TOWARD THE CONSTRUCTION OF A GENETIC MAP IN COFFEE

P. LASHERMES [1], M. PAILLARD [2], P. MARMEY [1], M. C. GAVALDA [1], E. COUTURON [3], V. PÉTIARD [2], A. CHARRIER [1]

[1] ORSTOM, 911 Av. Agropolis, BP 5045, F-34032, Montpellier, France
[2] FRANCERECO S.A., 101 Av. G. Eiffel, F-37390, Notre-Dame-d'Oé, France
[3] ORSTOM, BP 434, Man, Côte-d'Ivoire

Construction of a genetic map of the coffee genome based on molecular markers has been initiated. First efforts are focused on *Coffea canephora* which presents the advantages of being a diploid and highly polymorphic species. The generated information will be extended to other species including the allotetraploid species *C. arabica*.

The segregating population selected for linkage analysis consists of 100 doubled haploid genotypes (DH) derived from the heterozygous clone IF 200. DH were developed using haploid embryos occurring spontaneously in association with polyembryony (Couturon and Berthaud, 1982), and are characterised by a strict homozygoty which leads to considerable advantages for linkage analysis and agronomic evaluation.

The DH population is being evaluated for agronomic and technological characteristics (adaptation to industrial processing, quality). To overcome the important inbreeding depression exhibited by the DH genotypes, most part of the evaluation is carry out on top-crosses involving the different DH genotypes and a common homozygous parent tester (HD 160-02). Important traits such as yield, susceptibility to leaf rust, bean size and fruit maturation have been scored ; first observations showed large genetic variability within the DH population (Lashermes *et al.*, 1993a).

Both restriction fragment length polymorphism analysis (RFLP) and random amplified polymorphic DNA assay (RAPD) are performed in order to find polymorphic DNA markers. For RFLP analysis, genomic and cDNA clones originated from arabusta libraries (Duchateau and Paillard, 1993) as well as short repeat oligonucleotides (microsatellite DNA) are used as probe. RAPD involves primers constituted by arbitrary decamer oligonucleotides (Lashermes *et al.*, 1993b).

A large screening of genomic probes and primers for detection of polymorphism within the DH population, and between IF 200 (parental clone of DH's) and DH 160-02 (homozygous parent tester) is being done. A considerable polymorphism has been observed. Concerning RAPD, 40 % of the tested primers detected polymorphism between IF 200 and DH 160-02, and 11 % within the DH population. Segregations of

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polymorphic markers observed on a large number of DH genotypes were in agreement with mendelian expectations.

The development of this genetic linkage map will bring important informations on coffee genome and chromosomal organisation, and may open up interesting aspects of crop evolution. High density DNA marker map offers the most direct approach for genetic analysis of quantitative traits, and may eventually form the basis for identifying and cloning genes of agronomic interest.

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