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Genotyping-By-Sequencing of Soybean Breeding Lines from Africa, Brazil, Canada, and the USA

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Soybean improvement efforts at the International Institute of Tropical Agriculture (IITA, Nigeria) began in the mid 1970's. Release of high vielding varieties that are tolerant or resistant to biotic and abiotic stresses has contributed to increasing average yields in Sub-Saharan Africa in the last four decades. More recently, the Soybean Innovation Lab was established as an international consortium focused on sustainable soybean development in Africa. Plant breeding and germplasm research at the Soybean Innovation Lab includes the introduction of elite germplasm from the USA and Brazil, and improvement of IITA soybean varieties. We used genotyping-by-sequencing to assess the genetic diversity and structure of 298 IITA breeding lines, and to compare them to diverse panels of soybean varieties from the USA (94 lines), Canada (139 lines), and Brazil (103 lines). A total of 42.067 SNPs were obtained for the IITA dataset, which allowed a genome-wide characterization of nucleotide diversity, linkage disequilibrium (LD), and genetic structure. Pairwise values of Identity-by-State (IBS) distances showed that 27 pairs of lines were closely related (IBS distance values < 0.02). In order to compare diversity between datasets, a subset of 100 IITA samples was selected to compose a representative group of diverse breeding lines from Africa. Approximately 15,000 SNPs shared by the four datasets were used to compare their values of nucleotide diversity, LD patterns, and haplotype structures. Results indicated that IITA breeding lines are as diverse as varieties from the USA, Canada, and Brazil. Genetic structure patterns between the four groups were mainly influenced by differences in maturity groups, in addition to geographic origins of samples.

Back to: Genome Mapping, Tagging & Characterization: Legumes, Soybeans, Common Beans

<< Previous Poster | Next Poster >>

Home/Search

Browse by Day

Browse by Type

Poster Categories

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