Molecular characterization of the indigenous microbial communities living naturally in the rhizosphere of *Acacia senegal* trees in Kenya and Niger

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1. Introduction

Acacia tree species form a major composition of the leguminous trees in the ASALs in sub-Saharan Africa. They form symbiotic associations with strains of root-nodule bacteria (rhizobia) that are widely distributed in the rhizosphere (Brockwell *et al.,* 2005). Acacia *senegal* tree species, common in the semi-arid areas are the sources of gum arabic. Rhizobia can also stimulate production of non-wood forest products (gum arabic) once mature trees are inoculated with rhizobia (Faye *et al.,* 2006). Stimulation of gum arabic production could improve the livelihoods of farmers through its utilization as food and exchange for income. Understanding the relationships between microbial communities and their manipulation could be a way for a sustainable management of gum arabic production through improvement of soil fertility.

2. Overall objective

To assess the diversity of soil microbial (bacterial and fungal) communities naturally present in the rhizosphere of tree species in different Agro-ecological zones in Niger and Kenya before starting investigations on the functional communities in relation with N cycle.

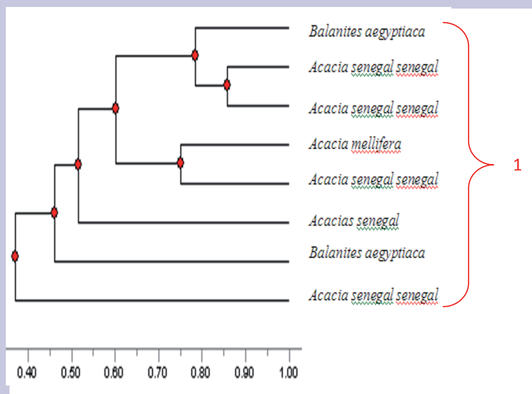
3. Sites and Methods

This study was conducted in nine sites within three districts in Kenya. Isiolo district (Ngare Ndare, Kula Mawe and Isiolo Town), Baringo district (Chepsigot, Rimoi, Solit and Kimalel), Kajiado district (Ldamat and Oloilila Ranch) and in seven sites in Niger (Azai, Bader goula, Begorou, Dogona, Kiki, Kokoiye and Tabe). These areas are in the ASALs in the sub-Saharan Africa. Soil sampling was done at the rhizosphere of Acacia species, other non-fixing tree species and on bare land (in Niger) at a depth of 0- 15 cm at four spots of equal distance and around the tree trunk, composited by mixing them thoroughly to form a sample per tree. Microbial diversity was assessed through DNA extraction, PCR amplification using universal primers gc-338f/518r for total bacteria communities and 403f/gc-662r for fungal communities. Amplified DNA was separated using Denaturing Gradient Gel Electrophoresis (DGGE) (Porteous *et al.,* 1997; Ercolini *et al.,* 2004; Assigbeste *et al.,* 2005). Digitized DGGE images were used to construct cluster dendograms and determine the Shannon-Weaver indices of diversity (Eichner *et al.,* 1999; Muyzer *et al.,* 1993). Means of diversity were subjected to ANOVA analysis and compared using Duncan New Multiple Range Tests (DNMRTs) at $P<0.05$.

4. Results

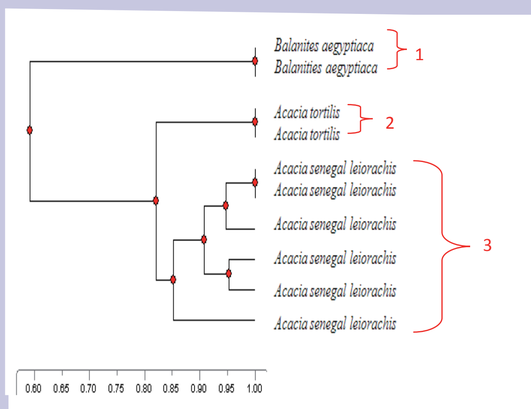
Cluster dendograms

A. Kimalel-Kenya



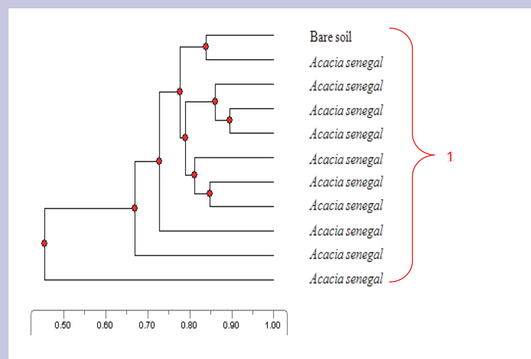
Fungal communities, non-specific clustering.

B. Kula Mawe- Kenya



Bacterial communities, specific clustering

C. Bader goula - Niger



Bacterial communities, non-specific clustering

Fig. 1(A, B and C): Examples of cluster dendograms of fungal and bacterial communities of Kenyan and Niger soils constructed using Unweighted Pair Group Method with Arithmetic Means (UPGMA).

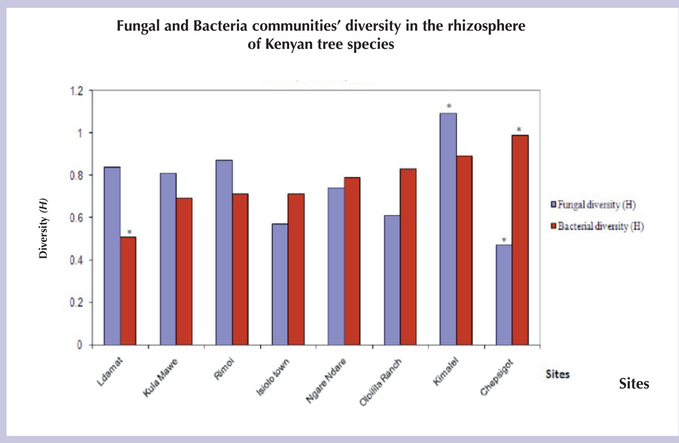


Fig. 2: Genetic diversity of soil microbial communities in Kenyan sites. * indicates significant differences between means of diversity.

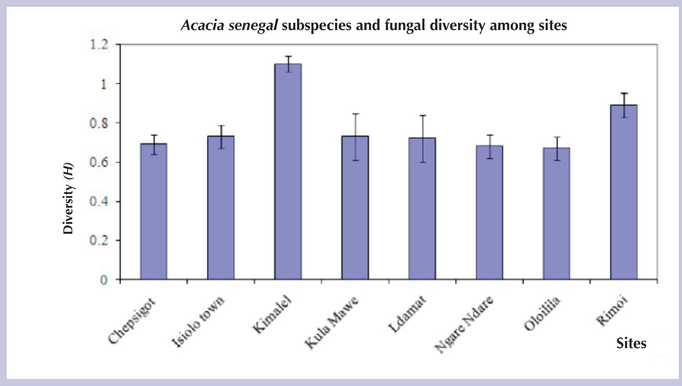


Fig.3: Genetic diversity of soil fungal communities under *Acacia senegal* subspecies in Kenyan sites

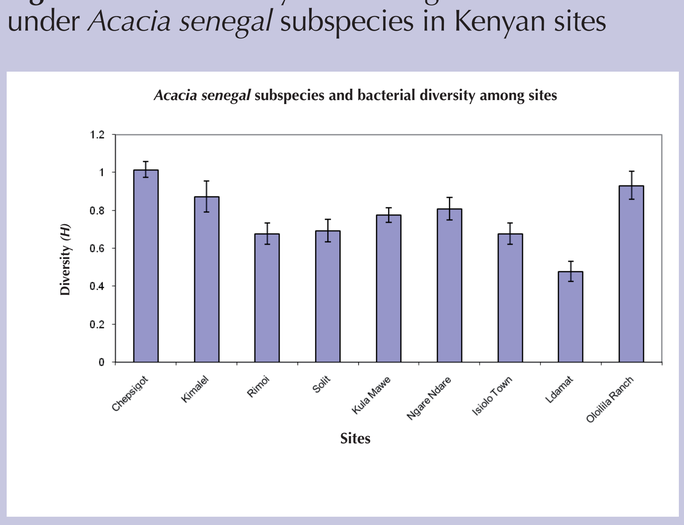


Fig.4: Genetic diversity of soil bacterial communities under *Acacia senegal* subspecies in Kenyan sites

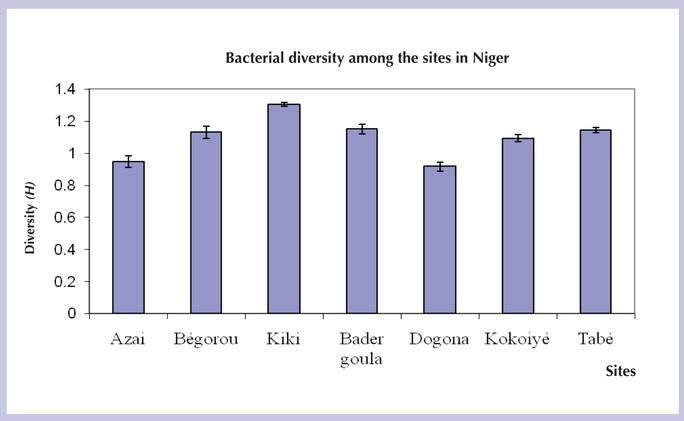


Fig. 5: Genetic diversity of soil bacterial communities in Niger sites

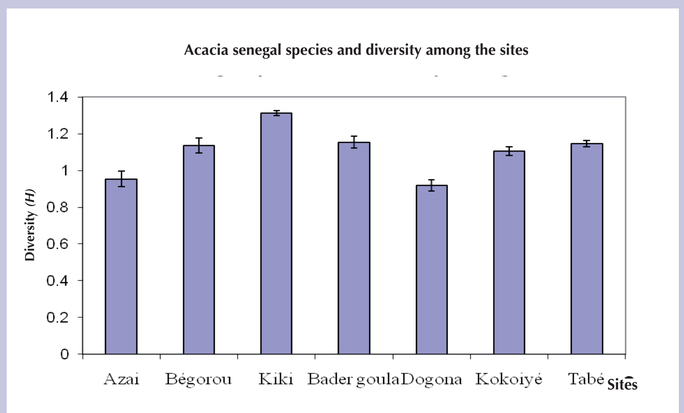


Fig.6: Genetic diversity of soil bacterial communities under *Acacia senegal* subspecies in Niger sites

5. Results and Discussion

Generally, there was specific clustering with bacterial communities according to the tree species in Kenyan soils. Fungal communities in Kenya and bacterial communities in Niger generally showed non-specific clustering with the tree species. (Fig. 1: A, Band C). This shows high similarity of bacterial species according to the tree species in Kenyan soils but high degree of variability with the soil fungal communities in Kenyan soils and bacterial communities in Niger soils. There were significant differences *($p< 0.05$)* between both fungal and bacterial communities in Kenyan soils with an interesting scenario of low fungal communities where bacterial communities were high and *vice-versa* in Chepsigot and Ldamat sites respectively. This suggests that the diversity of both fungal and bacterial communities is inversely related in Kenyan semi-arid soils. Bacterial communities' diversity was not significantly different among the sites. Fungal communities' diversity was significantly different *($p< 0.05$)* with high diversity in Kimalel, Rimoi, Ldamat and Kula Mawe and lowest in Chepsigot site. Effect of *Acacia senegal* subspecies on diversity of soil fungal communities was significantly high *($p< 0.05$)* in Rimoi and Kimalel sites. Ldamat site had significantly low *($p<0.05$)* diversity of bacteria with *Acacia senegal* subspecies. Bader goula and Begorou sites in Niger had significantly high *($p< 0.05$)* bacterial diversity both under *Acacia senegal* species and *Acacia senegal* species and bare land.

6. Conclusions and Recommendations

- Soil microbial communities (fungal and bacterial) diversity is varied in the rhizosphere of tree species in the semi-arid areas in sub-Saharan Africa.
- Generally, *Acacia senegal* subspecies did not significantly affect the diversity of soil microbial communities.
- Narrowing down to functional bacterial groups could provide more information.

7. References

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8. Acknowledgement

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