

Identification of molecular markers linked to a gene conferring resistance to coffee berry disease (*Colletotrichum kahawae*) in *Coffea arabica*

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Date: 2008-12

Abstract

Coffee berry disease (CBD) caused by *Colletotrichum kahawae* is a major constraint to Arabica coffee (*Coffea arabica*) production in Africa. One source of resistance to the disease is a natural interspecific hybrid between *C. arabica* and *C. canephora* and its derivatives. This study is aimed at deciphering the genetic basis of the host resistance and identification of molecular markers associated with it. CBD is a mature stage disease and in the absence of a mature mapping population, early detection of disease reaction phenotypes of mapping individuals is required. Two F₂ populations from crosses of cv. Catimor (resistant) and cv. SL28 (susceptible) were screened for resistance by a two step procedure. First, half of each population was screened 6 weeks after germination by inoculating hypocotyls with the pathogen. The surviving seedlings (G1) were considered to be resistant and were raised in a nursery together with the other unscreened halves (G2). Secondly, after one year, all the seedlings (G1 + G2) were screened by inoculation. Analysis of 57 microsatellites and 31 AFLP markers in 56 and 95 seedlings from G1 and G2, respectively, were performed. Eight AFLP and two microsatellites markers linked tightly to the resistant phenotype were identified and mapped to one unique chromosomal fragment introgressed from *C. canephora*. The gene conferring the resistance was localized within an 11 cM segment. It is concluded that the locus carries a major resistance gene designated Ck-1, which is likely to be synonymous to the T gene described in previous studies.