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Identification of QTLs linked to resistance for ceratocystis wilt in cacao.

Santos, R.M.F.¹; Clement, D.^{2,3}; Silva,S.D.V.M.³; Lopes, U.V.³; Mello, J.M.R.⁴; Damaceno, V.O.⁵; Pires, J.L.²; Micheli, F.^{2,6}; Gramacho, K.P.³.

¹Doutorando UESC/PPGBM; ²PhD CIRAD; ³PhD CEPLAC/CEPEC; ⁴Graduando IC CNPq/CEPLAC/CEPEC; ⁵Tecnica CEPLAC/CEPEC; ⁶Doutora DCB/UESC; E-mail: gramachokp@hotmail.com

Ceratocystis wilt (CW) of cacao, caused by *Ceratocystis cacaofunesta*, is a drastic disease that results in plant death. The pathogen was recently identified in the major cacao-producing region of Brazil-Bahia. The identification of genetic markers tightly-linked to disease resistance loci are valuable tools for the development of resistant cultivars using marker-assisted selection (MAS). The objectives of this study were to: i) test the segregation for CW resistance of a F₂ (Scavina-6 x ICS1) population; ii) understand the genetic control of CW resistance; and iii) detect the regions in the cacao genome that are possibly involved with CW resistance using a F₂. Branches of the 143 progenies of six years old were wounded by making a 3 mm deep cut from the outer bark into the wood with a sterile scalpel, and inoculated with a 20 ul drop of a spore suspension of 3 x 10⁴ CFU/mL. Twelve branches per genotype (3 plants x 4 branches) were used. The inoculated plants were monitored daily for death or wilting. After 15 days, each branch was sliced open vertically above and below the point of inoculation, and the length of xylem discoloration (LXD) was measured. The inoculation method used allowed to quantitative phenotype the population. The LXD followed a continuous distribution. These results imply that the resistance was quantitatively inherited. QTL analysis revealed two genomic regions (in linkage groups 3 and 9) associated with CW resistance. The QTLs explained individually from 6.9 to 8.6% of the phenotypic variation. The QTLs identified are crucial for identifying genes for resistance and might be applied in the genetic breeding of cacao aiming MAS.

Host: *Theobroma cacao*, cacao

Pathogen: *Ceratocystis cacaofunesta*

Disease: Ceratocystis wilt

Area: Genetic Breeding