

Division-4-05

Whole Genome Sequencing of Two *Musa* Species Towards Disease Resistance and Fiber Quality Improvement

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[Abstract]

Abaca (*Musa textilis* L. Nee) is a native *Musa* species from the Philippines known for its natural fiber. Abaca fiber a.k.a. Manila hemp extracted from its pseudostems is considered one of the strongest fibers in the world. This is used for commodities such as ropes, papers, and money bills. Abaca is vulnerable to pests and diseases such as the Abaca Bunchy Top Disease (ABTD) caused by Abaca Bunchy Top Virus (ABTV) and Banana Bunchy Top Virus (BBTV). Inosa, one of the varieties of abaca utilized in the Philippines, is highly susceptible to ABTD. In contrast, Pacol (*Musa balbisiana* L.), a close relative of abaca, is highly resistant to the same disease. Here, we report the sequencing and *de novo* genome assembly of both abaca var. Inosa and banana var. Pacol. A total of ~16 Gb and ~21 Gb raw reads for Inosa and Pacol, respectively, were generated using Pacbio Hifi sequencing method and assembled with Hifiasm. High-quality *de novo* assemblies of both *Musa* species with 99% recovered as per BUSCO analysis were obtained. The assembled Inosa genome has a total length of ~654 Mb and N50 of 7 Mb while Pacol has a total length of 527 Mb and N50 of 3 Mb which are close to their estimated genome size of ~638 Mb and ~503 Mb, respectively. The information that can be derived from the *de novo* assembled genomes would provide a solid foundation for further research in disease resistance and fiber quality improvement in abaca.

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