Oral Communication Abstract – SY28

DURUM WHEAT PAN-TRANSCRIPTOME AS A BRIDGE TO UNDERSTAND TETRAPLOID AND HEXAPLOID WHEAT GENE FUNCTION AND EVOLUTION

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The current study presents the transcriptome analysis of 13 elite durum wheat varieties representatives of the worldwide cultivated germplasm. cDNA libraries were produced from roots, seedling leaves and developing grains to study the gene expression pattern based on the reference genome sequence assembly of durum wheat cv. Svevo. As a result, 75.0, 70.5 and 74.5% of highconfidence Svevo genes were expressed across varieties in grain, leaf and root, respectively. Principal Component Analysis (PCA) analysis showed a gene expression clustering lead by tissues (leaves, grains and roots) and varieties accounting for 33.0% variance. We identified the differentially up- and down-regulated gene clusters based on tissues and varieties with 510 genes contributing to major variation pattern. Their functional enrichment analysis for three Gene Ontology (GO) terms showed that differentially expressed genes were significantly enriched in transport, kinase activity, binding, enzyme activity and protein metabolism. Variance expression analysis projected on the Svevo assembly revealed a trend towards increased expression variation in the distal chromosome regions across chromosomes. Clustering the gene expression and the cultivar's expression profiles evidenced several gene expression patterns related to the co-ancestry among cultivars, particularly for the grain, separating North American/old from Italian/CIMMYT varieties. The expression pattern database could be useful to identify genes regulated by eQTL, find the association between genotypic and phenotypic variation and to elucidate the function of candidate genes. Further, using the transcriptome of 13 varieties in relation to bread wheat reference genome (cv. Chinese Spring IWGSC RefSeq) we aimed to explore the gene loss/deletion during the polyploidisation events. The durum cultivar-specific reads that could not be mapped on Svevo (4-30% referred to the Svevo Illumina sequencing data) were successfully mapped to Chinese Spring. Unmapped reads were found in specific and narrow chromosome regions preferentially located on chr. 1A, 1B, 4A and 6B, suggesting the presence of commonalities between durum and bread wheat genomes. Reads that could not be mapped to Chinese Spring and 10 wheat genomes were mapped on Svevo, with the majority found on chr. 1A, 4A, 7A and 6B. Moreover, with the availability of the 10+ Wheat Genomes Project, which include cultivars that represent genetic diversity, we could infer strong allele fixation events (allopolyploidisation bottleneck).