

High through-put genomics in small grain cereals and applications to molecular breeding

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Identification of genes associated with beneficial traits has been one of the major goals in genetics. To facilitate this process in barley genetics, we applied microarray and *in silico* comparative genomics tools. For large-scale physical mapping of barley genes, we used the 22K Barley1 Affymetrix GeneChip to detect barley transcripts in wheat-barley chromosome addition lines harboring barley chromosome 2H, 3H, 4H, 5H, 6H, or 7H. In total, 5,543 barley transcripts were detected in the wheat-barley disomic chromosome addition lines, and they were physically mapped to six barley chromosomes based on their barley chromosome-specific detection patterns. Physical locations of these barley transcripts on each chromosome were validated by genomic PCR and *in silico* comparative mapping against the wheat and rice genomes.

We also used the Barley1 GeneChip to identify genes at the QTL for fungal resistance in barley. Deoxynivalenol (DON) is a trichothecene mycotoxin produced by *Fusarium graminearum* during infection and is an important quality-determining factor in harvested barley grain. Our objective was to identify genes associated with reduced DON accumulation. Using a pair of near-isogenic lines (NILs) carrying segregating alleles only at the QTL region on chromosome 3H associated with deoxynivalenol (DON) accumulation upon *F. graminearum* infection, abundance of 22,792 transcripts and their genetic association with DON accumulation were tested. We identified 7 barley transcripts showing differential abundance between the two NILs. By *in silico* comparative mapping, six genes were found on either barley chromosome 3H or

syntenous wheat or rice chromosomes. Our results show that detection of chromosome- or allele-specific transcripts using GeneChips in combination with *in silico* comparative mapping is an efficient tool to explore large-sized plant genomes to identify candidate genes.

We are currently conducting a similar study in wheat to identify genes for *Fusarium* head blight resistance located at the QTL on wheat chromosome 3BS. Candidate genes showing differential expression between two NILs carrying either resistant or susceptible alleles at the 3BS QTL were identified by the 66K Wheat Affymetrix GeneChip. In addition to transcriptome analysis in host plants, transcriptome change in *F. graminearum* through infection process is being investigated using the 18K *Fusarium* Affymetrix GeneChip. Simultaneous transcriptome investigation in plants and a fungal pathogen will facilitate understanding plant-microbe interaction and identification of defense response genes and potentially disease resistance genes.

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Publications

1. Cho S., Kumar J., Shultz J.L., Anupama K., Tefera F., F.J. Muehlbauer (2002) Mapping genes for double podding and other morphological traits in chickpea. EUPHYTICA 128 (2): 285-292.

2. **Cho S.**, Chen W., and FJ Muehlbauer (2004) Pathotype-specific Genetic Factors in Chickpea (*Cicer arietinum* L.) for Quantitative Resistance to Ascochyta Blight. *Theoretical and Applied Genetics* 109:733-739.
 3. **Cho S.** and F.J. Muehlbauer (2004) Genetic Effect of Differentially Regulated Fungal Response Genes on Resistance to Necrotrophic Fungal Pathogens in Chickpea (*Cicer arietinum* L.) *Physiological and Molecular Plant Pathology* 64:57-66.
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