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Comparative genetic diversity analysis of common beans grown in Kyrgyzstan using molecular and morphological markers

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INTRODUCTION

The Kyrgyz common bean market started to develop in the end of the 20th century. In 2010, 71,400 t of beans were produced (and 90% of it was exported mainly to Turkey, Bulgaria and Russia (STATCOM KR 2011). Kyrgyzstan has a moderate bean production compared with other grain-bean producing countries (Beebe et al. 2011), but ranks however among the top 20th bean grain exporters worldwide. The income from selling common beans (grains) is 1 billion Kyrgyz Soms (KGS) (approx. US\$ 20 million; FAOSTAT 2009). Kyrgyz farmers grow different types of market bean classes, and sometimes use cultivar mixtures because they believe these will give a higher yield. Furthermore, the market price for different types of seeds is not stable from year to year, which also supports these cultivation practices.

Keywords: Micro satellites • Qualitative morphological traits • *Phaseolus vulgaris* •

OBJECTIVES

The aim of this study was to assess the diversity of Kyrgyz common bean cultivars and a reference set of foreign common bean accessions based on qualitative morphological traits and microsatellite markers.

MATERIAL AND METHODS

Five widely grown Kyrgyz cultivars were selected along with foreign accession kindly provided by Michigan State University (East Lansing, MI, USA) and the United States Department of Agriculture (Pullman, WA, USA) (Fig. 1).

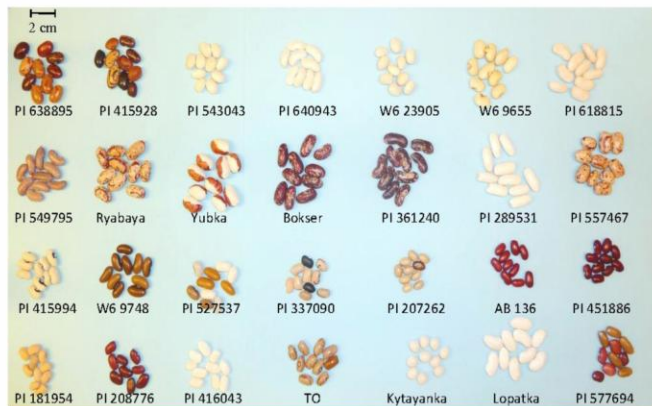


Fig. 1 Common bean accessions.

Data for 13 qualitative morphological traits were recorded on 10 randomly chosen individual plants per accession (Table 1). Microsatellite alleles were previously scored as per Hegay et al. (2012). Lab and statistical analyses were done following Hegay et al. (2012).

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 Hegay S, Geleta M, Bryngelsson T, Gustavsson L, Persson-Hovmalm H, Ortiz R (2012) Comparing genetic diversity and population structure of common beans grown in Kyrgyzstan using microsatellites. *Scient J Crop Sci* 1:63-75

RESULTS

Table 1 Microsatellite loci characteristics, the diversity at each locus and morphology traits used to estimate genetic diversity with simple sequence repeats (SSR)

Primer	Ng	IL	Trait name	Trait characteristics	
				Unit	Scale
EM30 ³	4	0.140	Seed color	11	Seed color per each plant
EM107 ⁴	4	0.248	Seed shape	4	Round (ovate), kidney, reniform/oblate, or elongate (cylindrical)
EM118 ⁴	2	0.444	Flower color	4	White, pink, violet (purple), or red
EM125 ⁴	3	0.322	Phenological	2	The light/brown, neutral or sensitive
EM303 ³	3	0.295	Seed sowing weight	4	Small (<25 g), medium (25-40 g), large (40-60 g), or very large (>60 g)
EM54 ⁴	3	0.235	100 seeds, gram	3	Green, red or pink
PVM075 ²	2	0.439	Stem color	3	Green, red or pink
PVM146 ⁴	4	0.229	Stem shape and size	9	Medium cordate, small triangular; large cordate, very small cordate, small ovate, large lanceolate, small lanceolate, medium ovate or medium lanceolate
PVM152 ²	2	0.340	Pod string	2	Measurement at half dry stage; present or absent
			Fiber	2	Measurement at half dry stage; present or absent
			Pod/bank position	2	Flaccid or curled
			Straight leaf hairs	2	Present or absent
			Plant habit	4	Determinate bush, indeterminate bush, indeterminate prostrate or subdeterminate climbing
Mean	3	0.299			

N_a = observed genotype number, H_e = average gene diversity (estimated as expected for dominant locus)

³After Hegay et al. (2012)

⁴Hill et al. (2003)

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⁶Hill et al. (2003)

Table 2 The best three predictors included seed size, trait shape and size, and pod/bank position (model is a bold) that explained together 80% of the total variation, and fit the minimum number of morphological traits for gene pool classification

Predictors	1	2	3	4	5	6	7
R ² (adjusted)	53.3	52.1	51.1	61.4	80.4	79.2	83
R ² (unadjusted)	53.3	51.5	50.9	60.2	80.2	79	82.3
Adjusted Cp	407.1	714.5	285.2	449	150.8	174.7	108.4
S	0.341	0.346	0.25	0.205	0.222	0.229	0.21

Trait name	1	2	3	4	5	6	7
Seed color							
Seed shape							
Phenological							
Flower color							
100 seeds, gram							
Stem color							
Stem shape and size							
Pod/bank position							
Pod string							
Fiber							
Straight leaf hairs							
Growth habit							

R² and R² (adjusted) = percentage of morphological traits variation and their relationship with other traits

Adjusted Cp = comparing models to find best separation of predictors (smaller value is better)

S = standard error of the regression, measured of the distance in the morphological traits data values explained deviation from the regression line.

Table 3 Discriminant analysis performed for grouping common bean accessions into gene pool based on morphological characters. Re-sampling and analysis were performed in Minitab 15 software

Trait name	Mesoamerican accessions		Andean accessions		All accessions		Preportion correct (%)	
	(A)	(B)	(A)	(B)	(A)	(B)		
Seed color	117	53	153	110	270	163	107	60
Seed shape	117	0	153	33	270	33	237	82
Flower color	117	92	153	41	270	133	137	49
Phenological	117	10	153	153	270	163	107	60
Seed size	117	110	153	123	270	233	37	86
Hypocotyl color	117	57	153	132	270	189	81	70
Stem color	117	66	153	122	270	188	82	69
Plant shape and size	117	61	153	103	270	164	106	61
Pod/bank position	117	117	153	93	270	210	60	84
Pod string	117	107	143	50	260	157	103	60
Fiber	117	10	143	143	260	153	107	58
Straight leaf hairs	117	87	153	110	270	197	73	73
Growth habit	117	94	152	109	269	203	66	75
Overall	117	116	132	132	249	248	1	99

(A) = Number of individuals put in a discriminant analysis (DA)

(B) = Number of individuals belongs in predicted analysis (EA)

(C) = Un-grouped

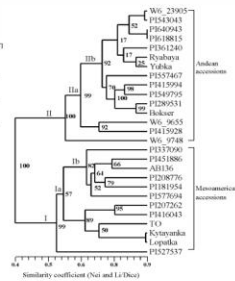


Fig. 3 DENDRA dendrogram of 27 and 11 clusters' similarity coefficient among 27 common bean accessions. The dendrogram was constructed based on a combination of morphological and microsatellite markers. There was a significant correlation between two approaches matrices ($r = 0.94$, $P < 0.01$).

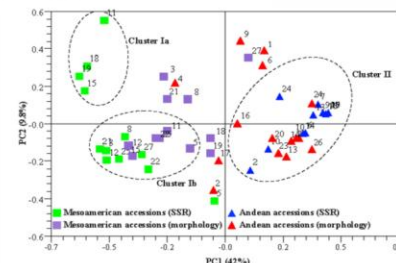


Fig. 2 Principal co-ordinate analysis based on morphological and microsatellite matrices from 27 common bean accessions. There was a significant correlation between the matrices ($r = 0.49$, $P < 0.01$) according to Lapointe and Legendre (1992).

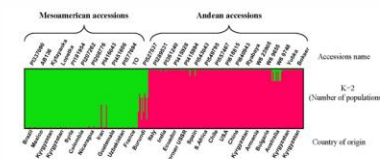


Fig. 4 Population structure for 27 common bean accessions estimated by the STRUCTURE program. The comparison included nine microsatellites and 13 phenotypic (qualitative) parameters. Accession names are given at the top while in the countries of origin are provided in the bottom.

SUMMARY

Cluster analysis grouped the accessions according to their gene pools. Andean accessions were less diverse than Mesoamerican accessions. This research confirms the ability of micro satellites and qualitative morphological traits to differentiate common bean accessions and to be able to assign modern cultivars to their gene pools.

Acknowledgements

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