

Anchor Markers for Comparative Mapping within the *Coffea* Genus

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SUMMARY

In order to unravel the *Coffea* genomic reorganization, we focused on comparative mapping within the *Coffea* genus and between *Coffea* and related families such as Solanaceae. Prerequisites for comparative mapping are a genetic linkage map for each species and a common set of DNA markers that can be used to align the maps. With this objective, we started developing anchor markers corresponding to two classes: 1) anonymous genomic sequences such as SCAR markers derived from AFLPs as well as microsatellite markers, and 2) coding genomic sequences (derived from ESTs: e.g. EST-SSR, COS). For all markers analysed in this study, we obtained good transferability among *Coffea* species even when considering species belonging to different phylogenetic clades. These locus-specific markers will facilitate assembly of a panel of “anchor” PCR-based markers for the study of similarities and differences in the structure and function between *Coffea* genomes. Furthermore, we have defined an initial set of 54 highly conserved, single copy genes—COS markers—which can be used as markers for comparative mapping between the tomato and coffee genomes. These comparative maps will not only shed light on the nature of genome evolution, but will also facilitate comparative mapping studies of qualitative and quantitative traits.