2ⁿᵈ World Biotechnology Congress

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The forefront of scientific progresses in plant science: Next generation crop breeding

Great success in crop improvement contributed to the green revolution, by creating high-yielding varieties/hybrids; but modern crop improvement programs face new challenges because of limited genetic resources for breeding demand, complexity of certain traits, demanding for fast breeding rates and novel approaches for crop improvement. Fortunately, rapid advances in molecular biology and quick development of genomic technologies have tremendously expanded our abilities to analyze and understand plant genomes and to reduce the gap existing between genotype and phenotype. Moreover, the recent completion of whole genome sequencing of many crop species opened the doors for more efficient gene discovery and offers us the opportunities to translate the genome information into improvement of crops through novel breeding strategies. This paper reviews the advances of our knowledge in plant biology and these cutting-edge technologies, such as development and utilization of the genomic resources for gene discovery, genotyping and QTL (quantitative trait loci) identification, development of DNA markers for the next-generation genotyping and marker-assisted selection, next-generation sequencing and genomics-assisted breeding (GSB), gene expression profiling and dissecting the networks of gene regulation in crop plants, plant functional genomics, molecular breeding and genetic enrichment of crops through transgenic approach. Furthermore, the latest invented technology, called "genome editing", represents an advanced plant breeding tool and holds tremendous promise and potential to facilitate precision crop breeding. It will also explore case studies of genotyping by sequencing applications to several crops differing in genome size, organization and breeding systems. Finally, the paper will demonstrate the application of those new tools in crop improvement in terms allowing more precise and quicker manipulation of crop genomes, more easily measuring traits and adding beneficial genes to various crop species around the world

Biography

Yinghua Huang is a Research Geneticist for USDA and serves as the Lead Scientist for the Plant Genetics Program, and an Adj. Professor of Oklahoma State University. His scientific background is in plant genetics and molecular biology, and he has considerable research experience in plant biotechnology, genomics and crop improvement. During his early career, he made a breakthrough in developing a reliable system for producing transgenic larch plant, which represents the first record of genetically engineered conifer tree, carrying the important traits including resistance to insects and herbicide. Recently, using cutting-edge microarray, RNA-seq and next-generation sequencing technologies, his lab has generated the expression profiles and genomic data, leading to the identification of the critical genes and networks that regulate the host defense against insect pests, crop yield, and bioenergy quality in crop species. The overall goals of his research are to conduct basic studies to enhance our understanding of biological processes in plants, to apply newly developing genomic tools to facilitate genetic improvement of crop plants, and finally to improve the production system for a better utilization of agricultural and natural resources.

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Page 45