

**ANALYSIS OF COMMONALITY TO ESTIMATE  
THE EFFECTS OF A  
QUANTITATIVE TRAIT LOCUS**

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**Abstract**

When a quantitative trait locus (QTL) is linked to a marker, an estimate of the QTL's effect on the phenotypic variation of a trait can be made. The best means of calculating the size of the effect is unclear. One method is through regression. The quotient of the sum of the squares associated with the variation of the marker and the sum of the squares associated with the variation of progeny among marker alleles is calculated. Another means of obtaining an estimate is through path analysis, which is analogous to path coefficients, but based on analysis of variance. Commonality has been used to identify relationships between fiber traits. To test these methods, a test population of  $F_2$ -derived  $F_3$  lines was developed. One parent was homozygous for a dominant morphological marker, pilose ( $T_1$ ), which is linked to loci that influence several quantitative traits of fiber; the other parent was homozygous recessive at  $t_1$ . Parents had widely different fiber traits. One hundred and forty-nine  $F_3$  lines were planted in two randomized complete blocks. Seven fiber traits (elongation, maturity, micronaire reading, perimeter, 2.5% span length, strength, and wall thickness) were measured. The  $t_1$  locus was found linked to loci influencing elongation, micronaire reading, perimeter, 2.5% span length, strength and wall thickness. The pilose marker accounted for 10 - 75% of the phenotypic variation of the linked fiber traits through the regression method. Analysis of commonality calculated pilose-linked fiber QTL accounted for 0 - 38% phenotypic variation of each trait. Most notably, the regression method calculated that the pilose-linked QTL for 2.5% span length accounted for 75% of the phenotypic variation, while commonality found only 17%. The ability of analysis of commonality to partition the influences of correlated effects gave more realistic estimates for the influence of a QTL on a trait.