Poster 13. De novo assembly and characterization of wheat root transcriptome.

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Root systems primarily provide plants water, nutrients and anchorage. While much progress has been made in understanding root development and growth in the model plant *Arabidopsis*, little is known in most crops such as wheat (*Triticum aestivum* L.). As the first step of wheat root genomics and genetics, we are sequencing, assembling, and annotating the wheat root transcriptome in reference cultivar Chinese Spring (CS). Messenger RNA was purified from the root tips at 4 d after germination and sequenced using 454/Roche Titanium platform. A total of 818,038 quality reads were assembled into 24,492 contigs with average contig length of 752 bp, N50 of 798, and a total assembly size of 16.2 Mbp using Newbler. These 24,292 Newbler-contigs were further assembled with 26,849 CS root ESTs deposited in NCBI using the CAP3 program. This hybrid assembly generated 27,852 transcripts (>100 bp) with average transcript length of 730.75 bp, N50 of 771, and a total assembly of 20.36 Mbp. Approximately 87% of the transcripts had BLASTX hits in NCBI nr protein database, of which 78% of the total transcripts were assigned with gene ontology (GO) terms and 18% were assigned with enzyme commission (EC) annotation. Of the 19,196 transcripts with GO assignments, top eight GO classes identified in biological process include cellular process (34.85%), metabolic process (34.3%), localization (6.26%), response to stimulus (5.37%), cellular component organization (5.34%), biological regulation (4.84%), cellular component biogenesis (4.38%), and signaling (1.71%). Important GO classes identified in molecular function include nucleotide binding (3.17%), transcription factor (0.5%), sequence specific transcription factors (0.17%), DNA binding (1.91%), transporter activity (1.28%), kinase activity (0.88%), and receptors (0.22%). Although the majority of the root transcripts also were found in the aboveground organs, putative root-specific transcripts account for ~12% of the assembled root transcriptome. More than 9,000 SSRs were identified comprising di- (11.48%), tri- (57.75%), tetra- (19.37%), penta- (5.35%), and hexa-nucleotide (6.05%) motifs. In addition, a very small fraction of the root transcriptome was found to contain transposable elements, mainly MITES. Assembly and annotation of wheat root transcriptome will lay a foundation for molecular biology to understand wheat root development and improve wheat tolerance to soil-derived abiotic stresses.

Poster 14. BREEDWHEAT: Breeding for economically and environmentally sustainable wheat varieties: an integrated approach from genomics to selection.

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Wheat represents a major renewable resource for food, feed, and industrial materials and is the most widely grown crop worldwide. With its high-yielding wheat production (~70 q/ha), France is a major producer and exporter (fifth producer and exporter) and wheat production contributes significantly to the French economy with a positive balance of more than 4 billion €. To face the challenge of delivering safe, high-quality, and health-promoting food and feed in an economical, environmentally sensitive, and sustainable manner while maintaining yield and stability across environments affected differently by climatic change, a paradigm shift is needed in wheat breeding. BREEDWHEAT is conceived to support the competitiveness of the French breeding sector as well as answer the societal demand for sustainability, quality, and safety. BREEDWHEAT gathers the best public and private partners (26) in wheat research and breeding in France to ensure that the knowledge, resources, and methods resulting from the project are translated rapidly into products and varieties. In an unprecedented effort, BREEDWHEAT proposes to break barriers that have thwarted the translation of knowledge and molecular resources into breeding as well as the exploitation of genetic resources to enlarge the genetic diversity of the wheat gene pool. BREEDWHEAT will not only provide a breakthrough in technological development of markers and phenotypes, but it uniquely will integrate high throughput genotyping, phenotyping, and modeling studies to decipher the molecular and ecophysiological basis of important traits. This long-term project (9 years) will include sequencing of a wheat chromosome (1B), detection of new structural polymorphisms, large-scale SNP production, genetic and physical mapping of those SNPs, 48,000 phenotyping trials, and the generation of 33 million genotyping data points for association genetics studies. Moreover, 5,000 wheat lines from INRA genetic stocks will be extensively characterized and used to identify new alleles to support a pre-breeding program aimed at developing varieties that can be directly exploited by the breeders. The efficiency and economic impact of various selection schemes will be assessed in a farm-scale breeding program. Finally, a robust bioinformatics platform enabling efficient association analyses and breeder friendly access to the data will also be established.