Alagu Manickavelu et al., Transcriptomics, 2:2
http://dx.doi.org/10.4172/2329-8936.S1.003

OMICS International
conferenceseries.com

International Conference on
Transcriptomics

July 27-29, 2015 Orlando, USA

Comprehensive analysis and utilization of Hexaploid wheat transcriptome

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Developing transcriptomic resource for 16 Gb hexaploid wheat is very important same time a challenging task. About 1 million Expressed Sequence Tag (EST) sequences comprising 125.3 Mb nucleotides were accreted from 51 cDNA libraries constructed from a variety of tissues and organs under a range of conditions, including abiotic stresses and pathogen challenges in common wheat (Triticum aestivum). Expressed sequence tags were assembled with stringent parameters after processing within build scripts, resulting in 37 138 contigs and 215 199 singlets. In the assembled sequences, 10.6% presented no matches with existing sequences in public databases. Functional characterization of wheat unigenes by gene ontology annotation, mining transcription factors, full-length cDNA, and miRNA targeting sites were carried out.A bioinformatics strategy was developed to discover single-nucleotide polymorphisms (SNPs) within ourlarge EST resource and reported the SNPs between and within (homoeologous) cultivars. Digital gene expression was performed to find the tissue-specific gene expression, and correspondence analysis was executed to identify common and specific gene expression by selecting four biotic stress-related libraries. For effective utilization, the ESTs were used to design custom microarray (GPL9805). Further the custom array was deputed to carry out the global gene expression of wheat genotypes against *Fusarium graminarium*. In microarray study, wheat temporal molecular response mechanism against this pathogen, gene expression analysis by using microarray was carried out in three genotypes (Japanese landrace cv. Nobeokabouzu-komugi - highly resistant; Chinese cv. Sumai 3 - resistant; Australian cv. Gamenya - susceptible) at two time points which spikes infected by *Fusarium graminearum*. Highest number of genes was up-regulated in Nobeokabouzu-komugi followed by Sumai 3 and minimum expression in Gamenya at 3 days after inoculated (dai) spikelets. Whereas at 7 dai, Sumai 3 expressed more genes compared to others. By systematic data analysis, the expressed genes were classified into three molecular response categories: Systemic defense-related genes, local defense-related genes and detoxification involved genes. In Nobeokabouzu-komugi, high expression of detoxification and systemic defense-related genes were identified at the early stage of infection, which is completely different from other resistant genotype, Sumai 3, containing mostly local defense genes. In Gamenya the expression of all three gene categories were minimized.The difference of these molecular responses with respect to time points confirmed the genotype variation. First time we reported the genes expressed in the FHB highly resistantcv. Nobeokabouzu-komugi and the possible underlying molecular mechanism. Overall, our effort of wheat transcriptome is vital for future research, especially in the sequencing era.

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