RESUMO - BIOTECNOLOGIA E GENÔMICA

GENETIC DIVERSITY AND SELECTION FOOTPRINTS IN THE GENOME OF BRAZILIAN SOYBEAN CULTIVARS

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To develop increasingly productive varieties, breeders must explore the genetic diversity available in a species. Thus, a wide genetic diversity is essential to breeding programs. A small number of studies analyzed the genetic diversity of Brazilian soybean, all of which found a narrow genetic base and limited genetic diversity. The objectives of this work were to analyze the population structure, genetic diversity and to identify selection signatures in the genome of soybean germplasms from different companies in Brazil. A panel of 343 soybean lines from Brazil, North America and Asia was genotyped through GBS (Genotyping by Sequencing). Population structure was assessed by Bayesian (STRUCTURE) and multivariate (Principal Component Analysis) approaches. Genetic diversity was analyzed using metrics such as the Fixation Index (FST), nucleotide diversity (p), genetic dissimilarity (IBS) and linkage disequilibrium decay (R^2). The software Bayescan was used to detect selection signatures between Brazilian and Asian accessions as well as among Brazilian

germplasms. Region of origin, company of origin and RMG (Relative Maturity Group) all had a significant influence on population structure. Varieties belonging to the same company and especially to the same RMG exhibit a high level of genetic similarity. This result was exacerbated among early maturing accessions. Brazilian soybean showed significantly lower genetic diversity when compared to Asian accessions. This was expected, as the crop's region of origin is its main genetic diversity reserve, as found by previous studies. Interestingly, when comparing brazilian germplasms among themselves, we found that portfolios containing varieties with a more diverse set of RMG values tend to exhibit a larger genetic diversity when compared to those comprised mainly of early maturing accessions. We identified 7 markers under selection between Brazilian and Asian accessions and 27 among Brazilian varieties developed by different companies. We found 96 QTLs for important soybean breeding traits associated to these markers such as flowering, maturity, plant architecture, productivity components, pathogen resistance and seed composition. Some of the QTL associated with the markers under selection have causal genes of great importance to soybean's regional adaptation. The results reported herein are a valuable resource to breeding programs, aiding in divergent parental selection as well as presenting regions under selection that can be explored by breeders to increase soybean productivity and adaptability in the many brazilian growing environments.