Transcriptomics: Open Access

Short Commentary

Transcriptome Analysis in Banana

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Short Commentary

DNA sequencing has become an inevitable platform for molecular biological studies. As a rapid and inexpensive method, the next-generation sequencing (NGS), offer high throughput through transcriptome profiling system called RNA-Seq [1]. As next-generation sequencing technologies provides deep coverage and at single base-pair resolution, RNA sequencing is preferred as an alternative to whole-genome sequencing as it analyzes only the transcribed portions of the genome [2].

NGS based transcriptome analysis have also been successfully applied to gene expression profiling by sequencing different mRNA species that measure the activity of thousands of genes in parallel and also quantify transcripts [3]. This helps in understanding the differential expression of genes at different biological conditions of cells and or tissues [4]. Besides that pathways, stress and environmental factors can be analyzed on a genome-wide scale using NGS technologies.

Banana (*Musa* spp.) belonging to the family Musaceae of the order Zingiberales is one of the most important food crops worldwide. It is derived from intra and inter specific crosses between M. acuminata colla (A genome) and M. balbisiana colla (B genome) which resulted to many genome groups such as AA, AB, AAA, AAB, ABB, AABB, AAAB and ABBB [5]. South-East Asia is considered as centre of origin of Musa species, where numerous wild species occur in an area stretching from Papua New Guinea to India. The major issues in the banana production are pest and diseases. Some pest and diseases are highly aggressive, easily spread and difficult to eradicate which dramatically reduced the yield affecting the economical balance in many banana producing states and countries [6]. The described draft sequence of 523-megabase genome of M. acuminata doubled-haploid genotype, providing a crucial stepping stone for genetic improvement of banana has been recently published [7]. Thus, banana is a good candidate for functional genomics because of its relatively small genome size and important characteristics such as climacteric fruit, parthenocarpy or vegetative propagation, which are absent in model organisms [8]. Recent advances in genetics and genomics including the use of molecular markers have enhanced our understanding of structural and functional aspects of plant genomes that can enhance our ability to improve banana [9]. The development of efficient and cost effective in vitro regeneration methods also has provided valuable options for improved production of superior planting materials [10].

Musa based Transcriptome analysis has been performed on root [2] and leaf [11]. Recently, a whole transcriptome from different tissues like leaf, root, sheath, flower bud, flower bract, pulp, and rhizome was performed by Backiyarani [12]. The identification of rapid activation and selective induction of cold tolerance genes ICE1 and MYBS3 and their pathways in plantain and banana, along with expression of other cold-specific genes provided useful information on the expression patterns using comparative transcriptomics [13]. Sequencing of the genomes and transcriptomes of two Fusarium oxysporum f. sp. cubense (Foc) isolates, the pathogens of banana that causes vascular wilt disease lead to the identification of genes putatively involved in root attachment, cell degradation, detoxification of toxin, transport, secondary metabolites biosynthesis and signal transductions and more importantly transporters and transcription factors for toxins and nutrients transport that may facilitate its ability to adapt to host environments and contribute to pathogenicity to banana [14]. The transcriptome analysis of the banana fruit during the ripening process revealed the underlying mechanism of ripening and also to the identification of a large number of novel differentially regulated genes associated with cell wall degradation and synthesis of aromatic volatiles [15].

Transcriptome analysis helps in interpreting the functional elements of the genome [16,17] and along with the recent introduction of next-generation deep sequencing could provide a platform for genetic improvement of economically viable crops such as banana or potato [18]. Its application in Musa could improve our understanding of the molecular mechanisms involved in defence [14], biosynthesis, and other biochemical processes [12,13,15] providing a potential resource for future genetic or genomic studies on this important food crop. It can also be expected to bridge a critical gap that exists in the Musa comparative genomics and could ultimately contribute to the evolutionary and functional studies of its genes and genomes.

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