MOLECULAR CHARACTERIZATION AND GENETIC DIVERSITY OF BRAZILIAN COMMON BEAN CULTIVARS AND ELITE LINES

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INTRODUCTION

The characterization and quantification of genetic diversity of common bean (*Phaseolus vulgaris* L.) cultivars and elite lines are useful for the breeding programs in the selection process of parents as well as in the determination of the genetic identity of superior genotypes (Cabral *et al.,* 2011). Currently, several classes of molecular markers are available for this purpose of which microsatellite markers (SSR – Simple Sequence Repeats) should be highlighted for being abundant throughout the genome, multi-allelic and suitable for semi-automated genotyping. Thus, the main goal of this work was to characterize and estimate the genetic diversity of "carioca" and black-seeded common bean cultivars and elite lines developed by the Brazilian Agricultural Research Corporation (Embrapa) and partners in Brazil, using 33 microsatellite loci developed and validated for common bean (Valdisser *et al.,* 2013).

MATERIAL AND METHODS

Seventeen cultivars and elite lines were analyzed, all selected for their high yield potential and consumer acceptance. Of these genotypes, 14 belong to carioca the commercial group ('Pérola', 'BRS Pontal', 'BRS Ametista', 'BRS Notável', 'BRS Cometa', 'BRS Horizonte', 'BRS Estilo', 'BRSMG Majestoso', 'BRSMG Madrepérola', 'CNFC 10429', 'CNFC 10431', 'CNFC 10432', 'CNFC 10467', and 'VC-6'), and three to the black group ('BRS Esplendor', 'BRS Supremo' and 'BRS Valente'). The DNA was extracted using samples composed of leaf tissue from 10 plants of each genotype collected in bulk, using the CTAB protocol. The 33 microsatellite loci were amplified as described by Valdisser *et al.* (2013). The amplified fragments were separated by capillary electrophoresis using an ABI 3500 Genetic Analyzer (Applied Biosystems ®) and markers were genotyped using software GeneMapper 3.5 (Applied Biosystems ®). The number of alleles per locus, allele frequency, genetic diversity, and the polymorphic information content (PIC) were calculated using the program PowerMarker (Liu & Muse, 2005). The genetic distances between genotypes were estimated by the method proposed by Smouse and Peakall, and grouped by Tocher's method of sequential clustering (Vasconcelos *et al.,* 2007), using software Genes (Cruz, 2013).

RESULTS AND DISCUSSION

Of the 33 SSR markers used in the analysis of 17 common bean genotypes, 26 (78.8 %) were polymorphic. A total of 109 alleles were identified, with an average of 4.0 alleles per locus, ranging from two alleles for the loci BM189, BM202 and PV169 to eight alleles for PV163. The mean genetic diversity of the SSR loci was 0.54, ranging from 0.06 for locus PV169 to 0.80 for BM187. In the genetic characterization of common bean cultivars from different commercial groups with AFLP and SSR markers, Cabral *et al.* (2011) and Perseguini *et al.* (2011) found mean scores of genetic diversity of 0.45 and 0.47, respectively, which are consistent with those estimated in this study. The PIC ranged from 0.05 for marker PV169 to 0.77 for BM187, with a

mean of 0.50. These results confirmed estimates of Díaz *et al.* (2010) who analyzed a set of 92 common bean landraces with 52 SSR markers (PIC = 0.54). The shortest genetic distance was found between 'BRS Ametista' and 'Pérola', while the longest was observed between 'BRS Majestoso' and 'CNFC 10432'. By Tocher's sequential clustering analysis, four groups were formed based on genetic distances estimated between genotypes according to Smouse and Peakall (Table 1). The results showed that the microsatellite markers were efficient to discriminate the analyzed genotypes. The black seeded genotypes were all clustered into a single group, along with the "carioca" seeded cultivars 'BRS Notável' and 'BRS Estilo'. The other "carioca"-seeded cultivars and elite lines were clustered into three distinct groups, which is consistent with the contrasts of these genotypes for several agronomic traits. The results confirm the existence of genetic variability among the tested genotypes, which can be exploited by the breeding programs in Brazil.

Table 1. Grouping of common bean cultivars and elite lines developed in Brazil by Embrapa and partners obtained by Tocher's sequential clustering, based on genetic distances of Smouse and Peakall estimated by 26 polymorphic SSR loci.

Groups	No. of Genotypes	Genotypes
I	4	Pérola[a], BRS Ametista[a], BRSMG Majestoso[a], and CNFC 10467[a]
II	7	BRS Cometa[a], BRS Pontal[a], BRS Horizonte[a], VC-6[a], CNFC 10429[a], CNFC10431[a], and CNFC 10432[a]
III	5	BRS Esplendor[b], BRS Valente[b], BRS Supremo[b], BRS Estilo[a], and BRS Notável[a]
IV	1	BRSMG Madrepérola[a]
Total	17	

[a]carioca and [b]black-seeded genotypes.

REFERENCES

Cabral PDS and Lima ABP (2011) Genetic diversity in local and commercial dry bean (*Phaseolus vulgaris*) accessions based on microsatellite markers *Genetics and Molecular Research*, v. 10, pp. 140- 149.

Cruz CD (2013) GENES - a software package for analysis in experimental statistics and quantitative genetics. *Acta Scientiarum*, v. 35, pp. 271-276.

Díaz ML and Buendía HF (2011) Genetic diversity of Colombian landraces of common bean as detected through the use of silver-stained and fluorescently labelled microsatellites. *Plant Genetic Resources*, v. 9, pp. 86-96.

Liu K and Muse SV (2005) PowerMarker: an integrated analysis environment for genetic marker data analysis. *Oxford Journals*, v. 21, pp. 2128-2129.

Perseguini JMKC and Chioratto AF (2011) Genetic diversity in cultivated carioca common beans based on molecular marker analysis. *Genetics and Molecular Biology*, v. 34, pp. 88-102.

Valdisser PAMR and Mota APS (2013) *Protocolo de extração de DNA e genotipagem de SSRs em larga escala para uso no melhoramento do feijoeiro*. Embrapa Arroz e Feijão (Comunicado Técnico 208), pp. 1-6.

Vasconcelos ES and Cruz CD (2007) Método alternativo para análise de agrupamento. *Pesquisa Agropecuária Brasileira*, v. 42, pp. 1421-1428.