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GENETIC DIVERSITY IN A COMMON BEAN (*PHASEOLUS VULGARIS* L.) *EX SITU* COLLECTION OF ITALIAN LANDRACES

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Landraces (LRs) are vital genetic resources for breeding purposes, diversification of production, developing new farming systems and new quality products. The extent and distribution of the genetic diversity in a crop depends on its breeding system, geographical, ecological and human factors. Conservation of genetic variability is essential for present and future human well-being.

To date, the *in situ* or *ex situ* conservation strategies have been applied with little information on the genetic diversity that was being conserved. In order to improve conserved germplasm management, it is necessary to understand the genetic diversity that is present in collections.

Common bean LRs have been obtained from Italian farms and local markets, mostly located in Central Italy, and their seeds samples were used to establish an *ex situ* collection in DBVBAZ. In this study the amount of genetic diversity and its distribution in 159 Italian LRs were assessed using different approaches that included morphological (international descriptors), biochemical (phaseolin seed proteins) and molecular analysis (*Simple Sequence Repeats* markers). Results obtained showed a wide variation overall morphological traits, especially seed characters. The three major phaseolin types were found, 'C' (38.9%), 'S' (33.1%) and 'T' (28.0%) types. Nine of ten loci analysed were polymorphic and 82 different alleles were detected overall SSR loci.

Our findings on the extent and distribution of different aspects of genetic diversity in this Italian common bean LRs collection is an essential prerequisite to determinate what to conserve and how to conserve it. In addiction all the information collected will offer the opportunity to rationalize the collection, to develop a core collection and to exploit these resources for valuable traits.