Association analysis using SSR markers to find QTL for seed oil content in soybean

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Brazil is known by its great variability and seed yield that may be used to extract vegetable oil or biofuel. The soybean is, up to now, the best alternative among these oilseed crops, because it is cultivated in a huge area throughout the country, has adequate levels of productivity and quality of oil (viscosity and cetane ratio), has a short-term cycle (nearly four months from seed to harvest) and it has a network of crushing industries available nationwide. The objective of this work is to identify molecular markers that can be used in a Soybean Breeding Program for biodiesel. Based on investigations in field conditions about 94 accesses of soybean (Plant Introductions, Brazilian and North American breeding lines), were separated in two groups consisting in high seed oil content (21-25%) and low seed oil content (12-17%). Genomic DNA samples were prepared from a lyophilized bulk of leaf tissue of 10 plants of each accession by mini-prep procedure. Amplicons were obtained in a touchdown program and visualized in 4300S DNA Analyser. A total of 142 SSR loci, evenly distributed over 20 chromosomes, were assayed for polymorphism. The 1142 alleles identified were used to estimate population structure and to analyze the genome-wide linkage disequilibrium. The accessions of soybean were highly structured, showing two subpopulations: a group of Brazilian and North-American germplasm derived from modern U.S.A and another group consisting in Plant Introductions and landrace from Asian. Relationship estimates based on SSR marker data, quantified in a Q matrix will help breeder's decisions regarding crosses. Twelve putative oil SSR loci were identified on the basis of highly significant markers. Five of these regions are where oil content has been mapped. The results presented strongly indicate that these SSR loci can be used in a Program of selection assisted markers.