DOMESTICATION HISTORY IN COMMON BEAN (\textit{Phaseolus vulgaris} L.): INFERENCES FROM MULTILOCUS SEQUENCE DATA

ROSSI M.*,**, MAMIDI S.*,***, MCCONNELL M.D.*,****, LEE R.K.*,****, BELLUCCI E.*,**, PAPA R.*,**, MCCLEAN P.E.*****

*) Department of Plant Science, University of North Dakota, Fargo, North Dakota 58105 (USA)
**) Dipartimento di Scienze degli Alimenti, Facoltà di Agraria, Università Politecnica delle Marche, Via Brecce Bianche, I-60131 Ancona (Italy)
***) Genomics and Bioinformatics Program, North Dakota State University, Fargo, ND, 58105 USA

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DNA sequence polymorphism carries genealogical information and allows for testing hypotheses on selection and population history, especially through coalescent-based analysis. Understanding the evolutionary forces at work in plant domestication and subsequent selection is of critical importance for the management of genetic resources.

In this study, we surveyed DNA sequence diversity in the wild–domesticated complex of common bean (\textit{Phaseolus vulgaris} L.). Cultivated common bean has two distinct gene pools (Middle American and Andean). Little is known about the effect of the separation of the common bean into gene pools and the subsequent domestication process on genetic diversity at the DNA sequence level.

Our objective is to study the effects of domestication and improvement on loci near and far from mapped domestication loci by sequencing 3’ portions of different genes in the three groups (wild, landraces and cultivar).

Overall, we analysed a sample of genotypes chosen on the basis of SSR data in order to represent the largest diversity within each set of accessions. We performed several statistical tests to identify the signature of selection due to domestication and crop improvement.

This very promising research provides the tools to identify genes of potential agronomic importance and to determine the effect of domestication and breeding on the structure of genetic diversity in the common bean genome.