MARKER-ASSISTED SELECTION INTEGRATED TO THE EMBRAPA COMMON BEAN BREEDING PROGRAM

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Several works developed during the last decade report the application of molecular markers in common bean (*Phaseolus vulgaris* L.) research for genetic diversity evaluation, evolution study, pedigree analysis, genetic mapping, gene tagging and breeding, including recurrent parent genome recovering in backcrossing programs and assisted selection of traits with high agronomic interest in segregating breeding populations (Barros & Souza 2012). Initially, codominant RFLP (Restriction Fragment Length Polymorphism) and dominant RAPD (Randomly Amplified Polymorphic DNA) markers have predominantly been used, allowing advances towards identification of molecular tools co-segregating with agronomic traits. Later on, a broad set of SCAR (Sequence Characterized Amplified Regions) markers have been developed from RAPD markers linked to disease resistance genes. Microsatellite or SSR (Simple Sequence Repeats) markers were also being gradually developed and utilized for a wide range of genetic analysis. Currently, many efforts is in course to discovery and use SNP (Single Nucleotide Polymorphisms) markers (Kelly et al. 2003; Barros & Souza 2012).

The establishment of a specific Marker-Assisted Selection Facility at the Embrapa Rice and Beans Biotechnology Laboratory, in 2014, has better supported the routine analysis with molecular markers demanded by the Embrapa Common Bean Breeding Program. In addition, it has also supported other Embrapa plant breeding programs, such as rice and cotton. Depending on the kind of genotypic analysis, DNA extraction is being performed using three different methods: (i) alkaline lysis – a simple and fast protocol widely used by many plant breeding programs worldwide but that results in DNA samples with low quality and, for this reason, it is more suitable for analysis in large scale without the need of DNA storing (Xin et al. 2003; Valdisser et al. 2013); (ii) CTAB (cetyltrimethylammonium bromide) – a very popular protocol that results in DNA samples with high purity, suitable for genotyping based on sequencing, hybridization or enzymatic digestion (Doyle & Doyle 1990; Ferreira & Grattapaglia 1998); and (iii) different commercial kits – fast and easy to use protocols which also results in a high quality DNA, e.g. the DNeasy Plant Mini Kit (Qiagen, Valencia, CA, USA).

Microsatellite markers have been used for genetic diversity studies (Brondani & Brondani 2006; Cardoso et al. 2014), confirmation of controlled crosses (Morais et al. 2016), marker-assisted backcrossing (Souza et al. 2014a), monitoring of allelic diversity and parental genetic representativeness in breeding populations (Batista et al. 2014), and assessig the genetic purity and identity of cultivars during seed production process (Morais et al. 2016). SCAR, SSR and STS (Sequence-Tagged Sites) markers have been validated and used for marker-assisted selection of genes associated with target traits such as resistance to *Bean golden mosaic virus* (BGMV) (transgenic event), anthracnose, angular leaf spot, rust, as well as to slow darkening of *carioca* grains (Ragagnin et al. 2009; Barros & Souza 2012; Souza et al. 2014a,b). SNP markers for some of these traits, such as resistance to BGMV, anthracnose and angular leaf spot, besides the slow darkening of *carioca* grains, are also being developed, validated and implemented in the pipeline of routine analysis. The consolidation of a genomic platform applied to large-scale genotyping in the Embrapa Common Bean Breeding Program is increasing the efficiency of the selection process of superior genotypes, but reducing time, handwork and datapoint cost.

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