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TITRE :
Identification of Theobroma cacao genes differentially expressed during Phytophthora infection.

RESUME :
Pod rot, caused by different species belonging to the genus Phytophthora, is the main cause of harvest losses worldwide for cocoa production. Between 15% to 80% of losses could be observed according to the Phytophthora species, P. megakarya being the most aggressive. Varieties' improvement with a sustainable resistance has been identified as a priority of research programs of producer countries with about 14 millions of workers getting their income from the cocoa cultivation.
Cocoa resistance to Phytophthora is quantitative and polygenic. The objectives of this project is to improve our knowledge of molecular mechanisms involved in the partial cocoa resistance in order to develop efficient tools of breeding to increase the resistance level of cocoa trees. This work aims to develop functional genomic approaches to identify candidate genes involved in this partial resistance.
Suppression subtractive hybridisation (SSH) was used to generate cDNA libraries representing genes differentially expressed in response to cocoa/Phytophthora interactions.
More than 15,000 ESTs were sequenced (in the frame of a GENOSCOPE project) and used for these studies. ESTs were analyzed by Blastn and/or Blastx search against NCBI data base. A little part of the clones had no homology with sequences and/or function already describe. The other part had significant matches to known genes. Among them, sequence homologies were found with pathogenesis related function knowledge, as PR protein (PR-1, glucanase, chitinase …), kinases, receptors (LRR), and transduction factors.
Gene expression was conducted on leaf tissues of a progeny created in Papoua Nouvelle Guinea derived from a cross implied forastero and haut amazonien. Two resistant individuals with the better allele combination and two susceptible individuals with the less allele combination were kept and used for this work.
Nylon cDNA macro arrays were used to assess the differentially expressed genes of the resistant and the susceptible cocoa clones infected by Phytophthora megakarya.. Libraries were screened with the inoculated-subtracted probes and non-inoculated reverse-subtracted probes, to reduce the candidate clones. We developed a novel set of macro arrays and obtained expression profiles during the several steps of phytophthora infection kinetic. Several genes differentially regulated between resistant/susceptible individuals revealed in this study are already known as integrated in signal transduction or in plant defence responses of other species.