

Mapping the Genetic Architecture of Complex Traits in Experimental Populations

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Understanding how interactions among set of genes affect diverse phenotypes is having a greater impact in biomedical research, agriculture, and evolutionary biology. Mapping and characterizing the isolated effects of single quantitative trait locus (QTL) is a first step, but we also need to assemble networks of QTLs and define non-additive interactions (epistasis) together with a host of potential environmental modulators. We proposed mixed-model-based composite interval mapping (MCIM) method and Henderson method III and Bayesian method, (HAB) for analyzing genetic architecture of complex trait including additive (A), dominance (D), and epistasis (AA, AD, DD) effects of QTL, as well as their interaction with environment (AE, DE, AAE, ADE, DDE). The predicted breeding merits of potential superior lines or hybrids can also be obtained. QTLNetwork was developed by C++ programming language. QTLNetwork-2.0 (<http://ibi.zju.edu.cn/software/qtlnetwork/>) is user-friendly computer software for mapping quantitative trait loci (QTL) in DH, RI, BC1, BC2, F2, IF2 and BCxFy populations, and for graphical presentation of QTL mapping results.

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