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Poster Abstract – A.41

MOLECULAR FINGERPRINTING OF ASPARAGUS ACCESSIONS *VIA* MICROSATELLITES AND ISOENZYME-DERIVED POLIMORPHIC SEQUENCES

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The overall goal of asparagus breeding in Italy is the development of all-male hybrids (HF1) from the combination of doubled haploid clones (Falavigna et al, 2002). The characterization of six HF1 commercial hybrids (Eros, Marte, Ercole, Giove, Italo, Zeno), their parents and the outgroup accession "Montina", belonging to *Asparagus maritimus* Miller, was performed by means of Simple Sequence Repeats (SSR) generated from a public expressed sequence tag (EST) collection (Caruso et al, 2007). All genotypes were also phenotypized and analyzed by means of isozyme-derived polimorphic sequences following the protocol developed by Wang and coworkers (2007) for the generation of new molecular markers. The isozymes were chosen on the bases of results obtained by Gonzales-Castañon (1999) and Falavigna and coworkers (2008). The sequences of the most polymorphic isozymes were retrieved from public databases for the analysis of conserved regions.

The results show the opportunity to use SSR and isozyme-derived PCR-based markers together with phenotypic descriptors for the univocal identification of asparagus hybrids. Furthermore, the development of PCR-based markers from isozyme gene families gives the access to a large amount of "old" data for the development of new molecular markers.

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