GENETIC DIVERSITY AND MOLECULAR MAPPING OF COFFEE

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The large number of named varieties and selections of arabica coffees hides the very narrow genetic diversity of the base populations from which they were selected (4). Historical evidence indicates that these base populations all descended from the few trees that survived various efforts to spread arabica coffee from Southern Arabia, now Yemen, into the main coffee-producing areas. The cultivars present therefore, a homogeneous agronomic behaviour characterised by a high susceptibility to many pests and diseases, and very low adaptability. Enlarging the genetic base and improvement of arabica varieties have become a crucial priority toward an economic and sustainable coffee production. Spontaneous accessions collected in the primary centre of diversity as well as wild relative *Coffea* species constitute a valuable gene reservoir for breeding purposes.

IRD aims to develop basic knowledges and genetic engineering strategies, required for an efficient and rational use of genetic resources. In recent years, molecular marker techniques have gained widespread applications in many fields of plant genetics and breeding. Regarding *C. arabica*, several lines of research are concerned (2).

GENETIC RESOURCES

In addition to germplasm collection screening for desired characteristics (3), molecular marker analyses are performed (13). These genetic diversity analyses have already increased our understanding of the relationships among coffee cultivars and between the cultivars and the spontaneous accessions collected in the primary centre of genetic diversity in Africa. We intend to propose improved management practices of collection and to assist breeding programmes in the identification of promising genitors.

GENOME CHARACTERISATION

C. arabica is the only polyploid species (2n =4x= 44) in the genus. By combining molecular markers (6, 10, 12) and DNA *in situ* hybridisation, we sought to gain insights into its genome organisation (8, 11). An amphidiploid structure was demonstrated and the diploid progenitor species identified. Further work should determine the degree to which the ancestral genomes have evolved in the amphidiploid, the chromosome meiotic pairing control, and the role of intergenomic interactions in gene expression.

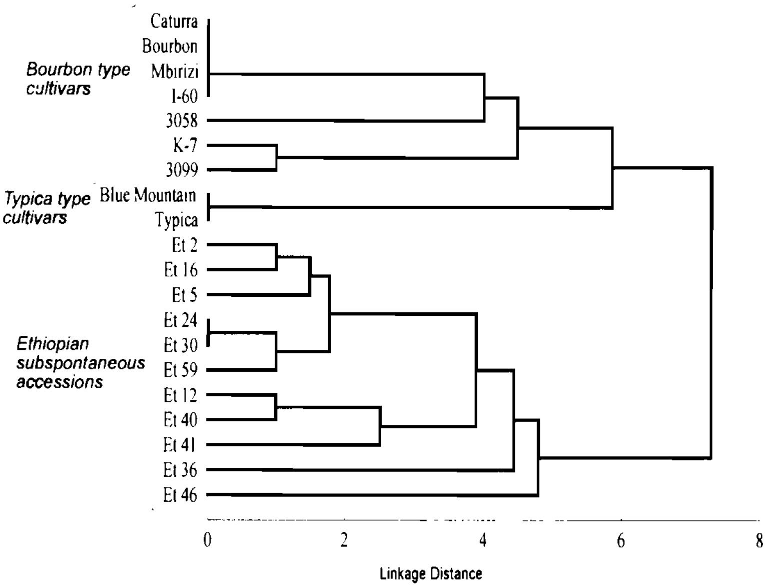

Fig. 1 Dendrogram of *Coffea arabica* accessions based on RAPD data and generated by single linkage cluster analysis (13).

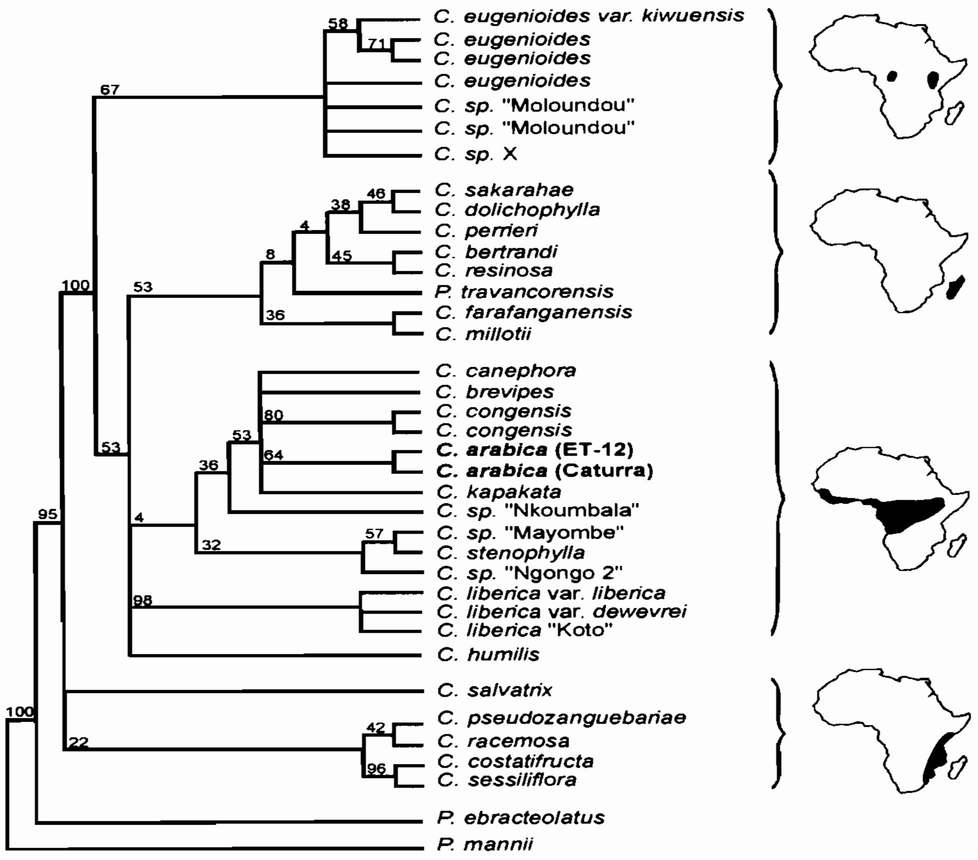

Fig. 2. Strict consensus Wagner tree resulting from parsimony analysis of ITS 2 (nuclear ribosomal DNA) sequence data. Numbers above the node represent bootstrap values (%). Geographical distributions of the majo groups are also indicated (10).

• GENOME MAPPING AND TAGGING OF USEFUL GENES

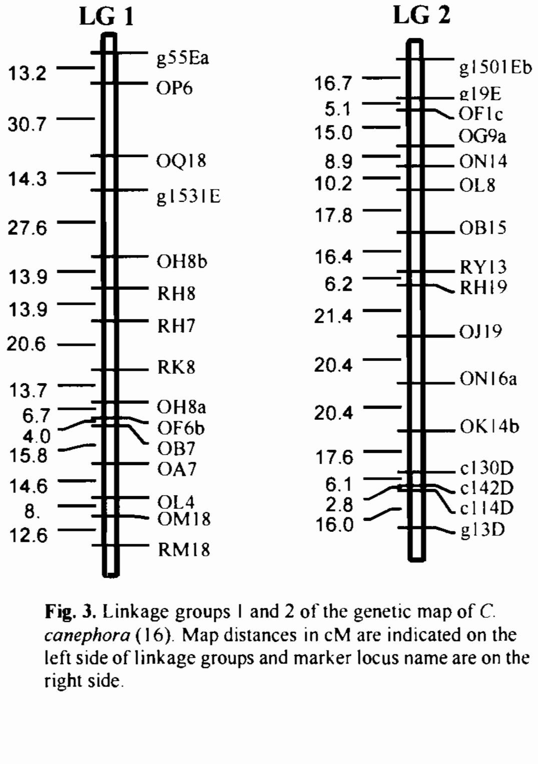

Fig. 3. Linkage groups 1 and 2 of the genetic map of *C. canephora* (16). Map distances in cM are indicated on the left side of linkage groups and marker locus name are on the right side.

A genetic linkage map of *C. arabica* is being constructed based on a F_2 population derived from a cross between an improved cultivar and a wild type. One objective is to determine the genome location and genetic contribution of genes controlling important traits of coffee plant. Gene cloning is also considered. Special emphasis is given to pest and disease resistances, quality-related traits, and male sterility (7, 9). Monitoring of gene introgression to *C. arabica* from wild diploid coffee species especially *C. canephora* and Timor Hybrid derivatives, is expected to be considerably facilitated by the development of molecular marker-assisted selection (14, 15). RAPD markers closely associated with the *T* gene of resistance to Coffee Berry Disease have been already identified (1).

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