

**W068 The Sequence of the Banana (*Musa acuminata*) Genome**

*Date: Tuesday, January 17, 2012*

*Time: 10:20 AM*

*Room: Pacific Salon 6-7 (2nd Floor)*

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We produced a reference genome sequence of banana. The *Musa* accession selected for sequencing is a doubled haploid of the accession 'Pahang' (DH-Pahang). This accession belongs to the *Musa acuminata* species (AA genome) *malaccensis* subspecies. We generated 20.5X coverage of the 523 Mb genome of DH-Pahang (estimated by flow cytometry) using paired and single 454 reads, complemented by Sanger plasmid- and BAC- End Sequences. An additional ~50X coverage of Illumina shotgun data was produced in order to ensure a high quality sequence draft. The assembly, performed with Newbler software, covers 472.2 Mb which represent 90% of the genome of DH-Pahang. A high-density genetic map was produced using SSR and DArT markers that enabled anchoring 70% of the assembly in 11 pseudo-chromosomes. We identified 36,542 protein-coding gene models using a reconciliation approach taking ESTs, protein sequences and *ab initio* data as input.

The general features of the *Musa* sequence and its comparison with other sequenced genomes, in particular from the Poaceae, will be presented.

This project is carried out in the framework and with the participation of partners of the Global Musa Genomics Consortium.

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