World-wide Common Bean (*Phaseolus vulgaris* L.) Diversity and Race structure.

CIAT (M.W. Blair, H.F. Buendia, L. Diaz, J.M. Diaz, M.C. Giraldo, N. Moreno, L. Gonzalez, M.C. Duque, D. Debouck)
CAAS-China (X. Zhang, S. Wang), CNPAF-EMBRAPA-Brazil (M.J. Peloso, R. Brondani, T. Olivieras Borba)
Cornell University (S. Kresovich, S.E. Mitchell) , ECABREN/SABRN-E. and S. Africa (A. Asfaw, P. Kimani, R. Chirwa)
Fundación Pairumani-Bolivia (T. Avila, X. Rojas, A. Davila) INIFAP-Mexico (H. Gil, N.M. Pérez J. Acosta) INCA-Cuba (S. Lorigados)

Acknowledgments

This research has been supported by CIAT, national program partners and the SP1 subprogramme of the Generation Challenge Program

Introduction

Cultivated common bean germplasm is especially diverse due to the parallel domestication of two genepools in the Mesoamerican and Andean centers of diversity and due to the introgression between these gene pools and between cultivated germplasm and wild common bean populations. The two genepools can be morphologically distinguished into various races, however the association of these phenotypic differences with genetic structure have not been clear. In a set of genotyping projects for common bean with international partners we are trying to determine the genetic diversity existing in international and national germplasm collections representing wide genetic variability from both primary and secondary centers of diversity.

Objectives

- To survey international and national collections with microsatellite markers.
- To determine population structure and correlation of groups with morphological races of common bean.
- To identify a useful microsatellite marker set for diversity analysis in beans.

Publications

Blair MW, Díaz JM, Hidalgo R , Díaz LM, Duque MC (2007) Microsatellite characterization of Andean races of common bean (*Phaseolus vulgaris* L.). Theor Appl Genet (in press)

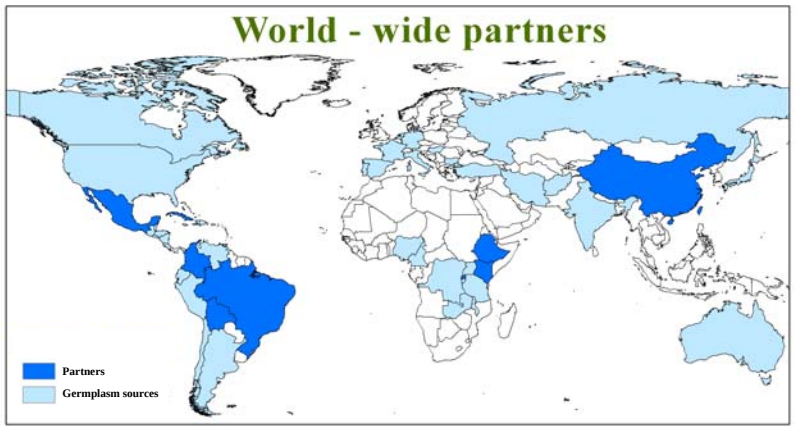
Blair MW, Giraldo MC, Buendia HF, Tovar E, Duque MC, Beebe S (2006) Microsatellite marker diversity in common bean (*Phaseolus vulgaris* L.). Theor Appl Genet 113:100–109

Díaz LM, Blair MW (2006) Race structure within the Mesoamerican gene pool of common bean (*Phaseolus vulgaris* L.) as determined by microsatellite markers. Theor Appl Genet 114: 143-54

Díaz LM, Díaz JM, Blair MW (2005) Diversidad genética de fríjol común (*Phaseolus vulgaris* L.) en Colombia. Fitotecnia Colombiana 5: 28-36

Research Summary

- Population structure in common bean is organized among gene pools (Meso and Andean) as well as races
- SSR analysis uncovers these groupings as well as finer levels of population structure which were not possible to distinguish with previous markers.
- Two major subdivisions are seen in each genepool validating the Durango-Jalisco, Mesoamerica, Nueva Granada and Peru races.
- Race Guatemala seems to be distinct within the Mesoamerica genepool and consists mainly of climbing beans; while the existence of race Chile within the Andean genepool is being confirmed.
- Introgression between the genepools is very evident as is probable introgression between cultivated and wild common beans.



Latin America	Africa	Asia
Brazil	Ethiopia	China
Bolivia	Kenya	
Colombia	Rwanda	World
Cuba	ECABREN	collection
Mexico	SABRN	CIAT

Training opportunities provided

NARs scientists:
- Asrat Asfaw, SARI - Ethiopia
- Gloria Santana, CORPOICA - Colombia
- Sandra Miranda Lorigados, INCA - Cuba
- Teresa Avila, CFP – Bolivia
- Tereza Oliveira Borba, EMBRAPA - Brazil

Graduate Students:
- Juan Manuel Díaz, Univ Nacional - Colombia
- Homar Gil, Univ. Tamaulipas – Mexico
- Lucy Díaz, Univ Nacional - Colombia
- Wilfredo Pantoja, Univ Nacional - Colombia
- Xiaoyan Zhang, IPGR-CAAS – China

UnderGraduate Students:
- Andrea Davila, Univ. San Simon - Bolivia
- Laura Gonzalez, Univ .Javeriana – Colombia
- Natalia Moreno –Uni.v Javeriana – Colombia
- Xímena Reyes, Univ. San Simon - Bolivia

Outputs and expected impact

- We have been able to select a reference set which represents the genetic structure found for the species which is divisible into the known genepools and two predominant racial groups per genepool.
- We have constructed a marker kit made up of both genomic and gene-based microsatellites.
- Impact on users will be two-fold:

1) better germplasm preservation strategies based on existing diversity across international and national collections.
2) better understanding of commercial seed classes and races to use in breeding combinations or in targeted introduction of germplasm.