Herbgenomics facilitates biological study of TCM

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Traditional Chinese Medicine (TCM) has been used for more than 5000 years and has attracted more and more worldwide attention because of its significant effect in prevention and treatment of diseases. However, the genetic background, the physio-ecological characteristics, and the molecular mechanisms of most herbs are poorly understood. The Human Genome Project opens the biological Era. Genomics triggered a revolution in system biology research and enabled people to have a deeper and comprehensive understanding of living organisms. With the development of high throughput sequencing technologies and bioinformatics, herb-genomics was put forward as a discipline to facilitate biological research of TCM [1]. It aims to uncover the genetic information, find gene functions, discover regulatory networks of herbs and to elucidate their molecular mechanisms in the treatment of diseases [2]. More and more biological studies were performed to examine the biology of traditional medicine including whole genome sequencing [3], adaptation [4], stress resistance [5], molecular identification [6] and evolution [7]. Herbgenomics will absolutely play an important role in research on modernization and internationalization of TCM.

In this special issue, a total of five articles have been devoted to herbgenomics study of TCM. HU YT et al. [8] identified transcription factor AP2/ERF related to camptothecin biosynthesis. They firstly made a systematic analysis of the AP2/ERF TFs family in Camptotheca acuminata including phylogeny, gene structure, conserved motifs, and gene expression profiles in different tissues and organs. A total of 198 AP2/ERF genes were identified and divided into five relatively conserved subfamilies. And then this paper compared gene expression patterns in different tissues and organs of C. acuminata, carried out the co-expression analysis with synthetic genes and performed the analysis of promoter sequences of key enzymes genes. They revealed that eight AP2/ERF TFs might be involved in CPT synthesis regulation in C. acuminata.

LV YN et al. [9] evaluated ITS2 and psbA-trnH as candidate DNA barcodes to identify species in Apocynaceae. Actually it’s really important to distinguish species within the Apocynaceae family because they are poisonous and some of them are used as traditional medicine. Based on 122 samples of 31 species from 19 genera, the PCR amplification of the two sequences were both 100%. Three identification methods including specific genetic divergence, BLAST1, and neighbor-joining trees were used to investigate their discrimination ability. Although ITS2 and psbA-trnH showed a high identification efficiency of 100% at genus level, they could not identify all samples at species level. The combination of ITS2/psbA-trnH can successfully identify 98% of samples. They demonstrated that ITS2 could be regarded as a core barcode and psbA-trnH was a supplementary barcode.

Cui YX et al. [10] focus on the expression analysis of PYL4 genes under abscisic acid (ABA) stress in G. uralensis. ABA as an important plant endogenous hormone plays a prominent role in different physiological phenomena, and lots of studies proved that it can regulate plant responses to abiotic and biotic stresses. Genome-wide identification of PYL can help to investigate the signal transduction of ABA and its regulatory mechanisms. The authors firstly identified 10 PYLs in G. uralensis using whole-genome sequencing data. They proved that 4 GuPYLs are significantly up-regulated under ABA stress. The characterization, phylogenetic and expression pattern analysis of PYLs were also carried out in this study.

In another two papers, four new chloroplast (cp) genome sequences were reported. Yang CH et al. [11] sequenced cp genomes of three original species of Pyrosiae Foliun, and Cui N et al. [12] firstly published the complete cp genome sequences of Salvia plebeia. Chloroplast is one of the most important plant organelles where photosynthesis takes place. In
addition, cp genome is one of three independent genomes. Knowledge of cp genome can provide sufficient information for phylogenetics and identification study. Chloroplast genome engineering also relies on the understanding of structure and function of cp genome. In these two articles, genome organization, specific barcode selection and phylogenetic analysis were performed for the four medicinal plants.

A lot of research work has been carried out in the past decade in understanding the biology of TCM whatever in gene or genome levels. Readers of this special issue will find not only different bioanalysis methods but also some important issues influencing quality of TCM. Biological issues lie in the whole indusrail chain of TCM, from the production of raw materials to the clinical medication. There are still some key questions to be resolved in the whole process including molecular breeding, biosynthetic and regulatory mechanisms, and action mechanism of effective components. We believe that herbgenomics provides an unprecedented opportunity to accelerate the internationalization research and application of TCM.

References


Dr. LI Xi-Wen is now an associate professor of Institute of Chinese Materia Medica, China Academy of Chinese Medical Sciences. His major is pharmcogonosy and research subjects are herbal identificaiton, cultivation and quality traceability. He has so far published 145 scientific papers on internationally recognized academic journals including Molecular plant, New Phytologist and Biol Rev. Dr. LI joined the Editorial Board of many journals including CHIN MED-UK, CJNM, APSB, etc., and he awarded the Second Prize of State Scientific and Technological Progress in 2016. Up to now, He awarded 3 first Prizes in provincial and ministerial level and won first Prize for International Contribution of Traditional Chinese Medicine.

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