

# Towards Genomics-enabled Banana Breeding



## Research GAP

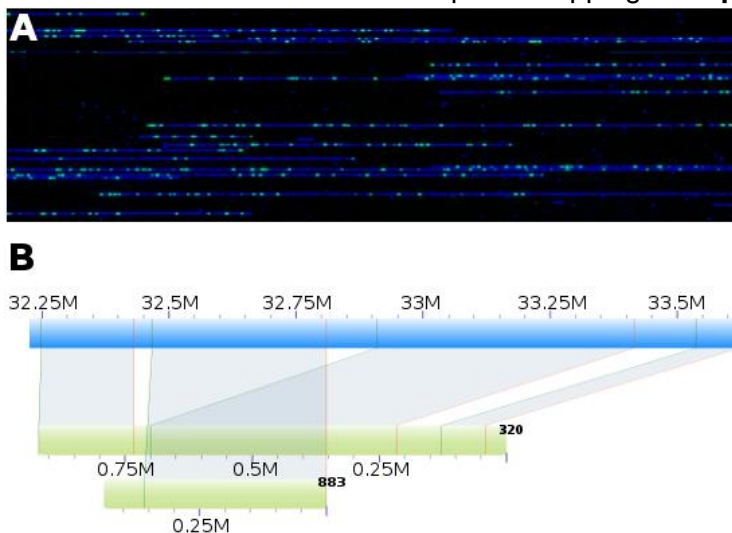
Efficient application of new breeding techniques requires us to identify genome loci that are responsible for important traits. As a majority of these traits of interest are affected by multiple genome loci, a detailed knowledge of the whole genome sequence is necessary to achieve this goal. **A reference quality genome sequence is not available, however, for any of the diploid or triploid banana clones that are cultivated in East Africa.**



## What WE DID

Genomic DNA of diploid *Mchare* type bananas, cultivar ‘Huti White’, was sequenced using illumina technology. Short overlapping reads were assembled to longer continuous DNA sequences (contigs), which were then ordered (scaffolded) to produce a draft genome assembly. However, some scaffolds were found to be chimeric, consisting of contigs originating from each of the two parental sets of chromosomes. In order to identify sequences specific for each of the two parental chromosome sets of ‘Huti White’, we further sequenced two hybrids (‘Huti White’ x ‘Calcutta4’). This information will help in splitting the chimeric scaffolds.

We also used optical mapping to improve the whole genome assembly:



(A) Linearized long DNA molecules (blue) in the nanochannels of Bionano Genomics Saphyr system; (B) Alignment of genome sequence (thick blue line) to optical maps (thick green lines). This revealed an incorrectly placed DNA sequence region between 32.4Mb and 32.8Mb (thick blue line), whose presence was not confirmed by the optical map no. 320. The region was aligned to optical map no. 883 and belonged to a different region of the genome sequence.



## What **WE ACHIEVED**

A draft genome version of a representative of *Mchare* banana was obtained and is **currently being improved to produce the first reference quality genome sequence for this type of banana.**



## Why **THIS IS IMPORTANT**

Access to a *Mchare* banana genome sequence will enable us **to employ the latest molecular biology, genomics and biotechnology tools** for improving this type of banana. This advance **will enable much more rapid and precise selection** of prospective parents for banana improvement and of progenies during early screening. Importantly, it will also be possible to **edit causal genome loci to enable us to biologically design our new banana varieties.** This work can then serve as a template for other groups of cultivated banana. Moreover, by delivering a genome sequence of unreduced gamete source of commercially important dessert bananas, this work has **significant impact beyond our current objectives and goals.**

### **For more information contact:**

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or see: <http://breedingbetterbananas.org/>