

Insights of Transcriptomic Study of Tea

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Keywords: *Camellia sinensis*; Next-generation sequencing; RNA-seq; Suppression subtractive hybridization

Commentary

Tea (*Camellia sinensis* (L.) O. Kuntze), an evergreen cash crop, is indigenous to Indo-China region [1]. These perennial shrubs intermittently encounter versatile stresses that impinge on production. However, tea consumption is escalating due to cheaper valuation. Hence, increased production entails appliance of advanced research and technological implications [2]. Concurrently, complex life cycle and out-breeding nature of tea poses several inadequacies for genetic improvement. Abolition of winter dormancy, quicker flushes, and faster germination demands deliberation. Incidentally, efficacy of DNA based markers for molecular or genetic characterization has been exploited. Though, genome sequencing and advanced molecular approaches have made possible genome-wide analysis of changes molecular expression, creating the opportunity for studying biological processes. Nevertheless, solitary technology as a 'stand-alone' cannot be adequate for gaining a comprehensive understanding [3]. Drought tolerance is a preferred criterion for tea and identification of differentially expressed gene profiles of tender roots was perpetrated by forward suppression subtractive hybridization (SSH) library. Upon generation of expressed sequence tags putative drought-responsive genes were identified that included candidate genes of ubiquitin-proteasome, glutathione metabolism and sugar metabolism pathways and several transcription factors [4]. Thus, SSH is crucial to learn drought-tolerance mechanism apart from dormancy that alters expression of genes. Sequencing and gene ontology analysis identified valuable public resource and preliminary insights into the molecular mechanisms of bud dormancy regulation [5]. *Helopeltis infestation*, a major menace for tea, because it incurs massive crop loss. Transcriptome analysis revealed alteration of flavonoid biosynthesis, purine and formate metabolism, jasmonic acid biosynthesis and signaling paving the way for crop improvement through transgenic approaches [6]. Similarly, endeavor to raise a blister blight resistant cultivar by identification of inducible defense-related transcripts in tea revealed potential candidates for resistance either by marker assisted breeding or by developing SNP and SSRs [7]. During another infection, gray blight, many genes are suppressed and enhancement of these genes may impart better disease tolerance to the plants [8]. SSH is effective to compare two mRNA populations and obtain cDNAs representing over-expressed or exclusively expressed genes in one population compared to the other. But the potential shortcoming of SSH technique is that, small quantity of poly(A)⁺ RNA from the two populations are needed in some cases, which may be difficult to obtain [9]. Transcriptome sequencing using next-generation sequencing (NGS) technologies is an impressive approach to generate genome-scale sequence resources of tea [10]. Currently, three available NGS platforms like Roche 454, Illumina Genome Analyzer and Life Technologies SOLiD can generate massive sequence reads at an extraordinary depth [11]. Using Illumina RNA-seq an extensive transcriptome dataset had been obtained from the deep sequencing of tea. The exposure was ample to ascertain all known genes of some major metabolic pathways [12]. Apart from that, floral transcriptome analysis for quantitative trait loci mapping, marker assorted breeding [13] and reasons for non-deciduous nature of tea was revealed by NGS [14]. A global survey of transcriptome profiles in response to non-freezing

temperatures and yields insights into the molecular mechanisms of tea plants during the cold acclimation process. Exploration of the cold-related genes facilitates the understanding of low-temperature tolerance and plant-environment interactions [15]. Collectively, noteworthy efforts on generation of transcriptomic data have been committed which will serve as platform for further research for discovering the genes, developing the genic markers, which is extremely important in absence of genome sequence.

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Received January 04, 2016; Accepted March 25, 2016; Published March 30, 2016

Citation: Mukhopadhyay M, Mondal TK (2016) Insights of Transcriptomic Study of Tea. *Transcriptomics* 4: 132. doi:10.4172/2329-8936.1000132

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Citation: Mukhopadhyay M, Mondal TK (2016) Insights of Transcriptomic Study of Tea. *Transcriptomics* 4: 132. doi:10.4172/2329-8936.1000132

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