

Genome wide selection in plant genetic improvement: A common bean case

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Introduction & Aim: The genetic sources of phenotypic variation have been a major focus of both plant and animal studies aimed at identifying the causes of disease, improving agriculture and understanding adaptive processes. Genome-Wide Association Studies (GWAS) offer high resolution through historical recombination accumulated in natural populations and collections of landraces, breeding materials and varieties. By exploiting broader genetic diversity, GWAS offers several advantages over linkage mapping. The common bean (*Phaseolus vulgaris* L.) is the world's most important legume for human consumption. Several groups have performed GWAS studies for common bean, but none have focused on Anthracnose (ANT) and Angular Leaf Spot (ALS) resistance. The breeders aim to obtain cultivars that are resistant to multiple diseases, as well as cultivars that have high levels of micronutrients such as iron and zinc. The aims of this study were to identify QRLs associated with resistance to ANT and ALS using SSR and SNP data. In addition to finding QRLs for the main diseases that attack common bean, the present work aimed to find associations for iron and zinc contents.

Methodology & Theoretical Orientation: Association mapping analyses were performed using a mixed linear model approach implemented in TASSEL. **Findings:** A total of 17 and 11 significant statistically associations involving SSRs were detected for ANT and ALS resistance loci, respectively. Using SNPs, 21 and 17 significant statistically associations were obtained for ANT and angular ALS, respectively, providing more associations with this marker. For the micronutrients evaluated, 9 SSRs were associated with the iron content and 7 SSRs showed association with the zinc content. A total of 10 SNPs markers were associated with iron content, whereas 6 SNPs markers showed association for zinc content. **Conclusion & Significance:** Our results demonstrate the great potential of genome-wide association studies to identify QTLs in common bean. The common bean is one of the most important staples in many areas of the world. Extensive phenotypic and genetic characterization of unexplored bean germplasm are still needed to unlock the breeding potential of this crop. Dissecting genetic control of flowering time is of pivotal importance to foster common bean breeding and to develop new varieties able to adapt to changing climatic conditions. Indeed, flowering time strongly affects yield and plant adaptation ability. The aim of this study was to investigate the genetic control of days to flowering using a whole genome association approach on a panel of 192 highly homozygous common bean genotypes purposely developed from landraces using Single Seed Descent. The phenotypic characterization was carried out at two experimental sites throughout two growing seasons, using a

randomized partially replicated experimental design. The same plant material was genotyped using double digest Restriction-site Associated DNA sequencing producing, after a strict quality control, a dataset of about 50 k Single Nucleotide Polymorphisms (SNPs). The Genome-Wide Association Study revealed significant and meaningful associations between days to flowering and several SNP markers; seven genes are proposed as the best candidates to explain the detected associations.