

Genetic Diversity in *Coffea* Genus Using Microsatellites Loci

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SUMMARY

The objective of this study was to precise the known diversity in this genus with a whole genome coverage microsatellite set. Microsatellites markers derived from three different origins (SSR enriched library, gene sequences and BAC library?) were applied to a set of 45 individuals representing 20 species. The aim of this work was to validate with a large set of microsatellites previous diversity studies made with other markers (RFLP, isozymes) and to relocate the genetic diversity of *C. canephora* in a global context. Our results clearly validate the previously described geographic groups of the *Coffea* genus. Considering the rapid evolution of microsatellites, the genome organisation and the origin of the *C. Arabica* genome is discussed. Moreover, the interspecific transferability of microsatellites defined on a specific species was very good. The focus made on several species allowed us to make some comparisons on several genetic parameters e.g. PIC and mean number of alleles. The results and the future work on the basis of this set of markers and individuals are discussed.