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

Alemayehu Teressa Negawo[1], Alemayehu Demeke Bedane[1], Michael Gashaw[1], Meki S. Muktar[1], Alice Muchugi[1,] Alieu M. Sartie[2] and Chris S. Jones[1,3]

[1]Feed and Forage Development Program, International Livestock Research Institute, Addis Ababa, Ethiopia; a.teressa@cgiar.org (A.T.N.); m.gashaw@cgiar.org (MG); M.Shehabu@cgiar.org (M.S.M.); a.muchugi@cgiar.org (A.M): c.s.jones@cgiar.org (C.S.J)

[2]Pacific Community (SPC), Suva, Fiji; sartiealieu@hotmail.com (A.M.S.);

[3]Feed and Forage Development Program, International Livestock Research Institute, Nairobi, 00100, Kenya

Introduction

Perennial soybean (*Neonotonia wightii* Wight & Arn.) is a herbaceous perennial forage legume that is mainly used as pasture or hay for animals[1-3]. It is a nitrogen fixing legume that can be grown as a cover or fallow crop[2] and contributes to improved soil fertility and productivity of crops [2,3]. It is a drought tolerant climate adaptive species[2,3] with an annual productivity of up to 10 tons DM/ha[2]. The ILRI Genebank holds over 400 accessions with little information on the collection. Generating information and understanding the collection through genotyping and phenotypic characterization 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.

Materials and methods

- Seeds of the selected accessions were grown in a greenhouse (Figure 1)
- Genomic DNA was extracted from young leaves collected from healthy growing seedlings and sent for genotyping at SEQART, ILRI Nairobi, Kenya.
- The genotyping data were used to assess the genetic distance/similarity among the accessions.
- The genetic relationship among the accessions was visualized using hierarchical clustering, principal component analysis, genetic relationship matrix and genetic distance.

Figure 1. *Neonotonia wightii* plants

Results

- The genotyping produced 31,064 SNP markers for 77 accessions.
- The hierarchical clustering (Figure 2) and PCA (Figure 3) show the genetic relationship of the accessions.
- The accessions were differentiated from each other with varying level of genetic distance (0.008-0.262 Nei's distance, 0.123-0.370 Roger's distance and 0.469-0.914 Hamming distance) (Table 1).
- No duplicate accessions were identified based on the GBS data, but there was high genetic similarity which generally aligned with the passport data.
- Thus, the results from this study demonstrate 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.

Figure 2. Hierarchical clustering of the accessions

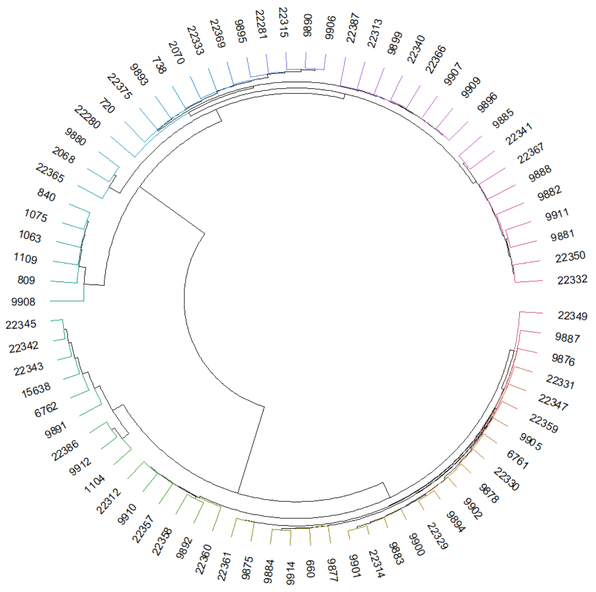

Figure 3. PCA using the first two axes contributing 39.9 % of the variation

Table 1. Genetic distance between pair of accessions suspected as duplicate based on passport data

Accession 1	Accession 2	Nei's Distance	Roger's distance	Hamming distance
6762	15638	0.028	0.169	0.648
9875	22329	0.012	0.153	0.531
9876	22330	0.015	0.163	0.627
9877	22331	0.018	0.177	0.631
9880	22365	0.045	0.235	0.888
9881	22367	0.157	0.335	0.859
9882	22369	0.126	0.323	0.742
9885	22341	0.189	0.296	0.914
9887	22343	0.091	0.188	0.626
9888	22313	0.175	0.327	0.872
9890	22340	0.158	0.361	0.548
9891	22345	0.041	0.233	0.690
9892	22347	0.014	0.220	0.723
9893	22375	0.155	0.291	0.726
9894	22359	0.015	0.123	0.469
9896	22281	0.119	0.281	0.650
9899	22366	0.151	0.300	0.750
9900	22361	0.026	0.146	0.532
9901	22358	0.016	0.224	0.633
9902	22357	0.018	0.224	0.664
9905	22332	0.262	0.343	0.653
9906	22280	0.122	0.37	0.742
9907	22387	0.149	0.305	0.792
9910	22312	0.026	0.241	0.796
9911	22350	0.187	0.318	0.780
9912	22386	0.011	0.198	0.721
9914	22349	0.008	0.209	0.686

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Chris Jones:
c.s.jones@cgiar.org, Feed and Forage Development program, International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia. ilri.org