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QTL mapping in a wheat breeding population by an IBD-based method - Crepieux, Sébastien [et al.]

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QTL mapping in a wheat breeding population by an IBD-based method

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Mapping quantitative trait loci in plants is usually conducted using a population derived from a cross between two lines. The power of such QTL detection and mapping strategies, and the estimation of the effects highly depends on the choice of the two parental lines. Thus, the QTLs found represent only a small part of the genetic picture and prove to be of limited economical interest in marker assisted selection. Besides, the cost of specific trials to perform QTL mapping is often a limitation for routinely map QTL.

On the other hand, conventional breeding programs use many different parents to perform pair-crosses. After several generations of self-pollination, the resulting progenies supply a more accurate picture of the improved material, on which a good range of quantitative traits are assessed in a wide set of environments during the selection process. As mentioned by Beavis (1998) "the integration of QTL mapping into existing breeding strategies is urgently needed". We developed and applied a two-steps IBD-based-variance component method to a Nickerson wheat plant breeding population, composed of 395 F6 individuals coming from 81 different parents. Results are presented for bread wheat quality related traits for which major gene and QTLs are known.

This method can provide an alternative to the development of specifically designed recombinant population, by exploiting the genetic variation actually managed by plant breeders. The use of these detected QTL in assisting breeding would thus be facilitated.

Calculation of the q-Values for a Two Stage Step-up Test Procedure that controls the False Discovery Rate

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After the paper of Weller et al (1998) the concept of the False Discovery Rate (*FDR*) (Benjamini Hochberg, 1985) is widely used in QTL mapping. The linear step-up multiple testing procedure of Benjamini and Hochberg, known sometimes as the BH procedure, controls the *FDR* at the desired level q for independent and positive dependent test statistics. More precisely, the BH procedure guarantees that $FDR \leq q \cdot m_0 / m$, where m_0 denotes the number of the true null hypotheses and m the number of all tests. If m_0 is known, then applying $q^* = q \cdot m / m_0$ instead of q increases the power of the BH procedure. Thus $FDR \leq q$ is fulfilled. Since in practice m_0 is unknown, several adaptive procedures were developed which use the BH procedure after estimating m_0. Benjamini, Krieger and Yekutieli (2004, BKY) provided a new two-staged procedure, where the linear step-up procedure is used at both stages but the level q^* used at the second stage depends on the number rejected at the first stage. They show that this new procedure controls the *FDR* at the desired level q. Moreover, the power of this procedure is substantial greater over the original BH procedure. For the case where the test statistics are positive dependent, they show, that among the procedures that exist in the literature the BKY procedure is the only one, which controls the *FDR*. Therefore, in this paper an algorithm will be demonstrated, which yield the q_i values for all hypotheses. For a hypothesis H_i the q_i value is the smallest threshold q for which H_i will be significant. If the q_i values are known and if a significance threshold, q, for *FDR* is given, then all H_i fulfilling $q_i \leq q$ are significant with respect to the BKY procedure.

References:

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