Assessment of genetic relationship in Musa using male flower descriptors and molecular markers

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Abstract:

The genetic relationship among twelve Musa accessions was assessed using male flower descriptors and two molecular markers: sequence related amplified polymorphism (SRAP) and amplified fragment length polymorphism (AFLP). Both systems were able to discriminate among accessions by showing good separation based on cluster analysis and by generating several unique markers for certain genotypes. The similarity matrices generated by the molecular markers presented a highly significant correlation and both molecular markers were significantly correlated with the morphological data. Among the male flower descriptors, the compound tepal basic colour was cream or white in Musa acuminata (A-genome) accessions, pink in M. balbisiana (B genome) and yellow in Musa ornata and Musa schizocarpa. Moreover, the compound tepal pink pigmentation was unique in all accessions having the B-genome (M. balbisiana, diploid (AB) and triploid (AA and ABB) hybrids), while both yellow-tinted free tepal and white ovary basic colour were distinct for M. ornata and M. schizocarpa. On the other hand, SRAPs and AFLPs showed several specific bands for certain accessions, with 31 and 25 bands, respectively, specific for M. ornata, and 8 and 25 bands, respectively, specific for M. schizocarpa. In addition, 2 and 4 bands were common between M. ornata and M. schizocarpa, and 9 and 4 shared among accessions having a B-genome: M. balbisiana, and triploid and diploid hybrids (AB and ABB, genomes), generated by each of the two markers, respectively. These specific markers for morphological and molecular descriptors are very important and could be helpful in Musa genotyping and genetic diversity assessment.

Keywords:

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