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.