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ORGANISATION, SEQUENCE DIVERSITY AND EVOLUTION OF A  
DISEASE-RESISTANCE GENE CLUSTER IN COFFEE TREE (*COFFEA L.*)

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Pathogen resistance (R) genes of the NBS-LRR class (for nucleotide binding site and leucine-rich repeat) are found in all plant species and confer resistance to a diverse spectrum of pathogens. Although the ability of plant species to survive over evolutionary time might depend on their ability to maintain and generate useful levels of diversity at resistance loci, little is known about the mechanisms that drive NBS-LRR gene evolution. Various genetic mechanisms, including point mutations, recombination, unequal crossing over, and gene conversion has been proposed to account for the evolution of R-genes. Furthermore polyploidy (whole genome duplication) that gives rise to organisms with multiple (3x, 4x...) sets of chromosomes, is a major evolutionary process in plants. It is now well established that most, if not all, wild and cultivated plants including those with small genomes (rice, *Arabidopsis*, grapevine) have undergone at least one cycle of whole-genome duplication during the course of their evolution. *Coffea arabica* is a young allopolyploid species and represents a good model to study mechanisms of gene evolution after polyploidization. By combining physical mapping using a bacterial artificial chromosome (BAC) library of *C. arabica* and sequencing of two BACs, organization of a cluster of disease resistance genes was established on the constitutive genomes of *C. arabica*. The relationships (orthology versus paralogy) of the different members of the resistance gene family identified on the two homeologous chromosomes was found out and sequence comparison between the two homeologous regions was carried out. In addition, the complete sequences of identified disease resistance genes were determined in different diploid *coffea* species representing the different biogeographical groups of coffee tree species. Evolutionary relationships and mechanisms were assessed based on DNA sequence analysis. Consequences in terms of speciation and evolution within the genus *Coffea* and coffee genetic resources preservation will be presented and discussed.

Ribas A, Etienne H, Combes M-C, Dechamp E, Lashermes P (2008) Organisation, sequence diversity and evolution of a disease-resistance gene cluster in coffee tree (*Coffea L.*). In *22nd International Conference on Coffee Science (ASIC), Campinas, Brazil, Sept. 14-19.*