[BIOINFO 2024]

Comparative genomics of Wolffia species: Investigating genome size evolution and the functional implications

Yejin Lee[1] and Yang Jae Kang[1,*]

[1] *Division of Bio & Medical Bigdata Department (BK4 Program), Gyeongsang National University*
**Corresponding author: kangyangjae@gnu.ac.kr*

Wolffia, the smallest aquatic monocot, is known for its rapid growth and significant nutritional potential and is also characterized by the absence of typical plant structures such as roots and stems. Recently, the draft genome of *Wolffia australiana* was reported to be approximately 400 MB, the smallest genome size among *Wolffia* species. In contrast, *Wolffia brasiliensis* has a genome nearly twice as large, approximately 800 Mb, though it remains understudied at the genomic level. This significant difference in genome size between closely related species provides an opportunity to explore the evolutionary mechanisms driving their genomic divergence. Larger genomes within a species are often attributed to events such as genome duplications, transposable element expansions, or variations in gene families, all of which may contribute to ecological adaptation and evolutionary strategies. In this study, we assembled the draft genomes of *W. australiana* and *W. brasiliensis* using long-read sequencing technologies on the PacBio platform. To elucidate the biological significance of genome size variation on gene content and repetitive elements during evolution, we conducted a comparative genomic analysis using the assembled genomes of *W. australiana* and *W. brasiliensis*. These findings offer significant insights into the evolutionary mechanisms driving the diversification and adaptation of *Wolffia* species, demonstrating the role of genome size variation and gene content shifts in shaping their evolutionary success.