



# Analysis of the genetic divergence of soybean lines through hierarchical and Tocher optimization methods

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Genet. Mol. Res. 15 (4): gmr.15048836

Received May 31, 20146

Accepted July 12, 2016

Published October 5, 2016

DOI <http://dx.doi.org/10.4238/gmr.15048836>

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**ABSTRACT.** This study aimed to evaluate the clustering pattern consistency of soybean (*Glycine max*) lines, using seven different clustering methods. Our aim was to evaluate the best method for the identification of promising genotypes to obtain segregating populations. We used 51 generations F5 and F6 soybean lines originating from different hybridizations and backcrosses obtained from the soybean breeding program of Universidade Federal de Uberlândia in addition to three controls (Emgopa 302, BRSGO Luziânia, and MG/BR46 Conquista). We evaluated the following agronomic traits: number of

days to flowering, number of days to maturity, height of the plant at maturity, insertion height of the first pod, grain yield, and weight of 100 seeds. The data was submitted to analyses of variance followed by average Euclidean distance matrix estimation used as measure of dissimilarity. Subsequently, clusters were formed using the Tocher method and dendrograms were constructed using the hierarchical methods simple connection (nearest neighbor), complete connection (most distant neighbor), Ward, median, average within cluster connection. The nearest neighbor method presented the largest number of genotypes in group I and showed the greatest similarity with the Tocher optimization method. The joint use of these two methodologies allows for differentiation of the most genetically distant genotypes that may constitute the optimal parents in a breeding program.

**Key words:** *Glycine max*; Genetic diversity; Genetic breeding