Johann Vollmann · Marjana Vasiljević · Leopold Rittler ·
Jegor Miladinović · Donal Murphy-Bokern

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Characterization of the population structure and genetic diversity of a Chinese soybean diversity panel

Juan E. Rosas[1], Jhon Larzábal[2], Qiu Lijuan[3], Yu Yongzhe[3], Victoria Bonnecarrère[1], Sergio Ceretta[2]

[1]INIA, Las Brujas, Uruguay, [2]INIA, La Estanzuela, Uruguay, [3]Chinese Academy of Agricultural Sciences, Institute of Crop Sciences, China

Soybean is a major commodity crop in Uruguay, and genetic diversity is essential for crop breeding programs to achieve genetic gain, adaptation, and stability. In this study, the genetic diversity and population structure of a soybean diversity panel from China were characterized by the Soybean Breeding Program of the National Institute of Agricultural Research of Uruguay (ISBP) in order to assess its potential for use in the program. A total of 230 lines derived from 49 original accessions (28 landraces and 21 cultivars) of soybean from eight Chinese provinces were genotyped using 5636 single nucleotide polymorphism (SNP) markers. The genetic diversity, population structure, and kinship were analyzed using principal component analysis (PCA), hierarchical clustering, and STRUCTURE analysis. The results showed that the Chinese soybean diversity panel exhibited a high level of genetic diversity, with an average expected heterozygosity of 0.35 and a polymorphism information content (PIC) average value of 0.34. The panel was structured into three major clusters, with no clear correspondence to the origin of the accessions. The kinship analysis revealed a low level of relatedness among the original accessions. We conclude that the Chinese soybean diversity panel is a valuable genetic resource for soybean breeding programs in Uruguay, as it exhibits high levels of genetic diversity and low levels of relatedness. The lines derived from the original accessions can be used to select for specific traits of interest, such as grain quality, disease resistance or yield potential to introduce novel genetic variation into the Uruguayan soybean germplasm. Overall, our results highlight the importance of having access to diverse germplasm through international collaboration, as it provides the material necessary for improving new breeding targets and for adaptation to changing environments.

Keywords: Germplasm, genetic variability, molecular markers, China, Uruguay