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How can we meet the challenges of efficient cereal mapping?

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Construction of high quality dense multilocus maps. Numerous mapping projects on cereal crops have generated an abundance of mapping data independently analyzed to create maps for each population. It is well recognized now that the quality of constructed maps vary broadly between populations, marker sets, labs, and bioinformatics tools. This calls for international collaborative efforts to re-analyze the accumulated mapping data, and build reliable dense multilocus maps that will fit the challenges of physical mapping, positional cloning, molecular breeding, and comparative genomics. Our experience allows declaring that using a verification process based on computing-intensive re-sampling approaches can significantly reduce the level of mapping inconsistencies. No less important is to integrate the mapping resources, and, when necessary, complement the existing marker sets by additional sets allowing better bridging between the maps. The currently employed approaches of building consensus maps are problematic. These approaches are based on identification of non-conflicting local orders on the map "pictures" and removing the conflicting markers, giving full credit to each of these "pictures". As a result, a paradoxical situation arises: with the increasing number of mapping populations, the number of conflicts increases, calling for removal of conflicting markers, and resulting in a reduced genome coverage by the "consensus" chromosome maps. As an alternative, we propose a different framework for joint analysis of multiple mapping populations, based on re-analysis of the original data rather than using the map "pictures".

QTL analysis. A huge amount of mapping results for cereal crops is spread in the literature, and for some cereals (e.g., barley) certain efforts have already been invested to summarize this information. Low accuracy of estimated chromosomal positions of detected QTLs is one of the major obstacles in application of QTL mapping results for marker-assisted selection and positional cloning of genes corresponding to the QTLs. As with map construction, the QTL mapping results have been obtained by different groups using different analytical (bioinformatic) methods, sometimes very simple, fast, and easy to use, at the expense of the efficiency and quality of mapping. Our experience suggests that a significant part of the mapping information carried in the row data remains untouched due to simplistic mapping approaches used. Thus, QTL mapping quality (detection power, resolution of the trait architecture components, accuracy of the estimated QTL position) can be tremendously improved by using more adequate and powerful analytical tools. In particular, our group is developing an efficient "*multiple-approach*" of QTL analysis that includes multiple-trait, multiple-environment, and multiple-family models combined with multiple-interval mapping (MIM). These combinations of methods proved very efficient, especially for increasing QTL detection power and mapping precision. One of the new interesting applications is "expression-QTL" mapping using microarray data. Like in multilocus map construction, joint QTL analysis of multiple row mapping data may result in a jump effect in terms of the foregoing criteria of mapping quality. The proposed new methodologies will be extensively illustrated on cereal mapping data (wheat, barley, and maize).