

Nondestructive, high-throughput phenotyping to study cereals under stress conditions.**Bettina Berger**¹ and M. Tester^{1,2}.

¹ The Plant Accelerator, The University of Adelaide and ² Australian Centre for Plant Functional Genomics, Waite Campus, Urrbrae, Australia.

Genetics and genomics are powerful tools for gene discovery. However, the ability to phenotype at high-throughput plant growth and function is forming a bottleneck in discovering the role of genetic loci in plants. Increasingly, efficient transgenic technologies are generating large numbers of GM crop plants; and the genotyping of mapping and mutant populations is now highly efficient. However, the ability to quantitatively phenotype these populations is limiting progress in plant science. The increasing power of digital imaging and computational technologies offers the opportunity to relieve this phenotyping bottleneck. The Plant Accelerator[®] is a new, 4,500-m² growth facility that provides -omic-scale shoot phenotyping of large populations of plants using automated plant handling and digital imaging. Current projects use the phenotyping capacity to analyze cereals under various stress conditions, including water deficit and salinity. First results and the experimental approach taken will be discussed.

POSTER ABSTRACTS***Poster 1. The International Wheat Genome Sequencing Consortium (IWGSC).***

The International Wheat Genome Sequencing Consortium. IWGSC, 5207 Wyoming Road, Bethesda, MD 20816, USA.

Bread wheat, the staple food for 35% of the world's population and the most widely produced crop, is one of the most important crop species. Genomics offers powerful tools for understanding the molecular basis of phenotypic variation as well as accelerating gene cloning, marker-assisted selection, and more efficient exploitation of genetic diversity. In 2005, a group of growers, breeders, and plant scientists launched the International Wheat Genome Sequencing Consortium (IWGSC) with the goal of securing a high quality, reference sequence of the bread wheat genome. The IWGSC facilitates and coordinates research projects and funding efforts at the national and international levels; develops and supports the design of research proposals; provides a framework for the establishment of common guidelines, protocols, and resources; and organizes scientific meetings and workshops. The IWGSC is governed by six co-chairs, a Coordinating Committee, and an executive director. General membership is open to any individual, laboratory, or entity with an active interest in meeting IWGSC objectives. The mission, goals, organizational structure, projects, and online membership registration are available at <http://www.wheatgenome.org>. IWGSC activities are guided by a milestone-based strategy coupled with short- and long-term roadmaps designed to provide breeders access to an increasing array of tools and resources without having to wait for the completed sequence. To reduce the complexity of the allohexaploid, highly repetitive, 17-Gb bread wheat genome, the IWGSC follows a chromosome-specific approach to develop physical maps, low coverage sequencing, and high quality sequencing of the Minimum Tiling Paths before moving towards a gold standard reference sequence. Physical maps have been completed or are underway for all 21 chromosomes of the reference cultivar, Chinese Spring. To facilitate anchoring, marker development, and to gain a first insight into the gene space composition, the IWGSC launched an internationally coordinated survey sequencing initiative that is providing breeders with survey sequences and the virtual gene order for all 21 chromosomes. High quality, BAC-by-BAC sequencing of chromosome 3B was completed in 2011 and sequencing of other chromosomes is under way. IWGSC activities and results will be presented.

Poster 2. The IWGSC Chromosome-Based Survey Sequencing Initiative.

The International Wheat Genome Sequencing Consortium. IWGSC, 5207 Wyoming Road, Bethesda, MD 20816, USA.

Applying advanced genomics to wheat breeding will play a central role in securing affordable and nutritious food. Bread wheat (*Triticum aestivum*) has one of the largest (~17 Gb) and most complex (allohexaploid, 6n=42, AABBDD) genomes. Although genome size varies in grasses, gene order, generally, is conserved along large chromosomal segments enabling comparative methods between related species. The IWGSC aims to establish a high quality, reference sequence