Evaluation of SSR allelic diversity on a broad sample of Musa species, discriminating ability at the species and subspecies level, and robustness of the results obtained.


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In order to insure further reliable diversity and phylogenetic analysis of Musa complex, the usefulness of 22 simple sequence repeat (SSR) loci is evaluated on a sample of 549 accessions. Robustness of the results was checked by comparing the genotyping results from 4 SSR on the same accessions, in two independent laboratories. We concluded that these markers are suitable for accurate diversity analysis when using appropriate standards, even if some problems linked to PCR amplification still remain with banana accessions leading to less than 10% of discrepancy. Looking at the allelic diversity of these markers within the 549 accessions, we observed good discrimination between Musa acuminata and Musa balbisiana, the main species in relation to edible bananas, while none at the intra specific level between Musa acuminata subgroups. Analyzing allelic diversity within the main triploids subgroups, we concluded to their likely monoclonal origin. The results also showed some discrepancies between the main groups leading to hypothesis on their evolutionary process.