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Whole Genome Sequencing and Gene Prediction of *Cynodon transvaalensis*

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[Abstract]

Cynodon transvaalensis belongs to the warm-season grasses and is one of the economically and ecologically important crops. *Cynodon* species with high heterozygosity are difficult to assemble, so genome research has not been actively conducted. In this study, hybrid assembly was performed by sequencing with Illumina and PacBio. As a result of the assembly, the number of scaffolds and the length of N50 were 1,392, 928 kb, respectively. The completeness of the assembly was confirmed by BSUCO at 98.3%. In addition, as a result of estimating the size of the assembled genome by K-mer analysis (k=25), it was approximately ~413 Mb. A total of 37,060 cds sequences were annotated in the assembled genome, and their functions were identified through blast. After that, we try to complete the assembled genome into a pseudochromosome-level genome through Hi-C technology. These results will not only help to understand the complex genome composition of african bermudagrass, but also provide a resource for genomic and evolutionary studies of grass and other plant species.

[Acknowledgement]

This work was supported by the National Research Foundation of Korea (NRF) grant funded by the Korean government (MSIT, No. 2022R1A2C1004127).

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