Nucleotide Diversity of Genes Involved in Sucrose Metabolism. Towards the Identification of Candidates Genes Controlling Sucrose Variability in *Coffea* sp.

D. POT[1,2], S. BOUCHET[1], P. MARRACCINI[1,2], F. DE BELLIS[1], P. CUBRY[1], I. JOURDAN[1], L. F. P. PEREIRA[3], L. G. E. VIEIRA[2], L. P. FERREIRA[2], P. MUSOLI[4], H. LEGNATE[5], T. LEROY[1]

[1]CIRAD (Centre de Coopération Internationale en Recherche Agronomique pour le Développement) TA 80/03 Avenue d'Agropolis, 34398 Montpellier Cedex 5 France
[2]IAPAR (Instituto Agronômico do Paraná) LBI-AMG CP 481 86001-970 Londrina (PR) Brazil
[3]EMBRAPA Café / IAPAR
[4]NARO-CORI P.O. BOX 185 Mukono Uganda
[5]CNRA Ivory Coast

SUMMARY

Quality and drought stress tolerance are two important targets for *Coffea* species cultivation. Currently, efficient genetic improvement of these traits is still hampered by the lack of early and cheap predictors. In this context, identification of molecular tools linked to these traits would significantly improve breeding efficiency. Based on the available literature, different metabolisms involved in the variability of both drought tolerance and coffee quality can be proposed. Based on this information, a study was initiated in *Coffea* species, aiming at estimating nucleotide diversity of four sucrose metabolism enzymes (Sucrose Synthase, Cell Wall Invertase, acid Vacuolar Invertase and Sucrose Phosphate Synthase). The two mains objectives of this work were i) to assess the level of variability of these genes within the whole area of distribution of *Coffea canephora,* and within 15 related *Coffea* species representing the four groups of diversity of this genus, and ii) to identify polymorphisms useful for mapping and association genetic studies. Almost 200 polymorphisms (SNP, INDELS, SSR) were identified through sequencing of *Coffea canephora* genotypes. In addition, analysis of the variability of these genes between different *Coffea* species allowed the identification of 300 additional polymorphic sites. Parallel in-silico analysis of EST resources confirmed the interest of this approach towards the identification of polymorphisms in *Coffea* sp. Identification of nucleotide polymorphisms will not only provide useful markers for traditional genetic studies (genetic mapping, population genetics, association studie) but also provide criteria to infer the evolutionary history of the analysed genes. Such information will be particularly relevant to select the best candidate genes to test in future association studies.