

Dovetail Genomics' Plantain Genome Enhances Food Security

Unlocking the genome of the plantain will improve breeding efforts and provide food for the communities that depend on it.



Figure 1: Plantain (*Musa spp.*)

Plantains (*Musa spp.*) are banana cultivars bearing starchy fruits and a staple crop in West Africa and Latin America, with the annual production exceeding 31 million tons. Plantains have a triploid genome, AAB, with two chromosome sets from one species of banana (*Musa acuminata*) and one from another species (*Musa balbisiana*). They originated several thousand years ago, and without a genome assembly, their origins have been somewhat mysterious.

“We cannot exclude the possibility that more than the two subspecies of *M.*

acuminata have played a role in their evolution, together with more complex mechanisms including multiple backcrosses” said Jaroslav Dolezel, Senior Scientist at The Centre of Plant Structural and Functional Genomics, part of the Institute of Experimental Botany in the Czech Republic. “By assembling the plantain genome, we can probably answer the question of where it comes from”.

As with other cultivated bananas, plantains do not produce seeds and must be maintained clonally. In addi-

tion, plantains are primarily grown by small farmers who do not have access to chemical fertilizers and other sophisticated agricultural methods and are dealing with a variety of diseases, pests and other pressures. Shortages have led to price increases, particularly in urban areas where breeding is impeded by seed sterility and poor knowledge of the genome. Though one banana genome has already been assembled, it is from a model species that is not cultivated. Sequencing an important crop like plantain could have tangible benefits for breeding programs and farmers.



Figure 2: Jaroslav Dolezel and Eva Hribova, Institute of Experimental Botany, Academy of Sciences of the Czech Republic

Plantain is the most diverse triploid subgroup of the genus *Musa* and although morphological differences are

recognized (French, Horn, False Horn and French Horn), their genetic diversity remains uncorrelated to the phenotype. Understanding the exact genomic constitution, as well as the morphotypes, is essential to advance plantain and any other banana subgroups as well.

For answers to these questions, Jaroslav Dolezel, Eva Hribova and colleagues wanted to assemble a high-quality plantain genome assembly. The Institute, which focuses on plant genome structure and evolution, has been collaborating with the banana and plantain breeding program of the International Institute of Tropical Agriculture to unlock the secrets of the plantain genome for improving breeding and feeding more people.

The Institute has a longstanding relationship with Dovetail, having previously collaborated on wheat and barley genome sequences. Using Dovetail's proprietary proximity ligation technologies, the team went through an iterative process to produce the *de novo* genome. Chicago® *in vitro* proximity ligation improved the genome N50 from 0.03 Mbp to 1.19 Mbp. Dovetail™ Hi-C then brought it up to 56.71 Mbp. "We have a high-quality assembly, which is really not easy," said Dolezel. "It's one thing to sequence the genome and it's quite another to have quality. That's why we like working with Dovetail – it's super high quality."

Assembling a plantain genome is a real breakthrough – the first cultivated

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	Draft (<i>De Novo</i>) Assembly	Post Chicago® Scaffold	Post Dovetail™ Hi-C Scaffold
N50	0.03 Mbp	1.19 Mbp	56.71 Mbp

banana clone ever assembled which is moreover a triploid. Now that the researchers and breeders have a high-quality reference genome which will be further verified by optical map construction, the team will conduct epigenetic and resequencing studies to better understand the plantain's different morphotypes, as well as investigate the genome's spatial organization in cell nuclei and how that affects gene regulation.