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Insights of Transcriptomic Study of Tea

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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.

References

1. Mukhopadhyay M, Mondal TK (2014) The physio-chemical responses of Camellia plants to abiotic stresses. Journal of Plant Science and Research 1: 105.
2. Mukhopadyay M, Bantawa P, Das A, Sarkar B, Bera B, et al. (2012) Changes of growth, photosynthesis and alteration of leaf antioxidative defence system of tea (*Camellia sinensis* (L.) O. Kuntze) seedling under aluminum stress. Biometals 25: 1141-1154.
3. Hegde PS, White IR, Debouck C (2003) Interplay of transcriptomics and proteomics. Current Opinion in Biotechnology 14: 647-651.
4. Das A, Das S, Mondal TK (2012) Identification of differentially expressed gene profiles in young roots of tea (*Camellia sinensis* (L.) O. Kuntze) subjected to drought stress using suppression subtractivehybridization. Plant Molecular Biology Reporter 30: 1088-1101.
5. Krishnaraj T, Prabu G, Senthilkumar P, Chandrabose SRS, Mandal AKA (2013) Analysis of dormant bud (banjhi) specific transcriptome of tea (*Camellia sinensis* (L.) O. Kuntze) from cDNA library revealed dormancy-related genes. Applied biochemistry and biotechnology 169: 1405-1417.
6. Bandyopadhyay T, Gohain B, Bharalee R, Gupta S, Das SK (2014) Molecular landscape of *Helopeltis theivora* induced transcriptome and defense gene expression in tea. Plant Molecular Biology.
7. Bhorali P, Gohain B, Gupta S, Bharalee R, Bandyopadhyay T, et al. (2012) Molecular analysis and expression profiling of blister blight defenserelated genes in tea. Indian Journal of Genetics and Plant Breeding 72: 226-233.
8. Senthilkumar P, Thirugnanasambantham K, Mandal AK (2012) Suppressive subtractive hybridization approach revealed differential expression of hypersensitive response and reactive oxygen species production genes in tea (*Camellia sinensis* (L.) O. Kuntze) leaves during Pestalotiopsis thea infection. Applied Biochemistry and Biotechnology 168: 1917-1927.
9. Al-Taweel K, Fernando WGD (2011) Differential gene expression is a promising tool for understanding host-pathogen interactions. The Americas Journal of Plant Science and Biotechnology 5:1-10.
10. Vaidya K, Ghosh A, Kumar V, Chaudhary S, Srivastava N, et al. (2013) De novo transcriptome sequencing in *Trigonella foenum-graecum* L. to identify genes involved in the biosynthesis of Diosgenin. Plant Genome 6:1-11.
11. Zhang HB, Xia EH, Huang H, Jiang JJ, Liu BY, et al. (2015) De novo transcriptome assembly of the wild relative of tea tree (Camellia taliensis) and comparative analysis with tea transcriptome identified putative genes associated with tea quality and stress response. BMC Genomics 16: 298.

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12. Shi CY, Yang H, Wei CL, Yu O, Zhang ZZ, et al. (2011) Deep sequencing of the Camellia sinensis transcriptome revealed candidate genes for major metabolic pathways of tea-specific compounds. BMC Genomics 12: 131.

13. Tan LQ, Wang LY, Wei K, Zhang CC, Wu LY, et al. (2011) Floral transcriptome sequencing for SSR marker development and linkage map construction in the tea plant (*Camellia sinensis*). Plos One 8: e81611.

14. Paul A, Jha A, Bhardwaj S, Singh S, Shankar R, et al. (2014) RNA-seq-mediated transcriptome analysis of actively growing and winter dormant shoots identifies non-deciduous habit of evergreen tree tea during winters. Scientific Reports.

15. Wang XC, Zhao QY, Ma CL, Zhang ZH, Cao HL, et al. (2013) Global transcriptome profiles of *Camellia sinensis* during cold acclimation. BMC Genomics 14: 415.