Instant sub-genome dominance and enhanced adaptability of synthetic allotetraploid in *Cucumis*

Xiaqing Yu[1], Jinfeng Chen[1*]

[1]College of Horticulture, Nanjing Agricultural University, Nanjing, 210095, China

[*]Corresponding author. Email: jfchen@njau.edu.cn

Background

Polyploidy is commonly known to play an essential role in plant evolution and speciation (Wendel et al., 2016; Van De Peer et al., 2017). However, the genomic changes following polyploidy has not been fully understood. Moreover, the feasibility of creating novel crop type with increased genetic diversity through polyploidization has rarely been tested. *Cucumis* ×*hytivus* is a newly synthesized allotetraploid in *Cucumis*, obtained through a wild cross between wild species, *C. hystrix* Chakr. (HH), and cucumber, *C. sativus* L. ‘BejingJietou’ (CC), followed by chromosome doubling (Chen and Kirkbride, 2000). The establishment of *C.* ×*hytivus* represents a breakthrough in the gene communication between distinct species with different chromosome bases.

Methods

In the present study, whole-genome shotgun sequencing, single-molecule real-time (SMRT) sequencing, high-throughput chromosome conformation capture (Hi-C) technology, and BioNano optical genome mapping were adopted to generate a high-quality genome sequence of *C.* ×*hytivus*.

Genome assembly of the unduplicated F1 homoploid hybrid and several early generations (S0, S4-S13) of *C.* ×*hytivus* were obtained through shotgun sequencing to differentiate the genomic consequences of interspecific hybridization from the genomic consequence of genome duplication.

We systematically examined individuals drawn from repeated rounds of self-pollination to reveal the genomic changes that occur after formation of the amphidiploid. By sequencing individuals that essentially define a time series through 14 generations of inbreeding, we reveal the genomic basis for the phenomenon of “diploidization” observed in allotetraploid.

Results

We used state-of-art sequencing strategy and obtained the chromosome-scale genome assembly of *C.* ×*hytivus*. By precise comparative analysis with parental genomes, we demonstrated the overwhelming dominance of CC-originated sub-genome. We also sequenced the genomes of F1 homoploid hybrid, the duplicated allotetraploid (S0) and subsequent generation individuals (S4-S13). Our results indicated that most gnomic changes occurred immediately after interspecific hybridization. By testing the root-knot nematode resistance and heat tolerance, we suggested that the fixed heterozygosity provides *C.* ×*hytivus* with increased stress adaptation.

Conclusion

Our study provides novel insights into plant polyploid genome evolution and demonstrates a promising strategy for the development of a wide array of novel plant species and varieties through artificial polyploidization.

Funding

This work was supported by the National Key Research and Development Program of China (2018YFD1000804), the National Natural Science Foundation of China (No. 31902006; No. 31902007), the 111 Project (B18029), the Natural Science Foundation of Jiangsu Province, China (BK20180536), National Key Research and Development Program of China (No. 2016YFD0101705-5; No. 2016YFD0100204-25) and the Priority Academic Program Development of Jiangsu Higher Education Institutions.

References

Chen JF, Kirkbride JH. A new synthetic species of *Cucumis* (Cucurbitaceae) from interspecific hybridization and chromosome doubling. Brittonia 2000, 52:315-319.

Van de Peer Y, Mizrachi E, Marchal K. The evolutionary significance of polyploidy. Nat Rev Genet. 2017, 18(7):411-424.

Wendel JF, Jackson SA, Meyers BC, Wing RA. Evolution of plant genome architecture. Genome Biol. 2016, 17:37.