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Small Millets Transcriptomics

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Editorial

With the advent of Next-generation sequencing and bioinformatic tools, gene expression studies have changed dramatically. Whole transcriptome studies are providing valuable resources for generating molecular markers like microsatellites and single-nucleotide polymorphisms and candidate genes. Transcriptome sequencing or RNA-Seq becomes more relevant in cases where whole-genome sequencing is not affordable. It provides cost-effective, functionally relevant information and generation of huge number of genomic resources in a reasonable time as compared to traditional approaches. The resulting information may be useful to address areas like differential gene expression, isoforms or allele-specific expression, characterization of regulatory elements, alternative splicing, RNA editing, population genetics and system biology etc.

Small millets are nutritionally rich, hardy and subsistence crops and gaining importance because of their potential role in nutritional food security and health benefits. Among small millets transcriptomic studies are available in finger millet (*Eleusine coracana* L. Gaertn.) [1-3] and foxtail millet (*Setaria italica*) [4]. There are other small millets like little millet (*Panicum sumatrense*), kodo millet (*Paspalum scrobiculatum* L.) and barnyard millet (*Echinochloa frumentacea*) etc. which are mainly cultivated in India and meager in genomic resources. Being future food security crops there is an urgent need to enrich the genomic resources of these crops. Our laboratory is involved in the generation of genomic resources in small millets. Three Bio-Projects have been submitted to NCBI on leaf transcriptomes viz. finger millet (BioProject ID: PRJNA268401), kodo millet (BioProject ID: PRJNA278353) and little millet (Bioproject ID: PRJNA267462). Transcriptome profiling of leaf samples of two finger millet cultivars (Blast resistant: GPU 28; Blast susceptible; PR 202) generated a total of 1,07,323 transcripts. Further, 56,404 Unigenes were discovered and their length ranged from 301bp to 13.1Kb, with an average length of 1,095 bp and N50 equal to 1735 bp. Differential gene expression analysis revealed TFs like WRKY transcription factor, kinases, disease resistance protein, cytochrome P450 etc. among the differentially expressed genes. A total of 12,510 repeat containing sequences were identified from the transcriptome data and finally 3,883 EST-SSR primer pairs were designed in finger millet (unpublished). Similarly, leaf transcriptome of variety OLM-203 generated 3,84,34,248 processed paired end reads and assembled in to 25,213 Unigenes with an average length of 904 bp and N50 value of 1176. Out of 25,213 Unigenes, 3,443 were assigned 123 KEGG metabolic pathways. From 25,213 Unigenes, 1576 non redundant EST-SSR primer pairs were designed (unpublished). Enormous transcriptome data generated in the form of candidate genes or molecular markers in these small millets would help in future genetic and genomic studies and would fasten the improvement of these less studied but nutritionally rich and sustainable crops.

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