

EX SITU CONSERVATION OF LOCAL TRADITIONAL VARIETIES OF MAIZE: AN EXAMPLE OF WORKFLOW FOR THEIR MAINTENANCE

LANDONI M.*, FERRARI F.*, ROSSI G.*, STAGNATI L.***, BUSCONI M.**,
MAROCCO A.***, GHIDOLI M.***, PILU R.***

*) Department of Earth and Environmental Sciences, University of Pavia, Italy

**) Department of Sustainable Crop Production, Università Cattolica del Sacro Cuore, Piacenza, Italy

***) Department of Agricultural and Environmental Sciences-Production, Landscape and Agroenergy, University of Milan, Italy

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Agricultural biodiversity, according to the Convention on Biological Diversity definition, includes all components of biological diversity of relevance to food and agriculture: animals, plants and micro-organisms, at the genetic, species and ecosystem levels, which are necessary to sustain key functions of the agro-ecosystem, its structure and processes.

Conservation of biodiversity is fundamental for the agricultural ecosystem but environmental changes, increased population, agricultural intensification, changes in land use, replacement of traditional varieties by modern cultivars are gradually leading to its loss.

Two main strategies, different but complementary, are used to preserve biodiversity: the *in situ* conservation that allow the maintenance of a species in its natural habitat, on farm or in the wild, and the *ex situ* conservation i.e. the conservation of a threatened taxa outside its natural habitat, as live plants in fields and botanical gardens or as seeds, tissues and DNA in a gene bank.

The high costs for *ex situ* conservation, mainly due to the gene bank management, can be reduced through an exhaustive characterization aimed at a correct/univocal identification of the different accessions. This procedure will avoid the waste of resources caused by the conservation of

identical accessions registered with different names.

The germplasm bank created in 2005 in the Department of Earth and Environmental Sciences (DSTA) of Pavia University, currently hosts more than 700 different species, among them crops (cereals and horticultural species) and wild species, for a total of more than 3400 different accessions.

The first step for *ex situ* conservation is a preliminary characterization of each accession using a form where the accession history is recorded (accession name and origin, farmer data, sampling site, ideotype description, how long the accession has been cultivated, etc.).

The ideotype identity and homogeneity is checked, through cultivation of different accessions in the same environment, and eventually restored through 2 or 3 years of recurrent massal selection/progeny test by controlled crosses.

The accessions corresponding to the original ideotype are sown together with some benchmarks and checked during the development to collect data required to fill the UPOV form.

If the parameters taken into account do not allow the univocal identification of the different accessions, further quantitative characters, not included in UPOV form, are measured. If a deeper characterization is needed a molecular analysis by SSR (Simple Sequence Repeats) molecular markers or Genotyping by Sequencing (GBS) is performed on the different accessions.

Last step, the accessions whose unique identity has been ascertained are registered and collected in the germplasm bank.

In this poster we will describe the workflow for the *ex situ* conservation of 40 maize traditional accessions, sampled on the Lombardy territory and stored in germplasm bank.