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USE OF SINGLE SEQUENCE REPEATS, SINGLE NUCLEOTIDE POLYMORPHISMS AND PLOIDY ANALYSIS IN GENOTYPING LANTANA CAMARA BREEDING CLONAL LINES

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In ornamental species breeding, molecular genotyping analyses provide useful information for planning crosses, predicting plant traits, assessing the genetic identity of varietal lots and protecting the legal rights of breeders (i.e. Plant Breeders Rights, PBRs). Due to the costs of the first sequencing platforms, most past genotyping studies have been accomplished with relatively few highly variable microsatellite loci (or SSRs). However, the progressive collapse of sequencing costs made HTS (High-Throughput Sequencing) platforms accessible also to minor crop species and ornamental plants, leading to a progressive replacement of SSRs with Single Nucleotide Polymorphisms (SNPs).

In this study, we used SNP and microsatellite datasets on 24 clonal lines of *Lantana camara* L. (2n=2x=22, 2C value: 2,93 Gb) to evaluate any concordances/discrepancies between the data obtained from the two types of analyses.

Since the number of chromosomal sets deeply influences the genotyping analysis, we firstly determined the ploidy of each accession. Ploidy is also relevant when planning crosses, since peculiar phenotypic traits were found to be associated with specific levels of ploidy. In particular, Lantana polyploids are characterized by unpleasant smells and apical dominance leading to habit asymmetries, whereas triploids are less fertile and hence useful to develop non-invasive varieties. The flow cytometry analysis allowed to observe three main different signals, consistently with the values available from the scientific literature for diploids, triploids and tetraploids. Furthermore, in parallel, a chromosomes count was carried

out on some random genotypes representing the three ploidy levels. The results obtained confirmed the observations made through the flow cytometry.

For the SSR genotyping, 13 markers available in the scientific literature for *L. camara* were tested and 8 resulted polymorphic. The genotyping analysis did not prove to be very effective in discriminating the 24 breeding lines. Although few accessions showed very low similarity values (as low as 27.3%) and the total variance explained by the two principal components was higher than 60%, a conspicuous number of samples resulted identical (100% genetic similarity).

On the contrary, the double digest Restriction Associated DNA sequencing (ddRADseq), allowed the identification of thousands of SNPs and each sample resulted perfectly distinguishable from the others. We demonstrated that ddRAD-Seq generated SNPs are only partially comparable to microsatellites for measuring genetic parameters.