

The use of molecular markers for determining genetic purity of open pollinated maize varieties

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Introduction

- ▶ Farmers in sub-Saharan Africa favor maize open pollinated varieties (OPVs) over hybrids; ZM 521 popular
- ▶ Danger of farmer exploitation by unethical seed traders – switch OPV seed with maize grain
- ▶ Identity and purity of maize OPVs cost-effectively tested by new bulked DNA fingerprinting method

Objective

- ▶ To optimize the bulked fingerprinting method by testing genetic purity among 35 seed lots of ZM521

Materials & Methods

- ▶ Thirty five seedlots of ZM521 from Zimbabwe, Zambia and Malawi
- ▶ References – breeder's seed from 14 unrelated OPVs and two hybrid varieties
- ▶ Twenty (20) seeds per seedlot randomly selected and sown for DNA extraction
- ▶ DNA extracted, bulked and analyzed – simple sequence repeat (SSR) analysis used
- ▶ Subset of 15 SSR markers used



Figure 1. Farmers in Malawi growing one of the maize open pollinated varieties.

Results & Discussion

- ▶ The 15 SSR markers used for fingerprinting were effective in discriminating the seedlots of ZM521 and all other maize OPVs.
- ▶ One of the seedlots of ZM521 95255 did not cluster into any group – its distinctness indicates a mislabeled seedlot.
- ▶ The breeder's seed of ZM521 (also used as the reference sample for this OPV) is in the first cluster, indicating that the seedlots in this group are highly similar to the original breeder's seed and have not been changed or contaminated during seed increase by the various seed companies.

Figure 2 shows a summary of PGMA dendrogram of the 17 selected seedlots of ZM521, 3 additional OPVs, and 13 SC513 grouped using 15 SSR markers. The seedlots are

clustered into 3 groups; one of the 17 seedlots of ZM 521 including the reference sample; two hybrids SC403 and Z578; and the third cluster is the seedlots of SC513.

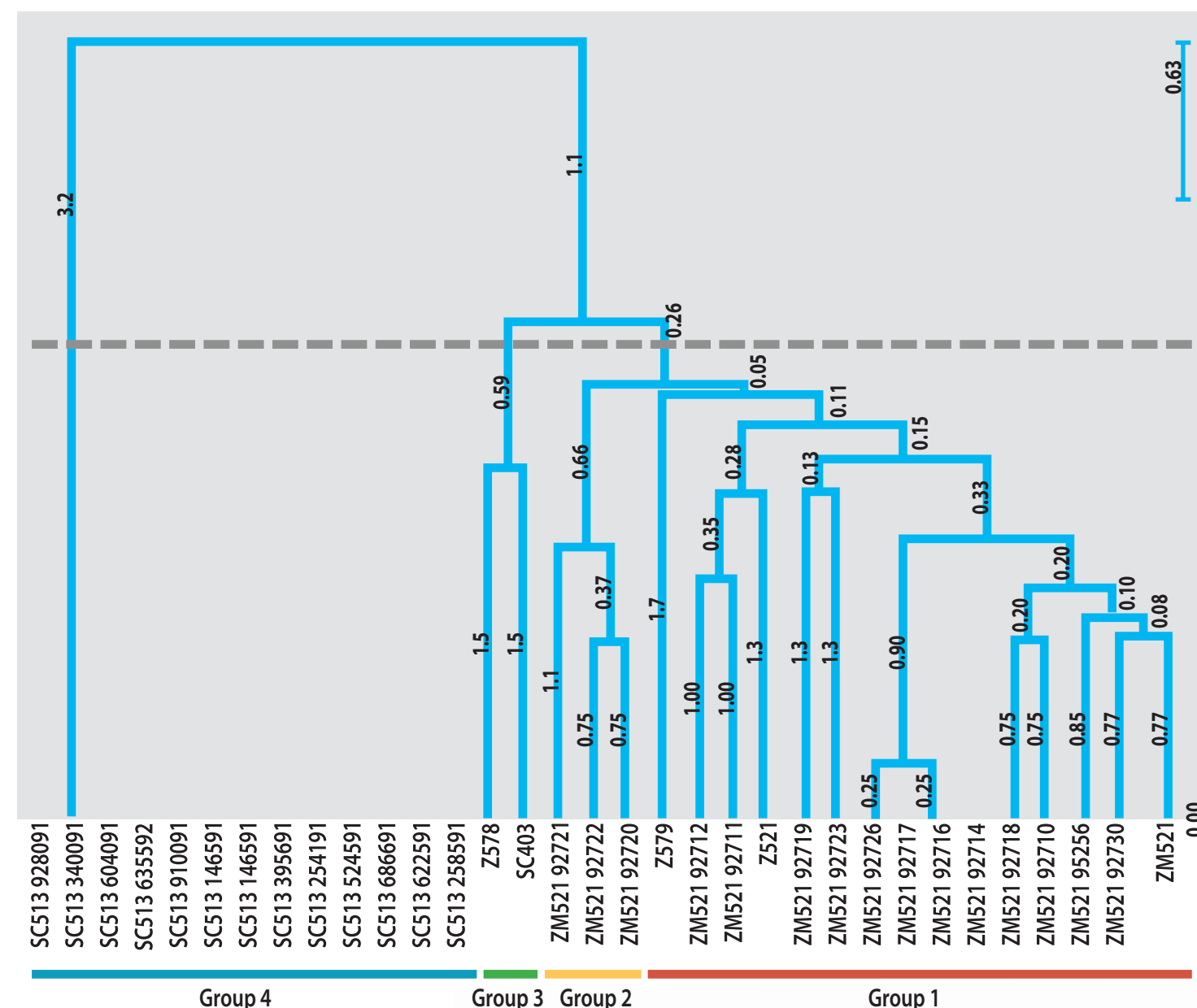


Figure 2. UPGMA dendrogram of the 17 seedlots of ZM521, 3 additional OPVs, and 13 SC513 grouped using 15 SSR markers.

Conclusion

- ▶ The 15 SSRs markers distinguished 15 unrelated CIMMYT maize OPVs and ZM521 seedlots.
- ▶ The seedlots in cluster C, which were all from company C in Zambia, were found to be genetically drifting away in terms of purity from the reference sample.
- ▶ The 15 SSRs markers are a quick and cost-effective tool for seed companies and NGOs to determine the genetic purity and identify their foundation and marketed certified seed.

References

- Dubreuil, P., M. Warburton, M. Chastanet, D. Hoisington, and A. Charcosset. 2006. More on the introduction of temperate maize into Europe: Large-scale bulk SSR genotyping and new historical elements. *Maydica* 51:281-291.
- Setimela, P.S., X. Mhike, J.F. MacRobert, and D. Muungani. 2005. Maize hybrid and open-pollinated varieties. CIMMYT, Mexico D.F.
- Warburton, M.L., P. Setimela, J.Franco, H.Cordova, K. Pixley, M.Bänziger, S. Dreisigacker, C.Bedoya and J. MacRobert. 2010. Toward a cost-effective fingerprinting methodology to distinguish maize open pollinated varieties. *Crop Science* 50: 467-477.