

Bayesian analysis of complex traits in multiple related plant populations

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Unraveling the genetic factors determining complex traits in agriculture has been a challenging task for breeders and geneticists for many years. Statistical methods have been devised to answer basic questions concerning QTL (e.g. number, modes and sizes of action) and to map QTL on the genome to facilitate their manipulation for breeding purposes. We developed a Bayesian approach to fit various genetic models to explain quantitative trait variation in a large set of full-sib populations of which the parents are related by pedigree. In the models the number of QTL, as well as the number of Major Genes (=unmapped QTL) are treated as unknowns; also a background polygenic component is part of the model. The individual genetic components can be accumulated to improve breeding value estimation. Also, the posterior probabilities on QTL positions and estimates for effect sizes can be integrated to facilitate genomic selection. We applied the Bayesian approach to an apple dataset comprising 27 related mapping populations generated within the EU-HiDRAS project (<http://users.unimi.it/hidras/>).