Abstract No: 42 ***Life Sciences***

HIGH-QUALITY GENOME OF AUSTRALIAN FINGER LIME

N.D.U.S. Nakandala[1,2], **A. Kharabian-Masouleh**[1,2], **A. Furtado**[1,2] **and R.J. Henry**[1,2*]

[1] *Queensland Alliance for Agriculture and Food Innovation, University of Queensland, Brisbane, Australia.*
[2] *ARC Centre of Excellence for Plant Success in Nature and Agriculture, University of Queensland, Brisbane, Australia.*
**robert.henry@uq.edu.au*

High-quality reference genomes provide a critical resource towards understanding the structural and functional basis of a genome, which can further support plant breeding. Currently, a few genomes are available for citrus with different accuracy and completeness levels. Australian finger lime (*Citrus australasica*) is a native citrus species in Australia with a high natural genetic diversity and tolerance to Huanglongbing (HLB) disease. A reference genome is not currently available for finger lime. Therefore, we have developed a high-quality, chromosome-level genome assembly for Australian finger lime to identify the genes related to disease resistance and other essential traits related to fruit quality. The genome was assembled using highly accurate PacBio HiFi long reads and Hi-C scaffolding technology and mapping against the previously published Australian wild round lime genome. The finger lime genome is diploid and heterozygous. The genome of finger lime was assembled into pseudochromosomes with high assembly contiguity and completeness (Benchmarking Universal Single-Copy Orthologs - BUSCO). Two haplotypes were assembled into chromosome levels using the Hi-C integrated Hifiasm option. The assembled genome will be structurally and functionally annotated to identify genes related to disease resistance and other essential traits in citrus. Five different accessions of finger lime have also been sequenced by Illumina short read sequencing (28X – 39X coverage of the genome) and will be compared for their genetic variation corresponding to pigmentation, volatile compounds synthesis and disease resistance. The newly assembled haplotype resolved finger lime genome will be a valuable genomic resource in understanding the genetic basis of HLB resistance and will provide an enhanced definition of evolutionary relationships with other Australian citrus species.

Financial assistance from the National Tree Genomics program for Horticulture (Grant No AS17000) is acknowledged.

Keywords: Haplotype resolved genome, Hi-C scaffolding technology, Huanglongbing (HLB) disease, PacBio Hifi long reads