



SDI Review Form 1.6

Journal Name:	American Journal of Experimental Agriculture
Manuscript Number:	2014_AJEA_10284
Title of the Manuscript:	GENETIC DIVERSITY OF DRY BEAN (<i>Phaseolus vulgaris</i> L.) ACCESSIONS OF KENYA USING SSR MARKERS
Type of the Article	

General guideline for Peer Review process:

This journal's peer review policy states that **NO** manuscript should be rejected only on the basis of '**lack of Novelty**', provided the manuscript is scientifically robust and technically sound.

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PART 1: Review Comments

	Reviewer's comment	Author's comment (if agreed with reviewer, correct the manuscript and highlight that part in the manuscript. It is mandatory that authors should write his/her feedback here)
<u>Compulsory</u> REVISION comments	The article cannot be accepted. The major deficiency is the low number of primers used for estimating the variability among the genotypes. This number must be a sample of bean genome. There are estimates of at least 100 loci. In these study only five were used, therefore five loci in a maximum of five chromosomes out of the 11 of the species. Besides in the results and discussion various analysis are mentioned and nothing in the material and methods. There are errors like cluster analyses using simple matching instead of UPGMA. Also the authors cited Colombia as a country of Middle America instead of South America. In conclusions there presented many discussions not appropriated.	An elaborated section on SSR markers is now included in the methods section. Seven SSR primer pairs (Promega Corporation, USA) were selected on the basis of the published dry bean microsatellite framework map for the genetic diversity analysis (Yu et al., 1999). Primers that revealed polymorphic banding patterns were selected while primers that showed monomorphic banding patterns were excluded from the study. Information on the SSR markers and PCR amplification, electrophoresis and visualization of PCR products, SSR data analysis, AMOVA and PCA analysis have been included in the methods. In addition, basis of the four populations has been inserted into materials and methods. The simple match coefficients were subjected to UPGMA thereafter dendograms were generated. Simple matching coefficients were determined because they generally take into account shared bands and shared absence of bands as factors that contribute to similarity between individuals. In this case since SSRs are co-dominant markers and beans are diploid species, a recognizable allele at a given locus is ordinarily associated with a single band at a unique position in a gel. Thus a homozygote has one band and a heterozygote has 2. Null bands are rarely seen (Kosman and Leonard, 1995: Similarity coefficients for molecular markers in studies of genetic relationships between individuals for haploid, diploid and polyploidy species: Molecular Biology 14; 415-425). This has been corrected Conclusion has been redone to reflect the discussed issues
<u>Minor</u> REVISION comments		
<u>Optional/General</u> comments		