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“Bridging the gap between increasing knowledge and decreasing resources”

Characterisation of Wild *Musa* Accessions Recently Introduced to the International Gene Bank

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Abstract

Bananas and plantains (*Musa* spp.) are one of the most important world trade commodities and are a staple food for millions of people in countries of the humid tropics. The production of bananas is, however, threatened by the rapid spread of various diseases and adverse environmental conditions. The *Musa* genetic diversity, which is of paramount importance for breeding of resistant cultivars, needs to be preserved and better characterised. The world's largest banana and plantain collection is managed by the Bioversity International Transit Centre (ITC) in Belgium and contains more than 1500 accessions maintained *in vitro*. The collection is being continuously expanded by new accessions representing various edible cultivars, improved materials and wild species from different parts of the world. Recently new germplasm was collected in Indonesia and successively introduced into the international *Musa* gene bank. The aim of this work was to characterise the genotype of these accessions in order to shed light on their genome structure and to confirm their taxonomic classification. A total of 21 wild *Musa* accessions were analysed and their nuclear genome size and the genomic distribution of ribosomal RNA genes were determined, showing a high degree of variability in both characters. Genotyping with a set of 19 microsatellite markers identified *Musa* species that are closely related to the studied accessions and provided data to aid in their classification. Sequence analysis of their internal transcribed spacers ITS1 and ITS2 suggested that some of the accessions are of interspecific hybrid origin and/or represent backcross progenies of interspecific hybrids.

Keywords: FISH, genome size, genotyping, musa, rDNA