Poster 10. Association of seed dormancy with red pericarp color in weedy rice arises from pleiotropy of a predicted transcription factor.

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Seed dormancy has been associated with grain color in wheat and rice, with the red-colored genotypes being more dormant than white-colored. However, whether the association arises from pleiotropy or linkage remains uncertain. We introduced a segment of chromosome harboring a cluster of QTL for seed dormancy (*qSD7-1*) and pericarp color (*qPC7*) from weedy into cultivated rice to clone and characterize their underlying gene(s). High-resolution mapping narrowed the QTL to the same locus of *Os07g11020* (a predicted transcription factor) and obtained a rare recombinant intragenic to the transcription factor. Sequence comparison for the 6,445-bp region identified 33 point mutations between alleles from the weedy and cultivated lines and that intragenic recombinant retains a segment of 2,000 bp from the weedy rice. A pair of dormant and nondormant isogenic lines was developed from the recombinant. These lines differed in seed dormancy, pericarp color (red vs. white), grain weight, and abscisic acid (ABA) content at about 10 days of seed development. The transcripts of the dormancy gene were detected in both seed and leaf tissues from the isogenic lines. Sequence comparison between the genomic DNA and the full-length cDNA identified eight exons and the 14-bp deletion in exon 7 that accounts for the molecular lesion for the aforementioned natural variation. We conclude that the above association in rice is a pleiotropic effect of the predicted transcription factor, and the dormancy allele cannot be used to improve white pericarp-colored varieties for resistance to preharvest sprouting. This research also suggests that the *qSD7-1* underlying gene may regulate the natural variation in seed dormancy and pericarp color by ABA- and pigment-related physiological pathways, respectively, and may have other effects on the traits expressed in the vegetative tissues.

Poster 11. GrainGenes: Serving the wheat community for 15 years, over a billion served.

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GrainGenes (graingenes.org) is a comprehensive database for molecular and genetic information on wheat, barley, rye, and oats. In addition, the GrainGenes project helps coördinate wheat community research projects, such as the International Triticeae EST Cooperative (ITEC), the mapping of ESTs in Chinese Spring deletion lines, development of the D-genome physical map, development of genome-specific SNPs, and analysis of Triticeae repeat sequences (TREP). The GrainGenes map collection comprises 165 mapping studies including genetic, consensus, and physical maps, viewable using the CMap comparative map display. Additional database tools are in development to build genotype, trait and QTL relationships for germ plasm to assist in wheat marker-assisted selection (Wheat CAP project, maswheat.ucdavis.edu). Other tools, such as preformatted Quick Queries, advanced SQL, and Batch Queries have been updated to aid user access to the database. The web log shows that 30,000 different people use GrainGenes per month. Most of you have not told us what you do not like about GrainGenes, either what data should be there that is not or questions about how to find what is there. Please speak up.

Poster 12. Influence of flanking sequences on transgene expression levels in the endosperm of transformed wheat.

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There is often no relationship between transgene copy number and expression levels in different transgenic plants transformed with the same DNA construct. We hypothesized that expression of the integrated DNA can be influenced