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Poster Abstract – A.72

SPECIES RELATIONSHIP AND HYBRID IDENTIFICATION IN *LILIUM* USING RAPD MARKERS

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Lilium, chromosome number, genetic diversity

The genus *Lilium* includes about a hundred species classified into seven Sections distributed through the cold and temperate region of the Northern hemisphere. This germplasm represents an important source of useful genes as well as a "reservoir" of allelic diversity for breeding purposes. However, gene introgression through the wide inter-specific hybridization is hampered by incompatibility barriers at pre- and post-fertilization levels including F_1 hybrid sterility.

In the present investigation, putative inter-specific hybrids of *Lilium* obtained by conventional crosses were characterized. The hybrids and their parents were analyzed by RAPD markers at an early seedling stage as well as by morphology at different developmental stages. In addition, RAPDs were used to estimate the genetic diversity in a sample of *Lilium* species that was also characterized for chromosome number and pollen stainability. The chromosome number of the material used in the experiments including different *Lilium* species (*L.bulbiferum, L.candidum, L. martagon ,L. .formosanum L miryophyllum,.L. pyrenaicum, L.pumilum, L.willmottiae, L.regale*) as well as some cultivars (Snow Queen, Cascade, Pollyanna) resulted diploid ($2n=2x=24$). The exception was represented by Elite cultivar that is triploid.

Inter-specific crosses were made between three species, *L. formosanum, L. miryophillum, L. regale*, and four cultivars: Cascade, Elite, Pollyanna, Snow Queen. Capsules were obtained from all cross combinations, except from Elite x *L. miryophillum*, Elite x *L. regale* and Pollyanna x *L. regale*. Average seed number per capsule was generally lower in the crosses than in selfings. Average germination time was also estimated: in particular, *L. formosanum* x Elite germinated significantly later as compared to parents.

Firstly, RAPD analysis was performed on the parental lines and on the other *Lilium* species. 35 random primers revealed polymorphic amplified DNA fragments. The percentage of polymorphic bands for each primer ranged from 0.1 to 9 %. Genetic similarities among *Lilium* species, estimated through simple matching coefficient, based on both shared and unique amplification products, ranged from 0.53 to 0.69 across nine species. The highest similarity was detected between *L. regale* and *L. myriophyllum*. The dendrogram obtained using UPGMA cluster analysis evidenced the *Lilium* species subdivided into two major groups, one including *L. formosanum* and *L. willmottiae*. To identify the hybrids, nine random primers were used since they were informative to discriminate between parents. So far, *L. formosanum* x Elite hybrids have evidenced the paternal band.

DNA markers generated by RAPDs allowed the identification of genotypes during a very early stage of plant development giving an helpful support to the breeding programmes of *Lilium*.