

M-03

Using latest genomic technologies to study soybean stress biology

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Soybean (*Glycine max*) is a legume crop with worldwide economic and environmental importance. It accounts for a majority of plant dietary protein for human and livestock as well as for oilseed production, and maintains soil fertility through symbiotic nitrogen fixation. However, the sustainability of soybean yields is threatened by climate change. On-year yield growth does not keep up with the increase in planted land area, suggesting that more soybean are being planted in marginal lands, where they are commonly challenged by drought and soil salinity, yet the current cultivars have limited ability to cope with the harsh environment.

To ensure food security, soybean genomics research becomes imperative for crop improvement. The first reference genome of the cultivar William 82 was released in 2010 and has greatly enhanced soybean research. Nevertheless, many valuable genetic traits, especially those that are involved in stress tolerance are likely to be lost during domestication. Traditionally, stress-response related quantitative trait loci were discovered by genome-wide association studies or QTL identification using bi-parental genetic populations using. Single nucleotide polymorphism and expression landscapes are profiled by re-sequencing and transcriptomics. Yet, results are confounded by heavy dependence on the single cultivar-based reference built with short-read sequencing, which is limited in capturing large-scale genomic structural variations. Representing a multi-disciplinary team at The Chinese University of Hong Kong, this presentation looks to utilize the latest genomic technologies to extend our knowledge in soybean stress biology.