

Wheat: A challenging genome to study.

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The hexaploid nature ($2n=2x=42$) and large genome size ($C=17,000$ Mb) of wheat make genomic analyses in this crop challenging. Nevertheless, a large number of resources have been built over the past five years, including BAC libraries of diploid, tetraploid and hexaploid wheats, more than 1 million expressed sequenced tags, and partial physical maps of the *Ae. tauschii* genome and of selected chromosomes of hexaploid wheat. Large-scale mapping of ESTs, and sequence analysis of regions carrying traits of interest and of randomly selected BAC clones has greatly increased our understanding of the organization of the wheat genome. The next big challenge will be to sequence the entire wheat genome. The development in recent years of new sequencing technologies has made sequencing the 17,000 Mb wheat genome an attainable goal. The short sequence reads associated with these techniques, however, make sequence assembly extremely challenging. My presentation will contain information on our current knowledge of the wheat genome, and some food for thought on strategies for wheat genome sequencing.

Wheat domestication and genetic diversity.

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Domestication of diploid einkorn wheat and tetraploid emmer wheat (*Triticum turgidum* subsp. *dicoccoides*, genomes AABB) was one of the key events during the emergence of agriculture in southwestern Asia. Emmer was the source of durum wheat and the tetraploid ancestor of hexaploid common wheat. Although einkorn wheat may have been domesticated in several places, genetic evidence based on single-locus and multilocus genotypes of restriction fragment length polymorphism at 131 loci suggest that domesticated emmer and the rest of the tetraploid wheats have a monophyletic origin. Emmer was domesticated west of Diyarbakir in southeastern Turkey. Subsequently, gene flow from wild emmer to domesticated emmer occurred across the entire distribution of wild emmer and enhanced its genetic diversity. This process was important particularly in southern Levant. Consequently, the Mediterranean emmer population has the highest genetic diversity of all domesticated emmer populations. Durum is closely related to the Mediterranean and Ethiopian domesticated emmer populations and probably originated in the eastern Mediterranean. Common wheat originated in Transcaucasia. Gene flow from domesticated tetraploid wheat and wild emmer wheat greatly enhanced genetic diversity in the A and B genomes. Gene flow from *Ae. tauschii* to the D genome was sporadic, and the D genome shows low gene diversity. Genetic diversity was estimated in 942 genes in one, two, or all three *T. aestivum* genomes, and the loci were mapped in *Ae. tauschii*. Genetic diversity varied among *T. aestivum* chromosomes in the A, B, and D genomes, the greatest diversity is in chromosomes 1A, 1B, and 2D, and the lowest in 4A, 4B, and 5D. Selection during domestication of tetraploid wheat or evolution of hexaploid wheat is principally responsible for variation in diversity among wheat chromosomes.