Identification of proteaginous pea cultivars (*Pisum sativum* L.) using microsatellites molecular markers

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Abstract: Conventionally morphological descriptors are routinely used for establishing the identity of varieties. This kind of descriptors has some disadvantages, namely most of them are quantitative, controlled by several pairs of genes, and their expression is influenced by environmental factors. Molecular markers have a potential to facilitate this procedure, increase the reliability of decisions, and substantially save the time and space needed for experiments. In this study we intended to identify 20 cultivars of proteaginous pea (*Pisum sativum* L.), registered in the Community Catalog of Varieties, by microsatellites molecular markers. After DNA extraction, seven different *loci* were analyzed. PCR amplifications were conducted and the resulting fragments were separated on an 3,5% MS-8 agarose gel in TBE buffer, at 90V/h. The gels were analyzed for the presence/ absence of bands and a table with binary code was made. The data were processed with the statistical software NTSYS-pc, using the SIMQUAL module and Jaccard similarity coefficient, followed by UPGMA cluster analysis. With the analysis of six polymorphic *loci* was possible to distinguish almost all of cultivars. The most informative *loci* were AD61 and AB53. The cluster analysis of SSR markers separated the pea genotypes into two distinct clusters. The first cluster included the five cultivars: Isard, Cartouche, Audit, Corrent and James. The second cluster included the remaining fifteen cultivars and was further divided in two subclusters. The first subcluster had the Portuguese genotype Grisel and second subcluster contained the remaining fourteen cultivars. In this subcluster Ideal and Alezan had 100 percent similarity. There was a low number of heterozygous *loci* which is consistent with the nature of self pollinated species. The results showed a high potential and resolving power of SSR markers in distinctness assessment. SSR markers might also be useful in *Pisum sativum* L. germplasm management and genetic diversity studies.

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