Comparative analysis of transcripts associated to all-stage resistance and adult-plant resistance to stripe rust in wheat.

Tristan E. Coram [1], Xueling Huang [2], Matthew L. Settles [3], Gangming Zhan [2], Gina Brown-Guedira [1], and Xianming Chen [2,4].

[1] USDA–ARS, Plant Science Research Unit, Raleigh, NC 27606, USA; [2] Department of Plant Pathology, Washington State University, Pullman WA 99164-6430, USA; [3] Department of Molecular Biosciences, Washington State University, Pullman, WA 99164-4234, USA; and [4] USDA–ARS, Wheat Genetics, Quality, Physiology, and Disease Research Unit, Pullman, WA 99163, USA.

Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici*, is a destructive disease of wheat worldwide. Genetic resistance is the preferred method for controlling stripe rust, of which two major types are race-specific and race-nonspecific resistance. Race-specific resistance includes the qualitatively inherited all-stage resistance, controlled by single major resistance (*R*) genes. Conversely, adult-plant resistance is race nonspecific, inherited quantitatively, and durable. Previously, we characterized the gene-expression signatures involved in *Yr5*-controlled all-stage resistance and *Yr39*-controlled adult-plant resistance using the Affymetrix Wheat GeneChip. For this study, we designed and constructed custom oligonucleotide microarrays containing probes for the 116 and 207 transcripts that we had found important for the *Yr5* and *Yr39* resistance responses, respectively. We used this custom microarray to profile the resistance responses of eight wheat genotypes with all-stage resistance (*Yr1*, *Yr5*, *Yr7*, *Yr8*, *Yr9*, *Yr10*, *Yr15*, and *Yr17*) and five genotypes with adult-plant resistance (*Yr18*, *Yr29*, *Yr36*, *Yr39*, and the adult-plant resistance gene in the *Yr8* line). The aim of this analysis was to identify common and unique gene-expression signatures involved in the two types of resistance, which were used to infer information regarding the general pathways involved in all-stage resistance and adult-plant resistance.

Balance and dosage interdependence of homoeolog gene expression in polyploid wheat.

Jasdeep S. Mutti and Kulvinder S. Gill. Department of Crop and Soil Sciences, Washington State University, Pullman, WA 99164-6420, USA.

Gene duplication by polyploidy (homoeologues) or other means (paralogues) is a prominent feature of angiosperm evolution. We studied gene expression among three homoeologues of hexaploid wheat that evolved from a common progenitor about 3 million years ago (MYA) and came into a common nucleus at different times, ~0.5 and 0.01 MYA. Gene expression corresponding to each homoeologue was identified by sequence comparison of cultivar Chinese Spring ESTs, and the results were confirmed by SSCP analysis of RNA using nullisomic-tetrasomic lines. Of the 632 genes analyzed, 58% were expressed from all three homoeologues, 33% from two, and only 9% were expressed from one of the three homoeologues. The largest percentage of genes (14%) were expressed in the anthers and the least (7%) were expressed in pistils. The highest number of homoeologues/gene were expressed in the roots (1.72 out of three homoeologues), and the lowest number were expressed from the anthers (1.03 out of three homoeologues). In general, the proportion of expressed copies decreased with an increase in homoeologue copy number. The most significant observation was that homoeologues for 87% of the genes showed different expression patterns in different tissues and, thus, have likely evolved different gene expression controls. About 30% of the genes showed dosage dependence as the expression of homoeologues changed in response to changes in structural copy number.