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Assessment of duplicates in perennial soybean (*Neonotonia wightii*) collection

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Abstract

Perennial soybean (*Neonotonia wightii* Wight & Arn.) is a herbaceous perennial forage legume that is mainly used as pasture or hay for animals. It is a nitrogen fixing legume that can be grown as a cover or fallow crop and contributes to improved soil fertility and productivity of crops. It is a drought tolerant climate adaptive species with an annual productivity of up to 10 tons DM/ha. The ILRI Genebank holds over 400 accessions with little information on the collection. Generating information and understanding the collection through genotyping and phenotypic characterisation is necessary to promote greater use and to rationalize and efficiently curate the collection. Preliminary passport data assessment showed some potential duplicates in the collection. In line with this finding, we used a molecular approach to study the identified potential duplicates. Genomic DNA was extracted from young leaves collected from healthy growing seedlings in the greenhouse and sent for genotyping at SEQART, ILRI Nairobi, Kenya. The generated genotyping data were used to assess the genetic distance/similarity among the accessions. Visualisation of the hierarchical clustering, principal component analysis, genetic relationship matrix and genetic distance were used to assess the genetic relationship of the accessions. The result showed the accessions are differentiated from each other with varying level of genetic distance (0.123–0.370 Roger distance and 0.4687–0.9136 Hamming distance). Thus, the result from this study demonstrates that genotyping data can be used to complement the passport and phenotypic data to assess potential duplicates and for efficient curation of germplasm in the genebank.

Keywords: Duplicates, genebank, genetic distance, germplasm, perennial soybean