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Poster Abstract - C.38

MOLECULAR MARKER-ASSISTED CHARACTERIZATION OF MULBERRY (*MORUS* SSP.) CULTIVARS FOR THE CONSTITUTION OF A CORE COLLECTION

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Mulberries are members of the genus *Morus* L., a taxonomic group showing a great genetic variability and adaptability to different environmental conditions. This study deals with the use of AFLP-based fingerprints as a tool for estimating genetic variability within as well as among three different mulberry species (i.e., *M. alba* L., *M. latifolia* Poir. and *M. bombycis* Koidz.) Preliminary flow cytometric analyses pointed out the presence of diploid as well as triploid accessions. A high level of polymorphism (72.2%) was found over all the 48 accessions analyzed. Genetic similarity (GS) within single *Morus* species ranged from 0.845 (*M. bombycis*) to 0.884 (*M. alba*) being intermediate in *M. latifolia* (0.869). The between-species mean genetic similarity estimates based on pair-wise AFLP marker fingerprint comparison were very similar ranging from 0.861 to 0.874. The partition of the genetic variation over the three *Morus* species was unexpected: a proportion of the among-species genetic diversity as low as G_{ST}=0.084 pointed out that about 92% of the total genetic diversity found among *Morus* accessions is due to DNA polymorphisms within a species, while only 8% of the total variation was highlighted among species. Our data indicate that some of the introduced accessions showing distinctive phenotypes, clearly differentiated from those revealed in the original habitat where they have been selected and adapted, hide an identical genotype. Current studies are aimed to set up a high reproducible identification method on the basis of accession-specific AFLP marker sequences to be used in simple PCR-based haplotyping.