

IN BRIEF

Genome Dominance and Interaction at the Gene Expression Level in Allohexaploid Wheat

Polyploidy is common in plants and confers advantages through a number of mechanisms, including fixation of heterosis (Comai, 2005). Commonly known as hybrid vigor, heterosis is a widespread phenomenon whereby hybrid plants outperform their parental lines. This effect can become fixed by polyploidization, which overcomes sterility in a hybrid. Understanding the molecular basis of heterosis is important both for its application in crop improvement and for understanding plant evolution and adaptation.

Allohexaploid common wheat (*Triticum aestivum*) arose as a hybrid between allotetraploid *Triticum turgidum* and diploid *Aegilops tauschii* and is known to out-compete its progenitors in a number of traits, including broader adaptability to various conditions and enhanced resistance to biotic and abiotic stresses. It is also possible to create newly synthesized wheat allopolyploids, as hybridizations between species may be followed by spontaneous chromosome doubling. These nascent allohexaploid wheat lines, which also show heterosis and adaptive traits (see figure), may to some extent recapitulate the original genetic status of ancient wheat hybrids. Li et al. (2014) apply this notion to an analysis of nascent allohexaploid wheat in comparison with its progenitor lines and common wheat.

The authors focus on the concept of genome expression-level dominance (ELD) in the early, heterotic stages of a new polyploid, which is defined as genes in polyploid progeny showing expression equal to one of the parents and not the other. This is contrasted with additivity (expression in progeny equals the average “mid-parent value” of progenitors) and nonadditivity (expression in progeny differs from the average and is higher or lower than either progenitor).

Many allopolyploid plants exhibit genomic asymmetry or genome dominance,



Nascent synthetic allohexaploid wheat (6x) compared with progenitors *T. turgidum* (4x) and *Ae. tauschii* (2x). Shown are 7-d-old seedlings (left), heading stage spikes (top right), and developing seed (bottom right). (Adapted from Li et al. [2014], Figure 1.)

where there is differential subgenome control of morphological traits. For example, in *T. turgidum*, some developmental traits are controlled by the A genome, whereas adaptive traits, such as responses to stress and disease, are controlled by the B genome. This is thought to arise by mechanisms such as intergenomic suppression of gene activity due to incompatible regulatory elements, chromatin modifications, or suppression of genes near transposable elements (Feldman et al., 2012). Recent work suggests that genome dominance is also present in natural hexaploid wheat (Akhunov et al., 2013; Pont et al., 2013).

Li et al. (2014) find that a high proportion of genes in nascent allohexaploid wheat exhibit parental ELD, with genes showing ELD similar to the *T. turgidum* progenitor more likely to be associated with develop-

ment, while those showing ELD similar to *Ae. tauschii* tending to be associated with adaptation, such as stress responses and photoperiod adaptability. This suggests that ELD in nascent polyploids may precede and give rise to genome dominance in later stages of evolution. An analysis of microRNA and small interfering RNA density suggested that small RNA-mediated regulation may influence homoeolog expression levels and contribute to heterosis in the nascent hexaploid wheat. This work provides insight into molecular mechanisms underlying heterosis and will motivate further experimentation on specific candidate genes.

Nancy A. Eckardt
Senior Features Editor
neckardt@aspb.org

ORCID ID: 0000-0003-1658-1412

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