

June 20-21, 2018 Rome, Italy

Lihong Xiao, J Plant Physiol Pathol 2018, Volume 6 DOI: 10.4172/2329-955X-C1-013 4th Edition of International Conference on

Plant Genomics

THE HIGH-QUALITY GENOMES OF PECAN AND CHINESE HICKORY PROVIDE INSIGHTS INTO THE GENETIC BASIS OF ADAPTIVE EVOLUTION AND NUTRITIONAL POTENTIALS



Lihong Xiao

Zhejiang A & F University, China

Pecan and Chinese hickory are the only two commercially cultivated tree nuts in the genus Carya. Their nutritional value and health benefits are superior to many other tree nuts contribute to growing consumption with potential to become major crops and suggest ability to improve world food security. Unfortunately, few resources are available to facilitate their genetic improvement. Here we report reference genome sequences for two highly heterozygous individuals - pecan cultivar (Pawnee) and a domesticated Chinese hickory. Both experienced two genome duplication events before divergence from walnut. The genomes encode 31,075 (pecan) and 32,907 (Chinese hickory) protein-coding genes.Gene family expansion highlighted the key genes and pathways involved in biotic (Chinese hickory) and abiotic (pecan) tolerance, accumulation on unsaturated fatty acid, non-structural polyphenol metabolism, nonessential amino acid and B vitamins. We also report the reduced-coverage genomes for 15 other hickories and two Juglans species, which, together with the two reference genome sequences, reveal the

evolutionary history and the disjunctive distribution of Carya species. We believe these genomic resources should be an important first step towards the genetic improvement of hickory nuts.

Biography

Lihong Xiao is senior most scientist at Zhejiang A & F University, China, her expertise in the improvement of tree nut quality and nutritional content based on Genome-Wide Association analysis (GWAS) and gene editing (CRISPR/Cas9). Her research interests are also focused on understanding fundamental mechanisms of plant abiotic stress responses to adverse environments and to explore the mechanisms and its evolution of stem cell maintenance by integrating extensive approaches, including "omics" (small RNA and mRNA transcriptome, proteomics and phosphate-protein, methylome) and Whole Genome Sequencing (WGS) as well as data analysis, genetics, cytology (including light, electron and confocal microscopy imaging), histochemistry, molecular biology, etc.

xiaolh@zafu.edu.cn