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The Musa Germplasm Information System Enhances Knowledge of Banana Diversity

Max Ruas, Stéphanie Channelière, Guilhem Sempere, Manuel Ruiz, Elizabeth Arnaud, Ines Van den Houwe, Jean-Pierre Horry, Nicolas Roux

Abstract

Bananas (*Musa* spp.) are a staple food and vital source of income for millions of people. These livelihoods in developing countries depend on over 1000 traditional varieties that are mostly consumed locally.

Because *Musa* cultivars are usually seedless, their genetic diversity must be conserved as full-size plants or plantlets, in field collections or in *in vitro* genebanks. More than 6000 accessions are conserved in about 60 *Musa* national collections. The Global *Musa* Germplasm Collection (ITC) in Belgium, managed by Bioversity International, stores more than 1400 *Musa* germplasm accessions in trust. The utilization of the germplasm in the collection depends on the availability of information relating to the characteristics of each germplasm accession. In 1997, the *Musa* Germplasm Information System (MGIS) was developed. It is a global exchange system and the most extensive source of data on *Musa* genetic resources. It contains information on 5522 accessions managed in 22 banana collections, including passport data (where and when the germplasm accession was collected, donated or developed), botanical classification, morpho-taxonomic descriptors, and evaluation data (characteristics such as agronomic traits, disease, and stress tolerance) as well as many different photographs. Each participating collection enters and manages its own accession data, which is centralized by Bioversity. Links have been created to external data sources such as the System-wide Information Network for Genetic Resources (SINGER), under which FAO in-trust accessions held by ITC are published. MGIS has been recognised by the Generation Challenge Programme as a model system for storing accession-level data. However, it represents an incomplete dataset due to either the lack of capacity or motivation by several collections to contribute to it. The database has undergone two upgrades (see new release <http://www.crop-diversity.org/banana/>) and new features should be made available in the coming months, such as links to a molecular database (TropGENE DB), Geographic Information System (GIS) information, data quality control and inter-collection data comparison.