

# Workshop Report

## **A Workshop Report on Wheat Genome Sequencing: International Genome Research on Wheat Consortium**

**Bikram S. Gill,<sup>\*,1</sup> Rudi Appels,<sup>†</sup> Anna-Maria Botha-Oberholster,<sup>‡</sup> C. Robin Buell,<sup>§</sup>  
Jeffrey L. Bennetzen,<sup>¶</sup> Boulos Chalhoub,<sup>&</sup> Forrest Chumley,<sup>\*\*</sup> Jan Dvořák,<sup>††</sup>  
Masaru Iwanaga,<sup>‡‡</sup> Beat Keller,<sup>§§</sup> Wanlong Li,<sup>\*</sup> W. Richard McCombie,<sup>¶¶&</sup>**

Figure 1.—Grasses as a single genetic system and recent coevolutionary history of cereals and

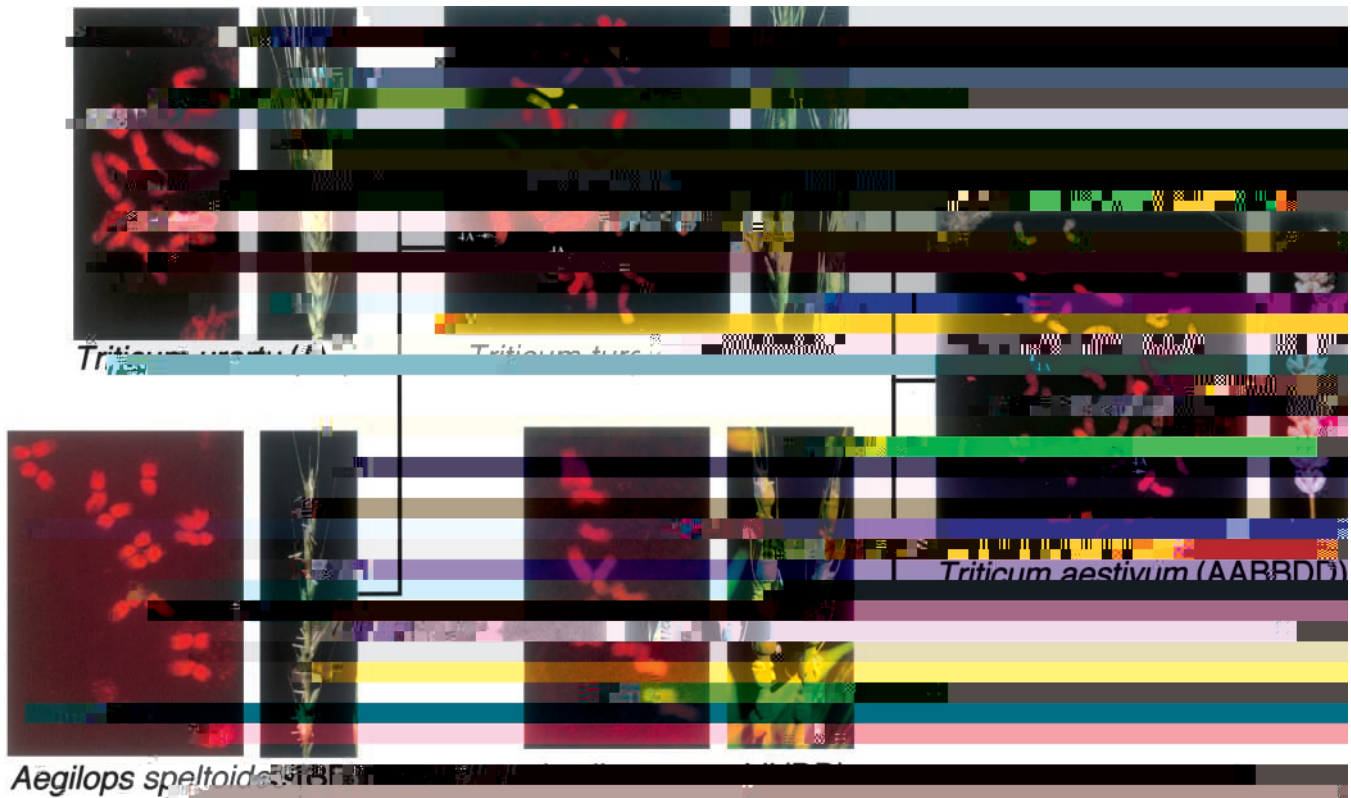


Figure 2.—By 1915, botanists had described three classes of cultivated wheats; the one-seeded monococcum ( $2x$ ), the two-seeded emmer ( $4x$ ), and the dinkel ( $6x$ ). The one-seeded wild relative of monococcum was reported in Greece and Anatolia between 1834 and 1884. The two-seeded wild relative of emmer was discovered by Aaronsohn in 1910 in Lebanon, Syria, Jordan, and Israel. Therefore, it was well accepted, as Candolle had suggested in 1886, that since wild wheats grow in the Euphrates basin, wheat cultivation must have originated there. Between 1918 and 1925, T. Sakamura and his student H. Kihara at Hokkaido University in Japan and K. Sax at Harvard University reported their classic studies on the genetic architecture of the three groups













- elimination of low-copy DNA sequences in polyploid wheat: a possible mechanism for differentiation of homoeologous chromosomes. *Genetics* **147**: 1381–1387.
- Feng, Q., Y. Zhang, P. Hao, S. Wang, G. Fu *et al.*, 2002 Sequence
- Rapid reorganization of resistance gene homologues in cereal genomes. *Proc. Natl. Acad. Sci. USA* **95**: 370–375.
- Li, W., and B. S. Gill, 2002 The colinearity of the *Sh2/A1* orthologous region in rice sorghum and maize is interrupted and accom-

- cloning of individual chromosome from bread wheat. *Plant J.* **39**: 960–968.
- Sandhu, D., J. A. Chanpoux, S. N. Bondareva and K. S. Gill, 2001 Identification and physical localization of useful genes and markers to a major gene-rich region on wheat group *1S* chromosomes. *S. Tanksley*, 2002 Deductions about the number, organization, and evolution of genes in the tomato genome based on analysis of a large expressed sequence tag collection and selective genomic sequencing. *Plant Cell* **14**: 1441–1456.
- Venter, J. C., M. D. Adams, E. W. Myers, P. W. Li, R. J. Mural *et al.*, 2001 The sequence of the human genome. *Science* **291**: