Exploring the functional roles of the Q gene homoeoalleles in wheat.

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The *Q* gene on chromosome 5A (*Q-A1*) has been referred to as a super gene in wheat, because it governs the free-threshing character and square spike phenotype. *Q* also pleiotropically affects many other traits associated with wheat development and domestication. The function of the *Q* homoeoalleles on chromosomes 5B (*q-B1*) and 5D (*q-D1*) is less understood. In this study, we further investigated the function of *Q-A1* through comparison of the wild type *Q-A1* allele with an EMS-induced *Q-A1*-knockout mutant in the hexaploid wheat cultivar Bobwhite. The phenotypic comparison confirmed the numerous pleiotropic effects of *Q-A1*. Relative quantitative-PCR (RQ-PCR) analysis revealed that the mutant allele, which has a premature stop codon, was transcribed at a lower level than the wild type. This result provided additional evidence that the amino acid at position 329 is important for homodimer formation, which may be a mechanism of self-regulation. We also initiated the functional analysis of the *q* homologs on chromosomes 5B and 5D. The genomic and cDNA sequences of *Q-A1*, *q-B1*, and *q-D1* share >90% similarity. Chinese Spring *q-B1* and *q-D1* deletion lines (5BL-14 and 5DL-5) had semispeltoid spikes instead of square spikes as observed in euploid Chinese Spiring. We developed a double deletion line lacking both *Q-A1* and *q-D1*, which exhibited more extreme speltoid spikes and tougher glumes compared to the single-gene deletion lines. In addition, alternatively spliced transcriptional variants were found for both *q-B1* and *q-D1* in spike tissues. Specific RQ-PCR assays were developed for each homoeoallele and their transcriptional variants, and the results suggested the presence of complex interactions among the homoeoalleles. This study demonstrated that the *q* homoeoalleles on 5B and 5D contributed to the suppression of speltoid characters and glume toughness but to a lesser degree than does the *Q-A1* allele on 5A. The mutation in *q-A1* that gave rise to *Q-A1* played a key role in the modern wheat evolution.

The Brachypodium genome structure and its potential as a model for wheat.

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Research in the grass crops, including wheat, has suffered from the lack of an appropriate model system and, thus, have not benefited from the potentials of such models similar to how *Arabidopsis* has revolutionized general plant biology. Although *Arabidopsis* has application to the grasses in areas of basic plant biology, *Arabidopsis* is a dicot, and a more appropriate tool for the dicots and less so for the monocots such as the grasses. Rice was originally proposed to fill this need for the grasses, but for a number of reasons, rice has not proven sufficient for all grasses. For example, rice has a longer life-cycle, is tropic/semitropic, is difficult to achieve flowering in most regions of the U.S., and is larger than appropriate for a model. In place of rice, the grass *Brachypodium distachyon* has been proposed as a more appropriate model system. Among its attributes, *Brachypodium* has an 8–10 week life cycle, a small genome (~320 Mb), can be transformed by *Agrobacterium* at a high efficiency, and is in the process of having the complete genome sequenced. As an added bonus for the Triticeae, taxonomic relatedness puts *Brachypodium* within a sibling tribe to the Triticeae and, thus, far closer in evolutionary distance to wheat than is rice. An overview will be given of what is known of the structure of the *Brachypodium* genome, an update on progress at developing tools necessary for *Brachypodium* to serve as a model system, the available results on how *Brachypodium* DNA sequences compare with available wheat genome information, and speculations on how *Brachypodium* will assist wheat research.