Crop Science Highlights QTL that Matter
by Marilyn L. Warburton and Christine H. Diepenbrock

Although there are now thousands of mapped quantitative trait loci (QTL) reported for crop species, very few varieties have been bred using marker-assisted breeding of these QTL. Noteworthy exceptions include the marker-assisted development of flooding-tolerant rice varieties, drought-tolerant maize, nematode-resistant soybeans, and disease-resistant chickpea and peanut varieties. QTL have been used to narrow down causal genes, often in conjunction with association studies, for traits including pre-harvest sprouting resistance in wheat, oil content and composition in maize, disease resistance and flowering time in soybean, and blast resistance in rice. The vast majority of mapped QTL, however, have neither led to concrete outcomes in advanced breeding materials nor released varieties. To QTL, however, have neither led to concrete outcomes in advanced breeding materials nor released varieties. To maintain a sufficient and nutritious food supply amidst changing demographics and climatic patterns and sustainability efforts, all available useful information for increasing genetic gain from selection should be put to use. A special collection of articles published in the July–August 2015 issue of Crop Science focuses on QTL that have made the leap into new breeding material or cultivars (in maize, perennial ryegrass, and soybean) or are in the validation phase (in maize, white clover, and soybean). Specifically, the articles expand on the difficulties encountered in incorporating QTL via marker-assisted selection into new varieties and what these successful examples would suggest as strategies for the identification, validation, and practical use stages of genomics-assisted breeding.

The main challenge is the time it takes to validate QTL in enough diverse environments and genetic backgrounds to ensure stable expression and understand their mode of action when placed in the presence of new environmental conditions or modifying genes. The time it takes to generate near-isogenic lines, transgenic lines, or find the same alleles in new backgrounds of recombinant inbred mapping populations and then to provide independent proof that these QTL are necessary and sufficient to achieve the phenotypes of interest deters their proper validation in most cases. This challenge can be ameliorated through early-cycle selection methods; an example can be found in Lightfoot (2015), which used highly correlated seedling phenotypes to identify plants resistant to the pathogen responsible for Fusarium root rot.

maximize translatability into breeding, validation should be planned at the start of a QTL identification study. Methods must be put into place to routinely validate QTL of large enough effect to justify the expense and to study QTL using meta-analyses when enough published data is available. Two examples of the former are provided in Semagn et al. (2015), in which a maize streak virus 3-SNP haplotype was validated using phenotypic outliers, and the most favorable haplotypes were then used to make double-haploid lines—a promising new tool for expediting marker-assisted selection strategies. This research group is also testing identified drought QTL in biparental families.

An additional confounding factor in the use of QTL in marker-assisted breeding is the existence of other routes to the same end for improving most traits in most crops. Transgenic technologies (especially pyramiding, as described in Lightfoot [2015]) and the use of genomic and/or phenotypic selection are often as effective as marker-assisted selection. It can be difficult to conduct accurate cost-benefit analyses to compare these methods given the varying cycle times, research costs, and number of markers involved for a given crop-trait combination, among other factors. As described in Diepenbrock and Gore (2015), increasing provitamin A levels in maize grain through breeding is a case in which marker-assisted selection for large-effect QTL, alone or combined with genome-wide selection models that account for residual polygenic effects, may offer substantial gains without use of transgenics, as the carotenoid biosynthetic pathway is native and active in the endosperm of maize grain (unlike in the case of rice). QTL for these and other traits will continue to be used in the future, especially as new technologies relying on information about causative variation such as genome editing come online. New QTL variation will also undoubtedly be needed as pathogens overcome resistance, environmental conditions and consumer preferences change, and genotyping and phenotyping platforms continue to increase in scale and precision and decrease in cost.

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