene was assessed. The robustness, the sensitivity of type-I error to some violation, of the statistical tests were also studied in the presence of half-sib relationship, a skewed phenotypic distribution, and unbalanced data cases (80% and 90% survival rate were used). The most powerful test, but also the most sensitive to half-sib relationship and skewness, was the Bartlett test. The log-ANOVA test is almost as powerful as the Bartlett test, and very robust to half-sib relationship and skewness. The Fain test was less powerful and less sensitive to skewness than that of the Bartlett test. The percentage of the major gene in the total phenotypic variance, showed as the difference of two homozygotes and the frequency of favorable allele, and the dominance of the major gene are two key factors affecting the power of detecting the segregation of a major gene. When 2a > 1.5 a_p and D a/2, the power to detect the segregation of a major gene in a base population is at least 58% and 81% for P(A)=0.1 and P(A)=0.5 respectively. For the same situation, the power to detect the segregation of a major gene in a half-diallel design is no less than 95%. Several diallel progeny test data of loblolly pine *(Pinus taeda* L.) from the North Carolina State University-Industry Tree Improvement Program were analyzed with those methods. The results showed that there was detectable segregation of major genes for tree height growth in the loblolly pine.

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[1] Department of Forestry, Box 8002, North Carolina State University, Raleigh, NC 27695