of the wheat genome (cv. Chinese Spring) that is anchored to the genetic and phenotypic maps to provide high resolution linkages between the traits and the underlying variations in sequence and polymorphisms. A first goal has been to obtain physical maps of the individual chromosomes/arms. To anchor the physical contigs, survey sequences were achieved using NGS technologies for a majority of the Chinese Spring chromosomes. The IWGSC then launched a short-term initiative to provide survey sequences of all 21 chromosomes. Sponsored by industry and government partners, the aim is to generate sequence and virtual order for most wheat genes. The sequences generated for each chromosome arm are assembled using the latest software tools. A first pass annotation is implemented over the draft assembly sequences where comparative genomics and colinearity with other grass genomes is used to derive a virtual gene order with an account of non-syntenic genes and pseudogenes. As sequences are generated independently for each chromosome, a second aim of this project is to characterize genomic variation between gene homoeologues (ie orthologous genes placed in different subgenomes), regulatory elements, and repeat content. An update of this initiative will be presented.

Poster 3. TriAnnot: a high performance pipeline for the automated structural and functional annotation of plant genomes - new developments.

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A versatile, easy-to-use, online, automated annotation pipeline, TriAnnot (Leroy et al. 2012. Frontiers in Plant Sciences 3:1-14; http://www.clermont.inra.fr/triannot), has been developed under the umbrella of the International Wheat Genome Sequencing Consortium, the TriticeaeGenome, and 3BSEQ projects to obtain a reference sequence of the bread wheat genome. Its modular architecture allows for the annotation and masking of transposable elements, the structural and functional annotation of protein-coding genes with an evidence-based quality indexing, and identification of conserved noncoding sequences and molecular markers. The performance of TriAnnot was evaluated in terms of sensitivity and specificity using curated reference sequence sets from rice (IRGSP build5, August 2010) and wheat (Choulet et al. 2010. Plant Cell 22:1686-1701). In less than 8 hours, TriAnnot was able to predict more than 83% of the 3,748 CDS from rice chromosome 1 with a fitness of 67.4%. On a set of 12 reference Mb-sized contigs from wheat chromosome 3B, TriAnnot predicted and annotated 93.3% of the genes among which 54% were perfectly identified in accordance with the reference annotation. It also allowed the curation of 12 genes based on new biological evidences, increasing the percentage of perfect gene predictions to 63%. TriAnnot systematically showed a higher fitness than other annotation pipelines that are not improved for wheat. The TriAnnot pipeline is parallelized on a 712 CPU computing cluster that can run a 1-Gb sequence annotation in 26 hours. It is accessible through a web interface for small-scale analyses and/or through a server for large scale annotations. For the later, the pipeline is launched automatically using a PERL script. After completion, the structural and functional annotation can be viewed through an online GBrowse and can be manually curated using Artemis and GenomeView graphical editors. As it is easily adaptable to the annotation of other plant genomes, TriAnnot is currently improved for other plant genomes annotations such as barley, rice, maize, and oak species, and should become a useful resource for the annotation of large and complex genomes in the future. Release 3.5 is on-line since January 2012, and a new release 3.6 is underway.

Poster 4. Current status of physical mapping on wheat chromosome 6B.

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For the purpose of better understanding the genome structure in wheat and accelerating the development of DNA markers for gene isolations and future breeding, the Japanese research consortium, as a member of IWGSC, is now conducting a project for the physical mapping and genomic sequencing of Chinese Spring chromosome 6B (914 Mb). With a