

Tues, 18 Oct 2022 | 11 am | DBS Conference Room 1

Hosted by Asst. Prof Lau On Sun

Genomic and Epigenetic Bases for Crop Improvement

Polyploidy or whole genome duplication (WGD) is a prominent evolutionary feature for all flowering plants and many animals. Most crop plants including wheat, cotton, and oilseed rape are polyploids, and many other crops such as maize and soybean are ancient polyploids. In allopolyploids, interspecific hybridization can induce “genome shock,” leading to genomic and epigenetic changes, the effects of which can be amplified by genome doubling (ploidy changes). Moreover, heterozygosity and heterosis between hybridizing parents are permanently fixed in allopolyploids. Here, I will present recent findings and perspectives of epialleles in allotetraploid cotton and inbreeding depression and transgenerational inheritance of epialleles in maize. These conceptual advances and genomic and epigenomic resources will help us improve the production of polyploid and hybrid crops for food security and carbon sequestration. Beyond plants, hybrid genetics is similar in sexually reproducing organisms including humans; the mechanisms associated with balancing ploidy and allelic variation may help us better-understand human health.



By Jeffrey Chen

Departments of Molecular Biosciences
The University of Texas at Austin, USA

Jeff Chen is a plant biologist. He started his faculty career in 1999 at Texas A&M University and in 2005, he was recruited as the recipient of the D. J. Sibley Centennial Professor of Plant Molecular Genetics at The University of Texas at Austin. He is known for his pioneering work on defining genomic and epigenetic changes in plant hybrids and polyploids with an emphasis on associating gene expression variation with phenotypic traits using Arabidopsis, cotton, and maize as experimental systems. His work discovered that epigenetic mechanisms drive genome-wide nonadditive expression of the genes in a number of regulatory pathways, including circadian clock genes that increase growth vigor, genes and small RNAs that mediate seed size, transcription factor genes that control fiber cell development, and epialleles responsible for inbreeding depression and trans-generational inheritance. He has led an international effort to sequence genomes of five tetraploid cotton species, including economically important Upland and Pima cotton. His research findings have significant impact, not only on advancing the field of genetics and epigenetics, but also on biotechnological applications to safely and effectively manipulate gene expression associated with growth vigor in plants and crops that produce food, feed, fiber, and biomaterials. He is an elected fellow of American Association for the Advancement of Science (AAAS) (2011) and recipient of Fulbright US-UK Scholar Award (2011) and Cotton Biotechnology Award (2016). He serves on editorial board of Genome Biology, The Plant Genome, Genes, Frontiers in Epigenetics and Epigenomics, and as guest editor of PNAS.