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Genetic diversity of Tanzanian advanced *Coffea arabica* germplasm and semi wild Ethiopian collection.

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•MTENGA, Damian J*., (damian.mtenga@tacri.org) KUSOLWA, Paul M., ** REUBEN, Shazia. O.W.M** and KILAMBO, Deusdedit L.*

•* Tanzania Coffee Research Institute P.O.Box 3004 Moshi, Tanzania

•** Sokoine University of Agriculture P.O.Box 3005 Morogoro, Tanzania

Introduction

Genetic diversity of Tanzanian cultivated arabica coffee is limited (Masumbuko and Bryngelsson, 2006; Masumbuko *et al.,* 2003). Efforts have been made through different approaches aimed at widening the genetic base of commercially cultivated arabica coffee through new introductions, collections and hybridization between cultivated varieties and semi wild types. Tanzania is one of the countries that benefited from the FAO coffee collection mission to Ethiopia of 1964 where 196 accessions were received and established in a field germplasm (FAO, 1968). Despite the wide publications of the genetic advantages of this germplasm in other countries, it has not fully been studied and exploited in Tanzania (Bertrand *et al*., 2014) The objective of this study was to establish the level of genetic diversity of coffee in the field maintained germplasm from Ethiopia and other germplasm at the Tanzania Coffee Research Institute using SSR markers.

Materials/Methods

Ninety one coffee arabica genotypes selected from Ethiopian collection (maintained at Tanzania Coffee Research Institute (TaCRI) and from germplasms and breeding fields at TaCRI Lyamungu were used. Forty five accessions were collected from Ethiopian while the rest were obtained from germplasm and breeding TaCRI Lyamungu fields. Young coffee leaves were picked from three trees per genotype from the growing tips and lyophilized for 72 hours for DNA extraction. The lyophilized coffee leaves were stored at -21° C before DNA extraction. Genomic DNA was then extracted from the leaves using the CTAB method (Diniz *et al.,* 2005) with minor modifications on annealing temperatures. The DNA was amplified with 30 SSR primer sets which were sourced from literature (Teressa *et al*., 2010; Chaparro *et al*., 2004; Baruah *et al*., 2003; Combes *et al*., 2000; Rovelli *et al*., 2000). A one hundred base pair DNA ladder was used as a molecular weight marker when scoring bands. Data analysis was performed using GenStat Release 15.1 (2012) by VSN International Ltd.

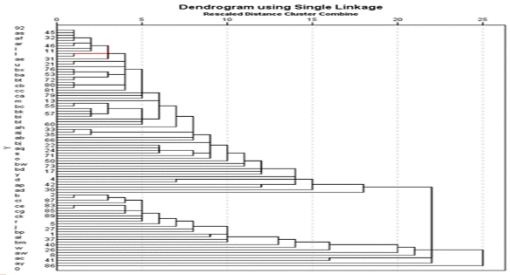

Fig.1 Dendrogram of 91 genotypes amplification by 30 SSR markers based on genetic

Table 1. Results of amplification of 91 coffee genotypes by 24 SSR markers

Components analyzed	Results
Total alleles produced	60
Average number of alleles per SSRs	2.5
Percent of polymorphic alleles (rP)	80.0
Observed heterozygosity (HO),	0.999
Gene diversity	0.527
Polymorphic information content (PIC)	0.413

Results/Discussion

The results revealed that six SSR markers (CMA055, CMA059, R209, R268, CM08 and CM16) were monomorphic while 24 SSR markers were polymorphic (80 %) and they gave good amplification of the coffee genotypes. The results (Table 1) revealed that the total number of alleles was 60 an average of 2.5 alleles per SSR marker. Gene diversity ranged from 0.500 to 0.775 with a mean of 0.527.

The marker which gave the highest coffee gene diversity was ssrAY2449 with the value of 0.7753. The observed heterozygozity was high with a mean of 0.999. The polymorphic information content generated ranged from 0.375 to 0.739 with a mean of 0.413. The marker that generated the highest polymorphic information was ssrAY2449 (Table 1). Single linkage dendrogram of the 91 genotypes studied (Fig. 1) using 30 SSR generated three main clusters. The first cluster was composed of the Ethiopian coffee genotypes while the second consisted of mainly the improved coffee breeding lines. The last cluster comprised the mixture of Ethiopian coffee genotypes, breeding lines, progenitors and commercial varieties. Even though, the overall genetic diversity of *Coffea arabica* is believed to be low, the populations in Ethiopia its place of origin and diversity, have a lot of genetic variability the fact that has been supported by many studies based on different techniques (Teressa *et al.* 2010).

Conclusion/Perspectives

This study revealed high heterozygozity among the coffee genotypes studied. Ethiopian genotypes were the most variable group. The information found from this study will facilitate selection of superior genotypes for development of superior varieties with broad genetic base for various traits. Marker ssrAY2449 was the most informative

References

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