Using Genotyping-By-Sequencing to Understand *Musa* Diversity

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ABSTRACT

**Background:** This project is part of a larger effort to apply genomics technologies to assess genetic diversity and to advance genetic improvement efforts in *Musa* (banana and plantain), a major staple food crop in the developing world. Most cultivated varieties of bananas result from intra- or inter-specific crosses of the wild diploid species, *Musa* acuminate (A genome) and *Musa* abelmoschiana (B genome). Somoclonal mutation and human selection has resulted in the many day bananas with a wide morphological diversity. The Cavendish (AAA) subgroups are believed to have derived from an individual unique initial genotype, and similarly for the subgroup plantain (AAB). However, little or no genetic diversity can be detected within these groups using conventional molecular markers such as RFLP, SSR, and DAR.

**Methods:** To assess genetic diversity with an improved resolution, we have selected 65 accessions with diploid and triploid combinations of the A and/or B genomes including AAB plantains and AAA Cavendish, and cultivated or wild *Musa* accessions from the core collection at the Global Musa Genomics Consortium (GMGC). A high-throughput reduced representation genome sequencing approach - genotyping-by-sequencing (GBS) is used to obtain high density sequence markers [1].

**Results:** Using GBS reads, genotypes were determined for each diploid and triploid accession, and dissimilarity computed across all accessions. Genetic diversity analysis was carried out using the DARwin software [2, 3].

**Conclusions:** GBS markers provide a high resolution approach to characterize the genetic diversity of Individual *Musa* subgroups.

METHODS

(1) A total of 65 *Musa* accessions including diploid and triploid combinations of the A or B genomes, AAB plantains, AAA Cavendish, and cultivated or wild *Musa* accessions were selected for GBS sequencing.

(2) About 1 to 4 million Illumina reads flanking PaTI sites were generated for each *Musa* accession. Approximately 200,000 candidate SNP locations with reference to the doubled-haploid *Pahang* genome were obtained from all 65 accessions combined (labeled as “ALL_SNP_POS”). Of which, approximately one-tenth were common locations and shared obtained across all 65 accessions (labeled as “COMMON_SNP_POS”). GBS markers obtained were distributed throughout the entire lengths of the *Musa* chromosomes (as expected) as shown in the chromosome position plot below.

**RESULTS**

(1) Factorial analysis was performed using 25,115 sites shared across all 65 *Musa* accessions. The accessions were clustered according to the expected genome composition. The A-only and B-only containing genomes were seen as the extremes of the first axis as expected.

(2) A neighbor-joining tree was constructed using 75,981 sites shared across 39 AAB accessions. The node for *Musa ornata* was grafted afterwards for tree rooting. The majority of the African AAB plantains (green labels) were clearly separated from other AAB accessions.

**CONCLUSIONS**

(1) Genetic diversity between the A and B versions of the *Musa* genome is higher than inter-A-genome variations, as expected.

(2) GBS markers provide a high resolution sequence-based approach to study genetic diversity for *Musa* subgroups such as the African plantains (AAB).

(3) Further analysis will be needed to compare the resolution of the GBS method with existing genotyping methods for studying *Musa* diversity.

REFERENCES


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