

GENOTYPING *CASTANEA SATIVA* × *C. CRENATA* AND *C. SATIVA* × *C. MOLLISSIMA* F1 HYBRIDS USING NUCLEAR SSRs

D. Batista, T. Valdivieso, L. Santos, O.S. Paulo, J. Gomes-Laranjo, R. Costa

Keywords: chestnut, controlled crosses, interspecific hybridization, microsatellites, molecular markers, allele segregation

Abstract:

In this study, full-sib progenies were established from controlled crosses made between *C. sativa* × *C. crenata* (SC) and *C. sativa* × *C. mollissima* (SM) for the introgression of resistance genes into the European chestnut. We report SSR genotyping of interspecific hybrids for 8 loci as an initial step towards identifying molecular markers associated to ink and blight disease resistance in chestnut. Preliminary results demonstrated one locus segregating at a ratio that was significantly different from the one expected (EmCs15) for the SC progeny. Compared to the parent trees, different alleles were observed in some individuals of both progenies. These data may provide a good basis for studying SSR mutation rates and the genetic stability of the species. On the other hand, new alleles were identified for *C. crenata* and *C. mollissima* in three different loci, providing useful information for the accurate characterization of these species and related hybrids. We expect that after a wide screening of these hybrid families with different molecular markers, specific genotypes will be associated to susceptible/resistant phenotypes.