

DEVELOPING RESOURCES FOR TRITICEAE GENOMICS

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Genetic variation is key to breeding improved crops, and next generation sequencing (NGS) enables us to generate draft reference genome assemblies for species with large genomes relatively quickly and cheaply, and to identify genetic variants by resequencing individuals from populations or crosses.

As part of the International Wheat Genome Sequencing Consortium (IWGSC) we have been sequencing and assembling a draft genome of hexaploid bread wheat (*Triticum aestivum* cv. Chinese Spring) using NGS technologies. This work is complemented by the design of an exome capture based on tetraploid wheat, which can be used in wheat resequencing experiments (in collaboration with the John Innes Centre and UC Davis). The availability of reference genomes and associated variants through publicly-accessible databases and genome browsers will enhance Triticeae research and complement existing resources for the improvement of these important crops.