software packages. In the first instance, we processed the raw reads by filtering them for low quality and then proceed to map them to the latest barley genome reference using Bowtie (Langmead et al. 2009) and Tophat (Trapnell et al. 2009) to consider spliced reads. These mapped reads were used for a downstream expression analysis study using the Cufflinks packages (Cufflinks, Cuffcompare, and Cuffdiff) (Trapnell et al. 2010) and R bioconductor packages (DESeq, NOISeq, and edgeR) (Anders and Huber 2010; Tarazona et al. 2011; Robinson et al. 2010). A comparison based on the results of these approaches indicated differences in the sets of genes reported with significant fold changes. Identification of the biological function of the nonoverlapping genes produced by the different analyses has been undertaken to explore the impact of using any one of these analyses in isolation.

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Poster 12. A triticale (x Triticosecale Wittm.) reference transcriptome.

Michele Frick [1], Yong Xu [1], Carolyn Penniket [1], Laurian S. Robert [2], Linda J. Harris [2], Frances Tran [2], Danielle Schneiderman [2], Patrick J. Gulick [3], and André Laroche [1].

[1] Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, AB, Canada, T1J 4B1; [2] Agriculture and Agri-Food Canada, Eastern Cereal & Oilseed Research Centre, Ottawa, ON, Canada, K1A 0C6; and [3] Department of Biology, Concordia University, 7141 Sherbrooke W, Montréal, QC, Canada H4B 1R6.

Triticale produces high biomass and grain yields and is resistant to many abiotic and biotic stresses. Hexaploid triticale (AABBRR) has a large genome similar to that of common wheat (AABBDD), and possesses large numbers of repeated sequences, making it difficult to sequence. Little is known about coordination of gene expression of rye and wheat genomes in this interspecific hybrid but understanding this interaction is crucial for improving its agronomic traits. We have produced cDNAs from four different triticale lines/cultivars; AC Certa, Alta, line 797, and line 1308, from different tissues including leaf, stem, and reproductive tissues at different developmental stages or exposed to different abiotic treatments (salt and drought). Reads were cleaned, and we assembled 6.7 M 454 reads and 276. 3 M Illumina reads together and identified, using a stringent assembly protocol, a total of 72,218 contigs with N50 and N90 values of 1,658 and 588 bp, respectively. Of these 72,218 contigs, 50,524 transcripts appeared to be full length after comparison to the sequences obtained from the four monocot sequenced genomes (rice, maize, sorghum and Brachypodium). The noncoding sequences appear to represent long, noncoding cDNAs, short ORFs, and precursors of microRNAs. At least 31,230 of these transcripts appear to be translated. In addition, we determined that approximately 20% of the genes had transcripts with alternative splice variants. Furthermore, nearly 60% of these transcripts were electronically annotated. Compared to our previous results with development of a rye transcriptome, the transcripts corresponding to the R genome in triticale were segregated from the sequences originating from genome A and B. A detailed molecular characterization of the transcripts into different functional groups as well differential expression of the rye and wheat transcripts under control and stressed conditions will be presented. We also will report on the utilization of fractionated DNA to further extend the 5' region of transcripts. Therefore, using next generation sequencing to de novo assemble a comprehensive reference transcriptome for triticale was possible. This approach would be useful for species with large, unsequenced genomes.