

Genetic integrity and diversity in *Urochloa brizantha* collection maintained in the ILRI forage genebank

Meki S. Muktar¹, Shimu D. Lema², Alemayehu T. Negawo¹, Yilikal Asefa¹, Chris S. Jones³

¹International Livestock Research Institute (ILRI), Ethiopia

²Oromia Agricultural Research Institute (OARI), Ethiopia

³International Livestock Research Institute (ILRI), Kenya

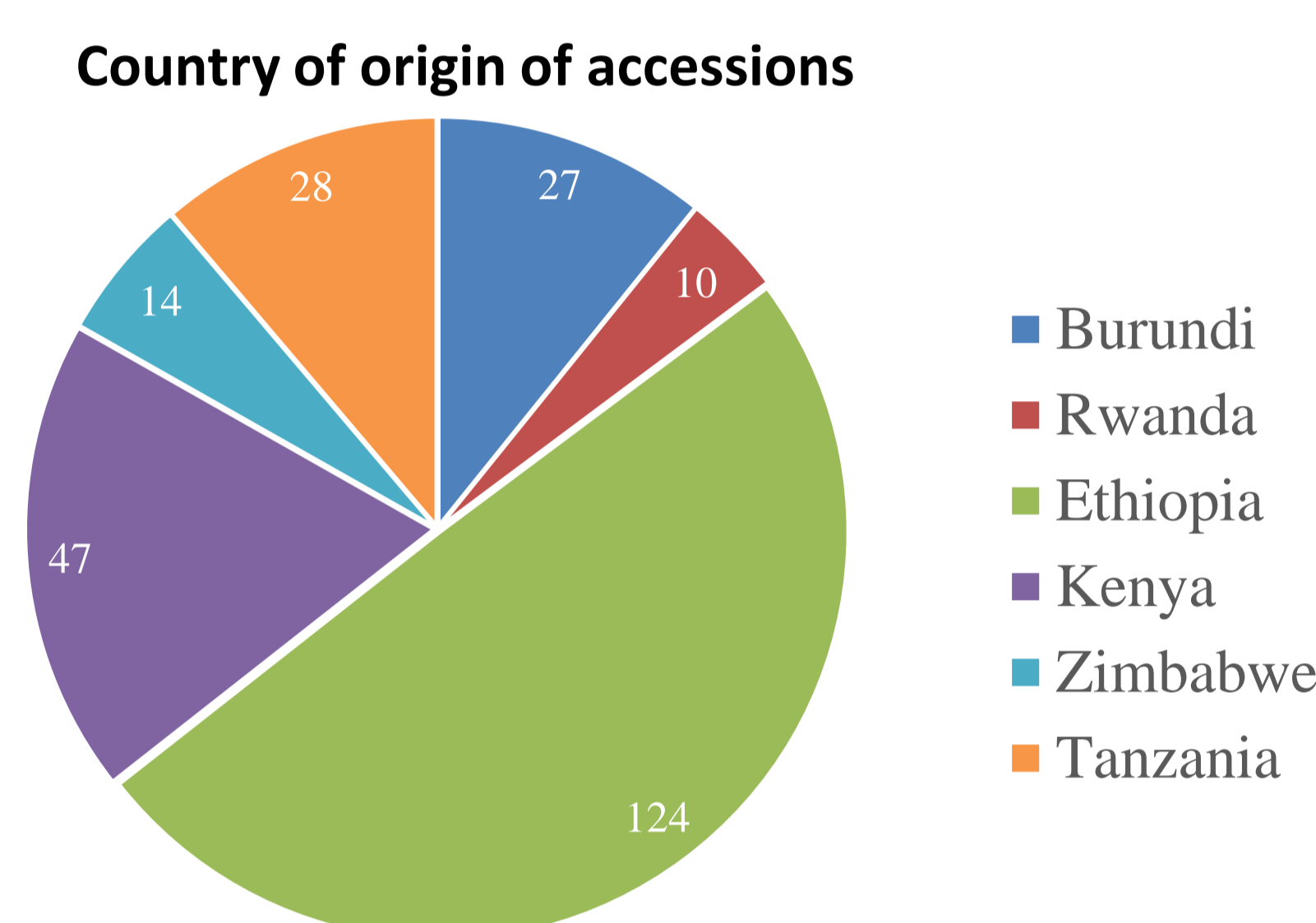
I. Introduction

The ILRI forage genebank maintains several different species of brachiaria grasses (*Urochloa spp.*) in-situ at its Zwai field site, Ethiopia, for over 30 years. We studied the genetic integrity in the *Urochloa brizantha* (*syn. Brachiaria brizantha*) collection, consisting of 252 accessions, in order to determine the integrity of plants within accessions and the genetic diversity exists in the collections. A total of 748 plants from 252 accessions, sampling two to three plants per plot per accession, were genotyped by the genotyping-by-sequencing (GBS) method of the DArTseq platform (Diversity Array Technology). A total of 162,002 SNP and 220,603 SilicoDArT genome-wide markers were generated. Of these, 51% of the SNPs and 39% of the SilicoDArTs were mapped onto the *U. ruziziensis* genome. The genetic integrity of plants within accessions was assessed based on a pairwise IBD (Identity-By-Descent) analysis using the Maximum Likelihood Estimation (MLE). Of the three plants sampled within a plot (within accession), 152 accessions (60%) were 100% true-to-type, indicating that there was no mix-up, mislabeling, or cross-pollination from other accessions. In 33 accessions (13%), one of the three plants was genetically different but showed a close genetic relationship (parent-offspring, full-sib, or half-sib) to the remaining two plants, indicating some level of cross-pollination had taken place in these accessions. In another 50 accessions (20%), one of the three plants was genetically distinct from the other two plants, while the three plants were unrelated to each other in another 17 accessions (7%), indicating that a mix-up or potential contamination had been taken place in this group of accessions. Clustering analysis using the discriminant analysis of principal components (DAPC) and hierarchical clustering detected four to five major clusters, each with further subclusters. The results of this study provides useful information for the management and conservation of the collection in the ILRI forage genebank. The substantial genetic diversity observed in the collection reveals the potential of the collection for further genetic studies and adaptations at different agroecological conditions of the world.

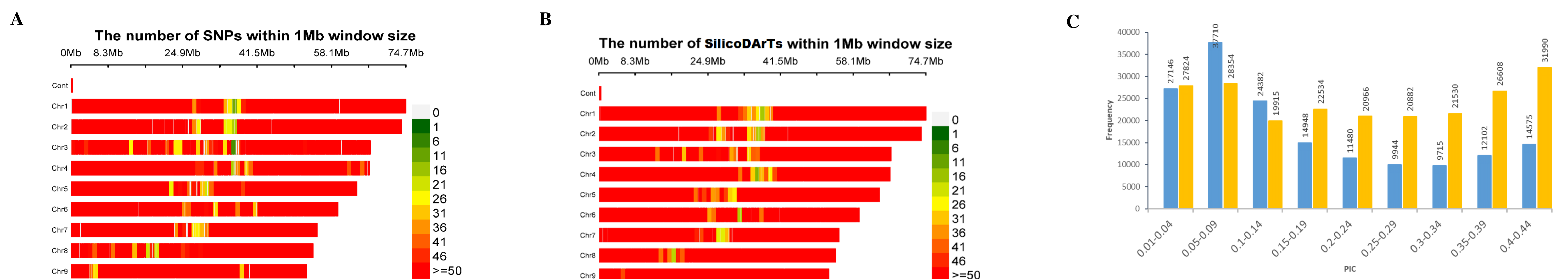


II. *Urochloa brizantha* collection used in the study

Figure 1. A total of 748 plants from 252 *Urochloa brizantha* accessions collected from different agro-ecological conditions of eastern and central African countries were analysed for genetic integrity and diversity. The number of accessions per country ranged from 10 from Rwanda to 124 from Ethiopia.



III. Genome-wide high-density SNP and SilicoDArT markers generated on the collection



IV. Genetic integrity of plants within accessions

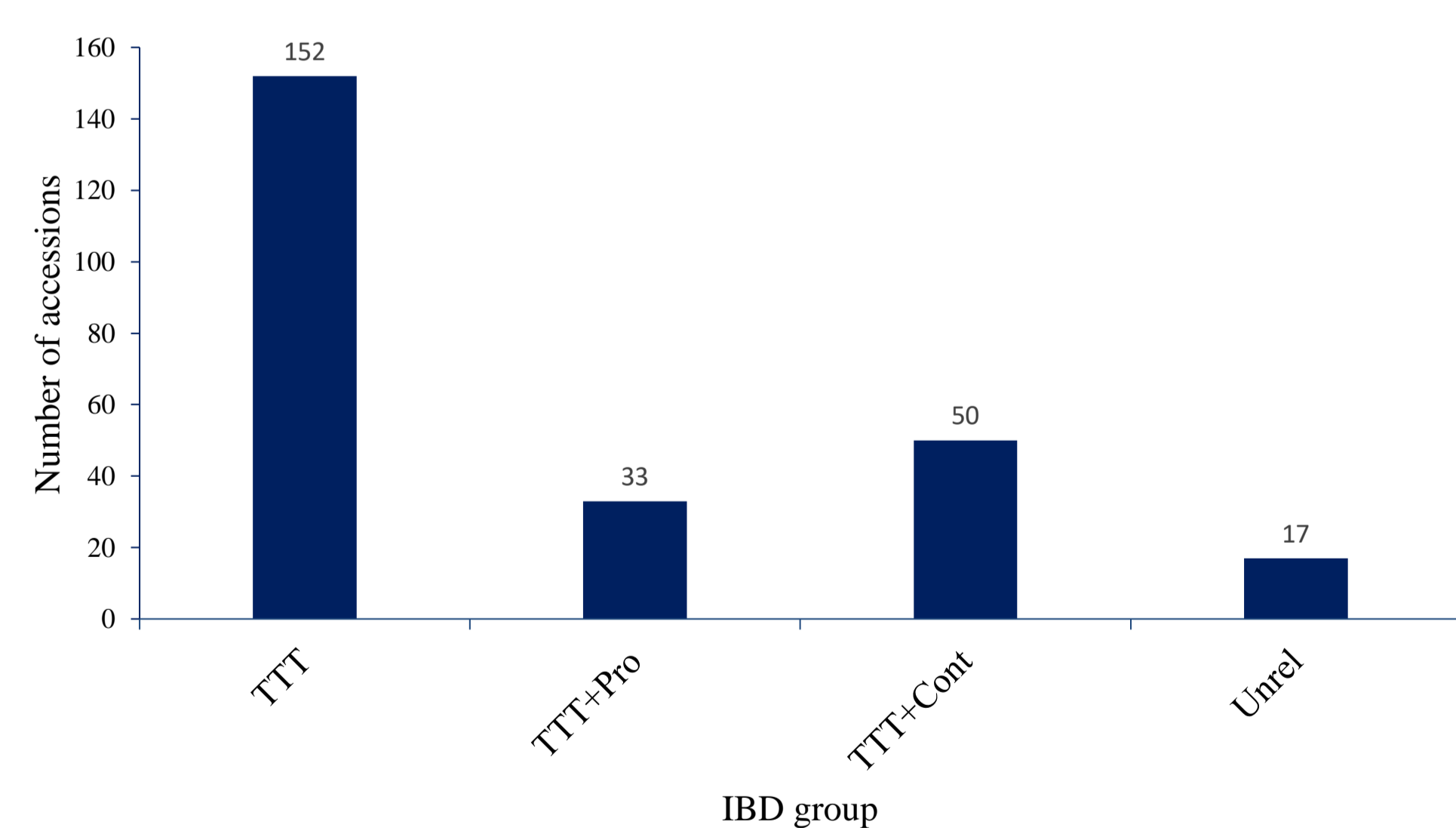
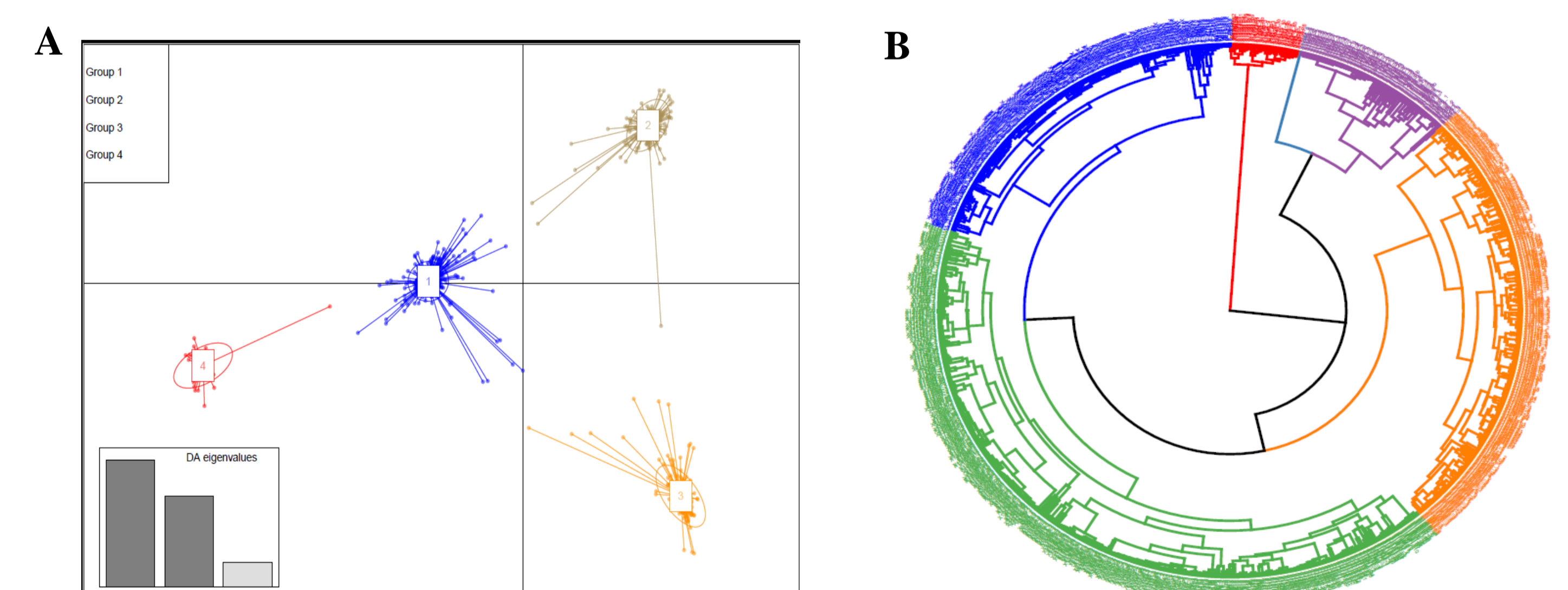


Figure 3. Genetic integrity of plants within accessions, assessed using Identity-by-descent (IBD) analysis, showed 52 accessions (60%) were 100% true-to-type (TTT); one of the three plants in 33 accessions (13%) was not similar with the other two plants (Pro); one of the three plants in 50 accessions (20%) was genetically distinct (Cont); and the three plants in another 17 accessions (7%) were unrelated to each other (Unrel).

V. Genetic diversity in the collection



VI. Conclusions

- The genetic integrity analysis showed that most of the accession (60%) were intact and there was no mix-up, mislabeling, or cross-pollination from other accessions.
- However, the analysis has also showed presence of some level of cross-pollination and potential contamination in some of the plots.
- The substantial genetic diversity observed in the collection reveals the potential of the collection for further genetic studies and suggested the importance the collection for agroecological farming.

Correspondence:
Meki S. Muktar, Feed and Forage Development, International Livestock Research Institute, Addis Ababa, Ethiopia, ilri.org; email: m.shehabu@cgiar.org



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VII. References

- Worku et al. 2021. DOI: 10.1002/agj2.20789

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