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Poster Abstract - C.33

THE USE OF AFLP MARKERS AND CHARACTERISATION DATA TO SAMPLE DIVERSITY IN A CORE COLLECTION OF PHASEOLUS VULGARIS L.

G. LOGOZZO*, L. MACALUSO*, N. LACERENZA**, M. DILUCA*, S. BENEDETTELLI**, P.L. SPAGNOLETTI ZEULI*

*) Dipartimento di Biologia Difesa e Biotecnologie Agro-Forestali, Università degli Studi di Basilicata, Viale dell'Ateneo Lucano10, 85100 Potenza (Italy) - logozzo@unibas.it
**) Dipartimento di Scienze Agronomiche e Gestione del Territorio Agro-Forestale, Università degli Studi di Firenze, Piazzale delle Cascine 18, 50144 Firenze (Italy)

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A core collection is a subset of accessions from a larger collection of a particular crop species that represents, with a minimum amount of repetitiveness, the genetic diversity of that crop species and its wild relatives. With limited resources, it is difficult to manage large germplasm collections. Criteria that have included geographical, morphological, biochemical and molecular data, have been used to analyze genetic diversity in order to construct core collections. DNA marker systems, which provide large number of polymorphic loci dispersed in the genome could be used efficiently for development of core collections. From base collection of common bean (*Phaseolus vulgaris* L.) including 560 accessions, a collection of 305 accessions, was sampled from different gene pools: 79.7% from European gene pool, 12.8% from South America and 7.5% from Middle America. This collection was analysed for seven seed traits (length, height, width, shape, colour, colour pattern and coat pattern- IPGRI descriptor), SDS-PAGE phaseoline patterns and E-AGT/M-GAC fluorescent AFLP primer combination. Core collections, consisting of $r = 0.18 \times n$ accessions, were sampled by several sampling strategies, simple random sampling, random-stratified by log frequency of accessions by continent, random-stratified by log frequency of phaseoline pattern, that are not dependent of molecular markers, and one marker assisted sampling that maximize genetic diversity at AFLP marker loci. An independent verification of the core collection sampling efficiency was performed using geographical, morphological, biochemical and molecular data by comparing the genetic diversity found in each core collection with the variability of base collection. The AFLP-based strategy allowed to include the largest number of AFLP loci (n=37) in the core collection, all classes for seed coat pattern and seed shape, but a smaller number of countries (n=21 out of 35 in the base collection). The no marker-based sampling strategies reduced AFLP marker loci richness from n=37 (base collection) to n=27 in the core collections.

Our results confirmed that strategies based on information obtained from marker loci lead to retention of the maximum number of loci and are useful tool for plant breeders and germplasm collection curators to better understand the genetic diversity within a germplasm collection.