

IDENTIFYING COMMON QUANTITATIVE TRAIT LOCI FOR A BIVARIATE PHENOTYPE

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High correlations between two quantitative traits may be either due to common genetic factors or common environmental factors or a combination of both. In this study, we develop statistical methods to extract the contribution of a common quantitative trait locus (QTL) to the total correlation between the components of a bivariate phenotype. Using data on a bivariate phenotype and marker genotypes for sib-pairs, we show that under the assumption of no dominance at the common QTL, the conditional cross-sib trait correlations (trait 1 of sib 1 - trait 2 of sib 2 and conversely) given the identity-by-descent (i.b.d.) sharing at the marker locus are increasing linear functions of the i.b.d. scores. Based on the above result, we propose a permutation test for linkage between a common QTL and a marker locus. The null hypothesis cannot be rejected unless there exists a common QTL. We use Monte-Carlo simulations to evaluate the performance of the proposed test under different trait parameters and quantitative trait distributions. We outline the issues and choices pertaining to possible extensions of the proposed method to incorporate multivariate phenotypes comprising more than two quantitative traits as well as larger sibship data. An application of the method is illustrated using data on two alcohol-related phenotypes from the Collaborative Study On The Genetics Of Alcoholism (COGA) project, each of which had provided evidence of linkage in the Alcohol Dehydrogenase (*ADH*) gene cluster on Chromosome 4 based on univariate analyses.