Sequence-based assembly of wheat chromosome 7A and comparison of its features to 7A from diploid progenitors

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This presentation provides a report on the sequencing the genome of chromosome 7A from wheat. The sequencing of chromosome 7A project (GRDC/BioPlatforms Australia-funded) has established the physical assembly of BAC clones prepared from flow sorted ditelocentric chromosomes. The Illumina Hiseq sequencing of BAC pools (AGRF) comprise physical contigs of 1-2 Mb genomic DNA which were assembled using the SNAPshot DNA fingerprinting of individual BACs with 5 restriction endonucleases. Extensive anchoring of the sequence assemblies was achieved initially using the 9K and 90K SNP chip-based molecular genetic maps and currently using the high-resolution map of chromosome 7A in the MAGIC population.

Although the assembly still needs refinement through additional sequencing of long insert mate pair libraries, comparative analyses have shown that the assembly is robust and capable of providing new insights into agronomically important loci. Some specific examples will be discussed which utilize an extensive in-house RNA-seq transcriptome for characterizing the genes in regions of interest.