



Genetic Diversity of *Mansonia altissima* (A. Chev.) and *Triplochiton scleroxylon* (K. Schum) in an Agroforest Scenario in Akure Forest Reserve, Nigeria

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INTRODUCTION

Problems of too much pressure on land for the production of food and wood for the increasing populace have necessitated the adoption of agroforestry practices such as Taungya and "on-farm tree" in recent times. However, genetic inventories of the tree component of these practices are missing. In the present study, genetic diversity of two important Nigerian timber species namely: *Mansonia altissima* and *Triplochiton scleroxylon* were assessed.

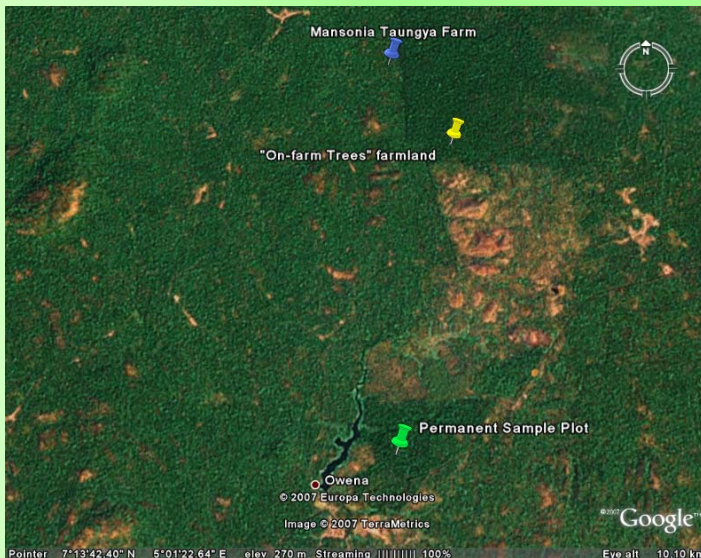


Figure 1: Location of sample plots

RESULTS AND DISCUSSION

Results of the genetic diversity within *Mansonia altissima* and *Triplochiton scleroxylon* populations are presented in Tables 1 and 2 respectively. In general, all the measures of diversity presented Table 1 indicate low genetic diversity in *Mansonia altissima* populations in the study area unlike what has been reported in the many literatures of most Tropical trees. The result also indicate that *Mansonia altissima* has higher genetic diversity in Taungya farm than in Primary Forest. The reason may be due to the fact that *Mansonia altissima* propagules in the Taungya Farm were collected from both inside and outside the Forest Reserve. In case of *Triplochiton scleroxylon*, the within-population genetic diversity is comparable to what has been reported in literature of most tropical trees. Although almost all the diversity estimates recorded (Table 2) in Primary Forest are higher than what was recorded in farmland with On-Farm trees, the disparity is not as wide as expected. Higher value of N_e in farmland with On-Farm trees is not unexpected according to Hollingsworth *et al.*, (2005).

CONCLUSION

These results reveal that trees on agroforest lands could show comparable levels of genetic diversity as those in the primary forests. In essence, agroforest lands could be reservoir of valuable genetic resources.

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MATERIAL AND METHODOLOGY

Fresh leaf samples of *Mansonia altissima* were collected from a Taungya Farm while *Triplochiton scleroxylon* leaves were also collected from a farmland with scattered "on-farm trees". To serve as control, fresh leaf samples of the two tree species were also collected from an old Permanent Sample Plot (PSP) which represents a Primary Forest (see Figure 1). Total genomic DNA was isolated from the leaf samples following DNeasy® 96 Plant Kit protocol of QIAGEN (QIAGEN GmbH, Hilden, Germany). Following the Amplified Fragment Length Polymorphism (AFLP) protocol of Vos *et al.* (1995), the total genomic DNA of each sample was digested with two restriction enzymes; EcoRI and MseI. EcoRI and MseI adaptors were then ligated to the ends of the restriction fragments to generate template DNA for Polymerase Chain Reaction (PCR) amplification, which consists of two successive steps; the pre-selective amplification and selective amplification. The pre-selective amplification was carried out with E01/M03 primer combination while the selective amplification was done using a fluorescent-labelled primer pair (FAM-E41/M63) primer combination. Reproducibility test was carried out using eight samples in order to exclude non-reproducible fragments from the analyses. Automated genotyping was done using an application software known as Genescan 3.7 while the resulting bands were scored manually with the aid of Genotyper Programme 3.7. Data matrix generated from the scoring were analysed using the software POPGENE 1.32 (Yeh and Boyle, 1997).

Table 1: Genetic Diversity within *Mansonia altissima* Populations

Population	PPL	N_a	N_e	I	H
Taungya Farm	21.30	1.213	1.051	0.063	0.0418
Primary Forest	12.04	1.120	1.045	0.045	0.0305

Table 2: Genetic Diversity within *Triplochiton scleroxylon* Populations

Population	PPL	N_a	N_e	I	H
"On-farm Tree" Farmland	55.20	1.552	1.374	0.320	0.2175
Primary Forest	62.70	1.642	1.359	0.333	0.2192

PPL = Percentage Polymorphic Loci, n_a = Number of Alleles per Locus, n_e = Effective Number of Alleles per Locus, H = Gene Diversity, I = Shannon Index.



Figure 2: A Mansonia Tree



Figure 3: A Farmland with "On-Farm" Trees

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