

Highlight yield forming and innovative technologies in tropical crops

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This special issue on tropical crops focuses on how these crops adapt to their tropical environment and accumulate carbohydrates in unique ways as well as recent technological innovations in genetics and breeding.

The tropics have an abundance of natural resources such as light, heat, water and great diversity of higher plants. It is estimated that about 100000 plant species originated in tropical and subtropical zones around the globe. Also, many cultivated crops evolved and were domesticated in tropical regions. The tropical crops, such as cassava, have highly efficient photosynthesis, energy transferability and biomass accumulation, as well as tolerance to drought and low fertility soil. In other words, tropical crops are like machines that can speedily create biomass from the extremely rich environmental resources. Consequently, they will be given much attention as sources of food, feed, bio-energy and green biomaterials in the near future. Different from the majority of crops in China and the world, research on tropical crops such as banana and other tropical fruit, cassava, rubber tree and sugarcane has been relatively limited, especially at the biological or genomic level, a situation that is not commensurate with their economic importance. The underlying problem is that few of institutes and experienced scientists engaged in this field of study because the most countries in tropics are developing country. Accordingly, until recently there has been less research on environmental response and biomass accumulation at molecular and cellular levels on tropical crops.

This special issue includes 10 articles on tropical crops, including banana, cassava, mangroves and rubber tree. These cover a wide range of important current research topics, encompassing yield formation, environmental response, and innovative transgenic technologies in special crops, as well as development of genomic tools.

On cassava (*Manihot esculenta*), proposed as a model plant of tropical crops, there are three research articles and one review add new resources and knowledge in genomics and transgenic technology. Large-scale comparative transcriptome analysis revealed the genes important in leaf, stem and storage root of cultivated cassava by comparison with its wild ancestor. This new understanding focused attention on specific genes for light harvesting and response, together with Calvin cycle genes in leaf, other genes for transport and key rate-limiting enzymes coupling ATP consumption in the glycolysis pathway in stem, and genes for sucrose degradation, amylose synthesis and hydrolysis. The expression of genes involved in three key steps in starch synthesis associated with storage has been enhanced during domestication. The coexpression network in each organ linked important transcription factors to their putative targets, and further confirmed some of important hub genes in photosynthesis, transportation and starch biosynthesis. Furthermore, the review presented several successful transgenic events on engineering protein content and improving resistance to viral diseases by RNAi in cassava and stated the potential utilization of this approach in cassava genetic improvement. A bacterial artificial chromosome (BAC) library with about 60 thousand clones with an average insert size of 125 kb has been released, and a physical map composed of 2485 contigs with average length of 336 kb based on fingerprint of 29952 clones was constructed, representing about 762 Mb of the cassava genome. This BAC-based physical map provides a valuable tool to understand the cassava genome and comparative evolution. Also, a full-length cDNA library containing 32640 recombinant clones from leaf and root of cassava cv. Arg7 and its wild ancestor W14 (*M. esculenta*) has been constructed. By sequencing of part clones, 5013 high-quality expressed sequence tags and 1259 unigenes were

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obtained and identified 24 important genes involved in starch metabolism. These advances contributed resources for elucidating the mechanism of highly efficient carbohydrates accumulation and genetic improvement in cassava.

Rubber tree (*Hevea brasiliensis*), yielding latex by tapping, is very different from all other crops, with a breeding cycle of up to 30 years that has greatly hinder the genetic improvement of desirable cultivars. The two articles in this special problem illuminate a pathway to its resolution. The secondary laticifer, a specific tissue in the secondary phloem of rubber tree, although already known, its number in the trunk bark of rubber tree was found to be positively correlated with rubber yield. Also, jasmonate was demonstrated to be crucial in the regulation of secondary laticifer differentiation, though the mechanism for the jasmonate-induced secondary laticifer differentiation remains to be elucidated. The study revealed that trichostatin A, an inhibitor of histone deacetylation, could induce the secondary laticifer differentiation in a concentration dependent manner, indicating that histone acetylation is essential for the secondary laticifer differentiation in rubber tree. In addition, the researchers report that the number of tapping-induced secondary laticifers was positively correlated to the rubber yield and invented a suitable parameter for early evaluation of yield potential of rubber trees, which has great potential for application in crossbreeding of rubber tree.

For banana (*Musa × paradisiaca*), a triploid crop, an efficient and reproducible transformation system using direct organogenesis was developed. This protocol could regenerate well-developed shoots for five different genotypes. Such a system will be of vital importance for facilitating the genetic improvement and functional genomics of banana. Comprehensive transcriptomic analysis revealed banana β -amylase genes are involved in regulating fruit development and ripening. Sixty-four cold responsive miRNAs and their 393 target genes were found in *Musa balbisiana*, a wild progenitor of banana with BB genome.

Finally, as Guest Editor, I would like to thank all authors and reviewers who have contributed to this special issue, and the *FASE* editorial team for their scientific input and consistent support.



Dr. Wenquan WANG, senior professor of genomics and molecular breeding of tropical crops including cassava, executive director of Key Laboratory of Tropical Crop Biology and Utilization of Genetic Resources and former coordinator of National Key Basic Research Program “The principal research on genetic improvement in cassava important tropical crop.” Dr. Wang received his PhD in nutrition genetics at the Chinese Agricultural University in 2000, and was a senior research fellow in The Boyce Thompson Institute, Cornell University from 2009 to 2010. During his academic career, Dr. Wang was dedicated to understanding molecular mechanism of carbohydrate accumulation in storage roots, developing new molecular tools for cassava based on genome and genomics and improving whole genome resolution for elite cultivar breeding in cassava and other tropical crops. His achievements include a third prize of National Science and Technology Innovation Award and two prizes of provincial Scientific and Technology Award, two patents and about 150 publications including articles published in *Nature Communications*, *Nucleic Acids Research* and *Scientific Reports*.