Indian J. Genet., 75(4): 522-525 (2015)
DOI: 10.5958/0975-6906.2015.00084.X

Short Communication

Genetic divergence in landraces of common bean (*Phaseolus vulgaris* L.) from the Nilgiris

S. Priya and Franklin Charles Jose*

Plant Molecular Biology Lab, Department of Botany, Government Arts College, Stone House Hill P.O., Udhgamandalam 643 002, Nilgiris, Tamil Nadu

(Received: November 2014; Revised: July 2015; Accepted: August 2015)

Abstract

Genetic diversity of common bean (*Phaseolus vulgaris* L.) was assessed based on morphological traits and RAPD markers. The principal component analysis identified eight components with eigenvalue above 1.0 and together explained 84.35% of the total variation. RAPD based dendrogram showed two major groups corresponding to the Andean and Mesoamerican gene pools. These bean landraces retain a considerable level of heterogeneity. Our results suggest that a deep knowledge of germplasm is the best strategy for preserving the diversity of common bean available with tribal farmers in remote villages of Nilgiri hills.

Key words: Genetic diversity, morphological markers, *Phaseolus vulgaris*, RAPD markers

Common bean landraces from Northern parts of India were well characterized with regard to morphological and molecular markers (Tiwari et al. 2005). So far only phaseolin based germplasm characterisation was done in common beans from the Nilgiris biosphere reserve (Franklin et al. 2010). Morphological markers and more reliable DNA based markers are considered to be the best tools for determining genetic relationship of crops. Hence, the present study aimed to investigate the variation among 20 landraces of common beans collected from the traditional tribal farming villages of the Nilgiris, Tamil Nadu, India.

The plant material consists of 20 landraces of common beans collected from tribal farmers in remote villages of Nilgiris. Seventeen qualitative and eight quantitative characters (IBPGR 1982) were studied among 20 landraces of common bean. The genomic DNAs of all the 20 common bean genotype were isolated using Qiagen DNeasy Plant Mini Kit (Qiagen Germany). The PCR was performed for 40 cycles in a reaction. All computations were carried out using the software package SPSS 9.0 for Windows.

On the basis of seed size common bean gene pools can be grouped as Andean comprising 45% plants, large seeded beans (>40 g/100 seed wt.), and Mesoamerican consisting 55% plants are small or medium-seeded (>25 g or 25-40 g/100 seed weight, respectively) (Singh et al. 1991). The seed weight, seed length, seed height, and pod length and pod width showed high positive correlation to each other. Highest correlations were observed between seed weight with seed length and seed width (Table 1).

The overall differences in morphological variables in the landraces were examined by Principal components identified (PCA). The first eight components having Eigen values greater than a one accounted for 84.35% of total variation (Table 2). The first component accounted for 20.48% of total variability; important variables with correlation values greater than 0.3. Similar to the present findings, when morphologically 116 accessions of common beans from Brazil were evaluated (Chiorato et al. 2006), it was found that the first two components were

*Corresponding author's e-mail: fcjooty@yahoo.com
Published by the Indian Society of Genetics & Plant Breeding, F2, First Floor, NASC Complex, PB#11312, IARI, New Delhi 110 012
Online management by indianjournals.com

Table 1. Pearson correlation coefficient for the eight quantitative traits in common beans

Characters	SWT	SL	SW	SH	PL	PW	PBL	NLP
SWT	1							
SL	0.828**	1						
SW	0.582**	0.278	1					
SH	0.811**	0.576**	0.691**	1				
PL	0.596**	0.847**	-0.05	0.326	1			
PW	0.570**	0.224	0.674**	0.671**	0.067	1		
PBL	0.613**	0.530*	0.262	0.303	0.429	0.322	1	
NLP	0.254	0.392	-0.12	0.222	0.435	0.154	0.009	1

**,*Correlation is significant at 0.01and 0.05 level, respectively; SWT = 100 Seed weight, SL = Seed length, SW = Seed width, SH = Seed height, PL = Pod length; PW = Pod width, PBL = Pod beak length and NLP = Number of locules per pod

Table 2. Principal components identified (PC1 to PC8), Eigen values, percent variation and component loadings in common bean landraces using morphological variables

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Eigenvalues	5.12	3.957	3.092	2.674	2.186	1.704	1.342	1.01
% of variance	20.481	15.829	12.369	10.695	8.745	6.814	5.368	4.054
Cumulative variance	20.481	36.31	48.679	59.374	68.119	74.934	80.302	84.355
Component loadings								
100-seed weight	0.397	–0.088	–0.151	–0.086	0.077	–0.001	–0.018	–0.077
Seed length	0.329	–0.053	–0.301	–0.044	–0.119	–0.078	–0.095	–0.073
Seed width	0.292	0.114	0.117	–0.057	0.301	0.201	0.089	–0.18
Seed height	0.381	–0.047	0.126	–0.191	0.038	–0.166	–0.05	–0.017
Pod length	0.257	–0.087	–0.329	0.052	–0.286	–0.071	–0.186	0.089
Pod width	0.329	–0.138	0.204	–0.082	0.1	0.108	0.141	0.276
Pod beak length	0.216	–0.25	–0.168	0.149	0.141	0.076	0.01	0.256
Number of locules per pod	0.073	–0.051	–0.098	0.193	–0.458	–0.25	0.327	–0.172
Seed coat pattern	0.113	0.205	–0.178	–0.36	–0.007	–0.086	–0.332	–0.283
Seed coat color	–0.004	0.279	–0.211	0.253	0.203	0.133	–0.186	–0.051
Seed shape	0.134	–0.003	0.133	–0.001	–0.243	0.459	–0.184	–0.477
Hypocotyl pigmentation	–0.135	0.14	–0.029	–0.308	–0.033	–0.032	0.427	–0.284
Emerging cotyledon color	0.114	0.268	0.259	0.184	0.111	–0.008	0.174	–0.203
Color of standard petal	0.269	0.238	–0.163	0.139	0.01	0.229	0.128	0.082
Color of wing petal	0.101	0.216	0.105	–0.036	–0.447	–0.168	0.116	0.039
Wing opening	0.159	0.073	0.419	–0.23	–0.015	–0.073	–0.045	0.02
Size of bracteole	0.113	0.309	0.085	–0.029	–0.135	–0.149	0.131	0.35
Shape of bracteole	0.127	0.051	–0.245	–0.02	0.279	–0.394	0.253	–0.254
Bracteole/calyx length	–0.062	0.048	–0.21	–0.355	0.04	0.284	0.232	0.181
Calyx/bracteole color	–0.129	0.248	–0.04	–0.355	–0.149	0.094	–0.23	0.103
Pod color	0.138	0.403	0.015	–0.069	0.074	0.049	0.097	0.261
Pod cross section	0.04	0.269	0.052	0.426	0.081	0.018	0.036	–0.131
Pod curvature	–0.043	0.243	–0.25	0.118	–0.228	0.332	0.098	0.096
Pod beak position	0.173	–0.039	0.341	0.167	–0.229	0.021	–0.2	0.045
Pod beak orientation	–0.074	0.323	–0.023	0.071	0.126	–0.37	–0.384	0.08

responsible for 33% of the variation, the first three components for 42.75% and the first four components for 50.52%. The PCA analysis allowed the identification of the redundant descriptors (Foschiani et al. 2009).

Both RAPD and SSR marker techniques have provided useful information regarding the level of polymorphism in common bean (Sajad et al. 2014). DNA extracted from 20 landraces was examined for their PCR-RAPD patterns. Out of 72 primers screened, 13 selected primers generated 102 amplification products, out of which 63 bands were polymorphic with an average of 7.8 bands per primer (Fig. 1). The Cluster analysis clearly discriminated the cultivars into three clusters (Fig. 2). RAPD markers were able to distinguish groups within both Andean and Mesoamerican gene pool.

The Mesoamerican group represented 35% of the total population; with seven landraces (LR2, LR7, LR8, LR9, LR14, LR19 and LR20) in cluster "M" and the Andean group 55% of world production of LRs in cluster, "A" out of which four are dwarf and seven are tall. In this cluster, two dwarf varieties (LR5 and LR17) formed a sub cluster with a similarity value of 0.79, are considered to be hybrids "H" between the Mesoamerican and Andean gene pools. In Nilgiris, majority of common beans under cultivation are from Andean gene pool. The same phenomenon was noticed in other common bean growing regions such as China (Zang et al. 2008), Italy (Ilaria et al. 2007) and Argentina (De Ron et al. 2004).

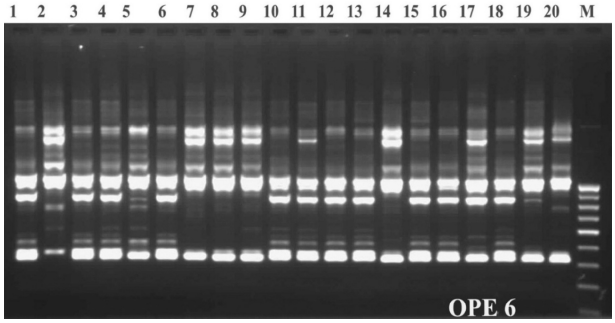

Fig. 1. RAPD banding pattern with OPE6 primer for 1-20 landraces of common bean. M-Molecular size ladder 100 base pairs

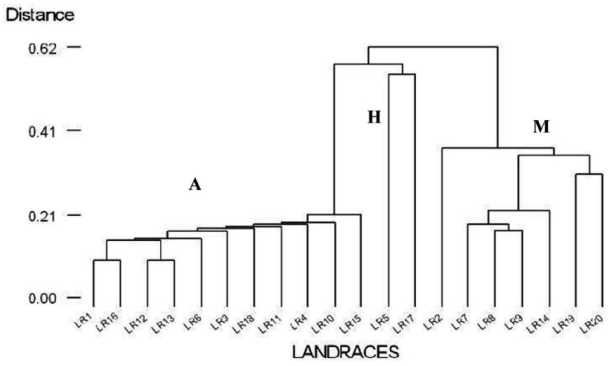

Fig. 2. Dendrogram based on Jaccard's coefficient among 1- 20 landraces of common bean using 63 RAPD marlers. M - Mesoamerican, A - Andean and H - Hybrid

These results indicated that the genetic variation has not eroded since the introduction of the common beans from the primary centers of domestication into Nilgiris. The level of polymorphism observed in the present study was moderately high, indicating a wide and diverse genetic base for the common bean landraces in Nilgiris. A clear-cut sign of introgression between the two gene pools as indicated by the hybrids, merits further evolutionary investigation. Moreover, in recent years farmers cultivate only a few highly priced, large seeded market classes. This could have contributed to a reduction in genetic diversity within the small seeded less desirable cultivars. Hence, an urgent action is the needed to conserve these landraces in gene banks or in botanical gardens from extinction.

Acknowledgements

The authors are grateful to the traditional 'Badaga' farmers of Nilgiri District who are conserving and cultivating this germplasm for many centuries. The second author gratefully acknowledges the grant from University Grants Commission (UGC), New Delhi, India, in the form of Major Research Project (UGC-MRP- 42-962/2013).

References

Chiorato A. F, Carbone S. A. M., Dias L. A. S., Moura R. R., Chiavegato M. B. and Colombo C. A. 2006. Identification of common bean (*Phaseolus vulgaris*) duplicates using agromorphological and molecular data. Genet. Mol. Bio., **29**: 105-111.

De Ron A. M., Marýa C. and Santalla M. 2004. Variation in primitive landraces of common bean (*Phaseolus vulgaris* L.) from Argentina. Genet. Resour. Crop Ev., **51**: 883-894.

Foschiani A., Miceli F. and Vischi M. 2009. Assessing diversity in common bean (*Phaseolus vulgaris* L.) accessions at phenotype and molecular level: a preliminary approach. Genet. Resour. Crop Ev., **56**: 445-453.

Franklin C. J., Sudheer Mohammed M. M., Sanil R., Dorai M. and Madanan M. G. 2010. Phaseolin and total

storage protein based diversity analysis of Nilgiri common bean landraces using SDS-PAGE. Indian J. Genet., **70**: 34-38.

IBPGR (International Board for Plant Genetic Resources). 1982. Descriptors for *Phaseolus vulgaris*. IBPGR, Rome, Italy.

Ilaria M., Alessandra B., Maurizio M., Pietro C. and Giovenni D. 2007. Characterization of some Italian common bean (*Phaseolus vulgaris* L.) landraces by RAPD, Semi-random and ISSR molecular markers. Genet. Resour. Crop Ev., **54**: 175-188.

Singh S. P., Gutiérrez J. A., Molina A., Urrea C. and Gepts P. 1991. Genetic diversity in cultivated common bean. II. Marker-based analysis of morphological and agronomic traits. Crop Sci., **31**: 23-29.

Sajad Majeed Zargar, Sufia Farhat, Reetika Mahajan, Ayushi Bhakhri, Arjun Sharma 2014. Unraveling the efficiency of RAPD and SSR markers in diversity analysis and population structure estimation in common bean. Saudi J. Biol. Sci., http://dx.doi.org/10.1016/j.sjbs.2014.11.011.

Tiwari M., Singh N. K., Rathore M. and Kumar N. 2005. RAPD markers in the analysis of genetic diversity among common bean germplasm from central Himalaya. Genet. Resour. Crop Ev., **52**: 315-324.

Zang X., Matthew W. B. and Shumin W. 2008. Genetic diversity of Chinese common bean (*Phaseolus vulgaris* L.) landraces assessed with simple sequence repeat markers. Theor. Appl. Genet., **117**: 629-640.