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Updated chromosome-level complete genome of *Mesembryanthemum crystallinum* L.: Insights into genome structure, molecular evolution, and non-coding regions

Ryoma Sato[1]Kyoka Takeuchi[2]Yuri Kondo[1]Hideki Hirakawa[3]Sachiko Isobe[3]Kenta Shiarasawa[3]Sakae Agarie[4]

[1]Graduate school of Bioresource and Bioenvironmental Sciences, Kyushu University, JAPAN

[2]School of Agriculture, Kyushu University, JAPAN

[3]Kazusa DNA Research Institute, JAPAN

[4]Faculty of Agriculture, Kyushu University, JAPAN

Abstract

The common ice plant (Mesembryanthemum crystallinum L.)., an annual herbaceous species of the Caryophyllales order and Aizoaceae family, is native to Southern Africa and represents the Mesembryanthemum genus. The ice plant is characterized by nine chromosomes (2n=2X=18) with an estimated genome size of approximately 370 Mbp. It exhibits resilience under salinity and desiccation stresses and possesses mechanisms to convert its photosynthetic processes. Our prior work detailed a genome assembly based on short reads from the Illumina platform; however, the resultant genome's quality was subpar. While one study has reported chromosome-level genome sequences of this species, their accessibility remains a difficulty. We generated a chromosome-level genome using the PacBio platform, public Hi-C data, and advanced bioinformatics techniques to solve this problem. We successfully assembled chromosome-level genome sequences matching the estimated genome size. With 98.2% of terrestrial higher plant BUSCO genes covered, our assembly surpasses previous studies in integrity. Interestingly, roughly 51% of the ice plants' genome is constituted of repetitive sequences, potentially underscoring their role in governing species-specific physiological adaptations. Further, phylogenetic analyses employing