

# Genetic structure of *Albizia gummifera* and local adaptation to the associated mycorrhiza

J. S Nantongo<sup>1</sup>, J. B. L Okullo<sup>1</sup>, G. Eilu<sup>1</sup>, D. Odee<sup>2</sup>, I. R. Ramonta<sup>3</sup> and S. Cavers<sup>2</sup>

<sup>1</sup>Faculty of Forestry and Nature Conservation, Makerere University

<sup>2</sup>Center for Ecology and Hydrology, Edinburgh

Correspondence: [jbokullo@forest.mak.ac.ug](mailto:jbokullo@forest.mak.ac.ug) / [okullo66@yahoo.com](mailto:okullo66@yahoo.com)

## Background

*Albizia gummifera* is an indigenous tree found in both East Africa and Madagascar with potential for restoration of degraded forests/landscapes. It grows fast in gaps, forms mycorrhizal and rhizobial associations. For successful restoration, an assessment of genetic structure of such a tree is important as it influences the adaptive potential of a species. The aim of this study was to assess the extent to which genetic structure of *A. gummifera* is an important factor in selecting germplasm for restoration in East Africa and Madagascar. The specific objectives were (i) to compare the genetic structure of three populations from East Africa and Madagascar and (ii) to assess local adaptation of various *A. gummifera* seed sources from different countries to mycorrhizae.

## Materials and Methods

The study populations consisted of three forests communities one from each of the selected sites in Kenya, Madagascar and Uganda. The study had two major components; *A. gummifera* genetic structure and adaptation to soil mycorrhizae. To determine genetic structure, leaves were collected from 30 trees (Fig1a) separated by at least 100 m in each country. Leaves were immediately preserved in silica gel. DNA extraction and Chloroplast RFLP amplification were carried out at CEH (Fig1b).

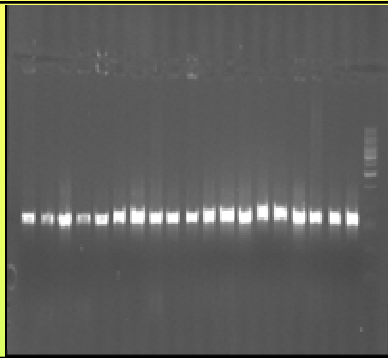


Fig1a: *A. gummifera* tree (left).

Fig1b An agarose gel scan of PCR1 amplification

To assess local adaptation of the species, a transplant experiment was set up using soils collected below the trees from which seeds were collected in each country (Fig2a.). Fungal spores of arbuscular mycorrhiza were extracted from part of the same soil by wet sieving and decanting, followed by sucrose centrifugation. Spores were enumerated using direct microscopic counts (Fig.2b).

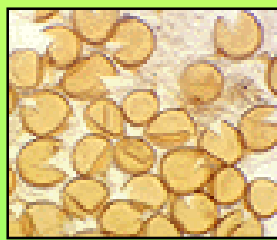


Fig 2a: Lay out of transplant experiment aggregatum

Fig2b. spores of *Glomus*

## Data analysis

For genetic structure, estimates of genetic diversity, gene flow and differentiation were obtained. For adaptation, ANOVA for seedlings heights and correlations between heights and micorrhiza diversity were run. Shannon Weiner's diversity indices were generated for myco diversity.

## Results

### Genetic structure of *A. gummifera*

The species is genetically diverse with 14 cpDNA haplotypes. Ugandan samples were most diverse followed by Madagascar and Kenyan. Although majority of variation was distributed within populations, significant population differentiation ( $P < 0.005$ ) was observed and each population contained private haplotypes. Greatest genetic distance was observed between Kenyan and Madagascar populations and lowest between Ugandan and Kenyan populations (Fig.3).

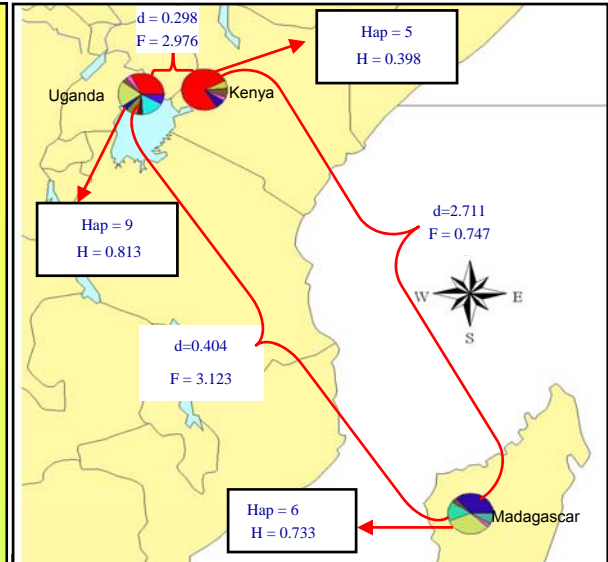


Fig. 3: Genetic structure of *A. gummifera*: H= Genetic Diversity, d= Genetic Distance, F = Gene flow. Fixation Index  $\Phi_{ST} = 0.249$

### Mycorrhizal diversity and adaptation of *A. gummifera*

The diversity of the mycorrhizal community varied among sites with Ugandan soils being more diverse than those of the Kenyan counterpart. For the old soils, fungal diversity was highest in Kenya, followed by Madagascar and then Uganda. Based on the growth performance measurements, there was no evidence of adaptation of *A. gummifera* provenances to local mycorrhizae though plant performance for inoculated plants was higher than that of the control (Fig. 4).



Fig. 4: Response of provenances to soil inoculation with mycorrhiza

### Inferences from study

From this study, the specific kind of mycorrhiza the *A. gummifera* plants are exposed to seems not to be important, although the trees can benefit from exposure to the mycorrhiza. The tree populations also seem to have genetically differentiated and transferring them to sites outside their own may pose a genetic threat. More research is however needed to ascertain adaptive differences of *A. gummifera* to abiotic and other biotic factors, the suitable founding genetic diversity and other factors that may affect its introductions to other sites. The exact mycorrhizae that colonise the plants also need to be identified.

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