

GENETIC STRUCTURE AND DIVERSITY IN *PHASEOLUS COCCINEUS* L. BY USING SSR (SIMPLE SEQUENCE REPEAT) MOLECULAR MARKERS

P. ARCALENI*, B. TIRANTI*, G. SPATARO*, G. ATTENE**, R. PAPA***,
P. SPAGNOLETTI ZEULI****, V. NEGRI*

*) Department of Plant Biology and Agro-environmental and Animal Biotechnology, University of Perugia, Borgo XX Giugno

**) University di Sassari

***) Università Politecnica delle Marche, Ancona, Faculty of Agriculture

****) Università della Basilicata

P. coccineus, genetic diversity, molecular markers, SSR, European germplasm

P. coccineus L. ($2n = 2x = 22$) originated in Mexico and Central America. It was introduced in Europe after the discovery of America and, nowadays, is widely cultivated because of its suitability to cool environments.

A first taxonomic treatment recognized five subspecies: *coccineus*, *formosus*, *glabellus*, *griseus* and *darwinianus*. Two of these subspecies are cultivated, *coccineus* and *darwinianus*, but only the former was present in Europe. A recent classification redefined the subspecies *darwinianus* as *P. dumosus*.

At the present, few information about the level of genetic diversity of the whole European germplasm of *P. coccineus* are available, even though genetic variation and structure in some landraces and populations of this crop from Spain, Central Italy and Poland were carried out. All these studies detected a high level of polymorphism.

The aim of this study was to compare the level of genetic diversity in landraces of *P. coccineus* from European and central America by using SSR (Simple Sequence Repeat) molecular markers. The comparison between the European and the Mesoamerican germplasm “core collections” allowed to:

- I. investigate the genetic variation and structure in *P. coccineus* landraces from a worldwide collection.
- II. improve the knowledge of the evolutive process of the European landraces, evidencing that genetic diversity was reduced and that a distinct genetic pool originated;
- III. obtain an overall picture for future plant breeding activities.

Data show that two distinct runner bean gene pools exist. The diversity present in Mesoamerican gene pool is higher in respect to the European gene pool. Introduction in Europe has originated a particular gene pool which should be the primary source of genetic variability for breeding activities in Europe.