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Macrofungal diversity in Yangambi Biosphere reserve and Yoko reserve rainforests of the Democratic Republic of the Congo

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Detecting and understanding patterns in the distribution of taxa is a fundamental element in implementing biodiversity conservation. Regarding fungi, understanding how functional diversity varies with forest types helps to define their niche and allows predicting the impact of forest degradation on communities of macrofungi. It also allows better understanding of the way in which they realize their ecological function and nourishment purpose. This study aimed to assess the species richness and functional diversity of macrofungi within rainforests from Yangambi Biosphere reserve and Yoko reserve in the Democratic Republic of the Congo. Results from this study show significant differences in number of macrofungi species between forest stand types (p -value <0.001). Based on all macrofungi functional groups, the most species-rich forest stand was the *Gilbertiodendron dewevrei*. Of the five reported functional groups (saprotrophic fungi, ectomycorrhizal fungi, insect parasitic fungi, plant parasitic fungi and termites' symbiotic fungi), the saprotrophic fungi were the most abundant trophic group represented 210 species of a total of 341 fungal taxa. The results revealed also that woody decaying and terrestrial saprotrophic are mainly characteristic of mixed forests while the occurrence of ectomycorrhizal taxa depends on the presence of ectomycorrhizal trees. In addition, strong relation has been demonstrated between fungal composition and the composition in vascular plants. Each forest stand type is characterized by specific floristic composition which has a corresponding and fairly predictable mycological composition. The study gave evidence that species richness and functional diversity of macrofungi are strongly influenced by vascular plants composition. The various reported functional groups differently intervene in nutrients cycling, and then play key role in forests functioning.

Key words: Species richness, functional diversity, macrofungi, rainforests, DR Congo.

INTRODUCTION

Detecting and understanding patterns in the distribution of taxa is a major topic in ecological studies and a fundamental element in implementing biodiversity conservation (Gaston, 2000; Purvis and Hector, 2000; Tilman, 2000; Schmit 2005; Caiafa et al., 2017; Dvorack

et al., 2017). Regarding fungi, the most important aspect of biodiversity assessment is the measures of species richness (Schmit et al., 1999; Hawksworth, 2001). Insight into fungal species richness is vital for biodiversity management, especially when the conservation status

needs to be evaluated (Caiafa et al., 2017). Next to a number of classical qualitative and quantitative traits, functional traits are now also being used for evaluation (Caiafa et al., 2017). Understanding how functional diversity varies with forest types helps to define their niche and allows predicting the impact of forest degradation on communities of macrofungi (Caiafa et al., 2017).

Several studies (Hawksworth, 1991; Hawksworth, 1997; Hawksworth, 2001; Mueller and Schmitz, 2007; Schmitz and Mueller, 2007; Caiafa et al.; 2017; Dvorack et al., 2017) have reported that species richness and composition of fungal communities are strongly related to the diversity and composition of the vegetation. As fungi developed different strategies to interact with plants and their habitats, they have been classified into three major functional groups (Read and Perez-Moreno, 2003; Lindahl and Borberg, 2008; Lonsdale et al., 2008): Saprotrophic fungi that grow on scraps on organic matter and decompose litter and dead trees or branch, mutualistic fungi that develop mutualistic relationship with host plants or other living organisms and parasitic fungi which grow in or inside other living organisms and lives totally depending on them (Read and Perez-Moreno, 2003; Lindahl and Borberg, 2008; Lonsdale et al., 2008; Tedersoo et al., 2010; Härkönen et al., 2015; Piepenbring, 2015).

However, some fungal species are selective with numerous plants trees, creating habitat filtering on their occurrence (Härkönen et al., 2015; Piepenbring, 2015). Functional trait-based approaches allow determining the relative importance of habitat filters and fungal species ability in fungal community assembly (Aguilar-Trigueros et al., 2015). Regarding this, specific groups of fungi may colonize particular groups of vascular plants or may occur on particular substratum (Munguia et al., 2005; Gómez-Hernández and Williams-Linera, 2011; Härkönen et al., 2015; Piepenbring, 2015). In addition, different fungal species develop in association with wide range of host plant or on various substratums (Lodge et al., 2004; Piepenbring, 2015). Hence, substratum reflects the strategy of macrofungi nourishment and therefore indicates the way in which fungi intervene in nutrient cycling.

Since fungal diversity is affected by host plant diversity (Härkönen et al., 2015; Piepenbring, 2015), rainforests from the Democratic Republic of the Congo are expected to host high numbers of fungal species. Although fungi are omnipresent and highly diverse within rainforests from the Democratic Republic of the Congo, little attention has been given to the assessment of fungal species richness. This paper is the first attempt to assess

the species richness and functional diversity of macrofungi within various types of rainforests found in the Yangambi biosphere reserve and the Yoko forest reserve. The aim of this study was to investigate patterns of distribution of macrofungi species and their functional diversity associated with different forest stand types.

MATERIAL AND METHODS

Study area

The two study sites (The Yangambi Biosphere reserve and the Yoko reserve) are located in the Tshopo province of the Democratic Republic of the Congo. Extended on the two sides of equator, the province of Tshopo is located in the central Congo basin, between -2° of south latitude and +2° of north latitude, and from 22° up to 28° Eastern longitude (Lejoly et al., 2010). As reported by Lejoly et al. (2010), the Yangambi Biosphere reserve is located within the Congo River Basin west, laying around 90 km west of Kisangani (Isangi territory) while the Yoko site is located in the Ubundu territory 32 km south-East of Kisangani in the Democratic Republic of the Congo (Figure 1). The biosphere reserve is home to a widespread range of virgin tropical rainforests hosting about 32,000 tree species and with about 2200 km² of surface (<https://www.protectedplanet.net/yangambi-biosphere-reserve>).

As part of the equatorial region, the Yangambi Biosphere reserve is characterized by a rainy and hot climate (Lejoly et al., 2010). The climate is characterized by monthly average temperature between 22.4 and 29.3°C, and annual average surrounding 25°C. The annual rainfall ranges from 1600 to 2200 mm with an average surrounding of 1828 mm (Mohyont and Demarée, 2006). Rainfall is irregular throughout the year. The average year has a long rainy season interrupted by two small drier seasons from December till January and from Jun till August (Mohyont and Demarée, 2006).

Fungal sampling and identification

The mycological inventories were carried out in November of the year 2012 and 2013, and during the main rainy season (between March and May) of the years 2015 and 2016. Fungal sampling was performed every two weeks within different types of forests (forests dominated by *Gilbertiodendron dewevrei*, *Brachystegia laurentii*, *Julbernardia serretii*, *Uapaca heudelotii* and *Uapaca guineensis*, and mixed forests) and along the main forestry roads trails and transects (Hueck, 1951; Lodge et al. 2004). Plots (100 x100 m) divided in 20 x 20 grid were demarcated in each forest type, except the *Uapaca heudelotii* in which plots were less than 100 x 100 m, that is 25 m x 50 m. The locations of all sampling plots were recorded with a Global Position System (GPS) device using the WGS-84 geographical coordinate system.

In each plot, the above ground encountered fungi fruiting bodies of Basidiomycetes and Ascomycetes have been surveyed and harvested (Arnolds, 1981). The fresh collected fruiting bodies were dried and voucher specimens were deposited at the Botanic Garden Meise (Belgium). Species identification was based on macro and micromorphological features referring to the description found in several documents (Heinemann, 1954; Heim, 1955;

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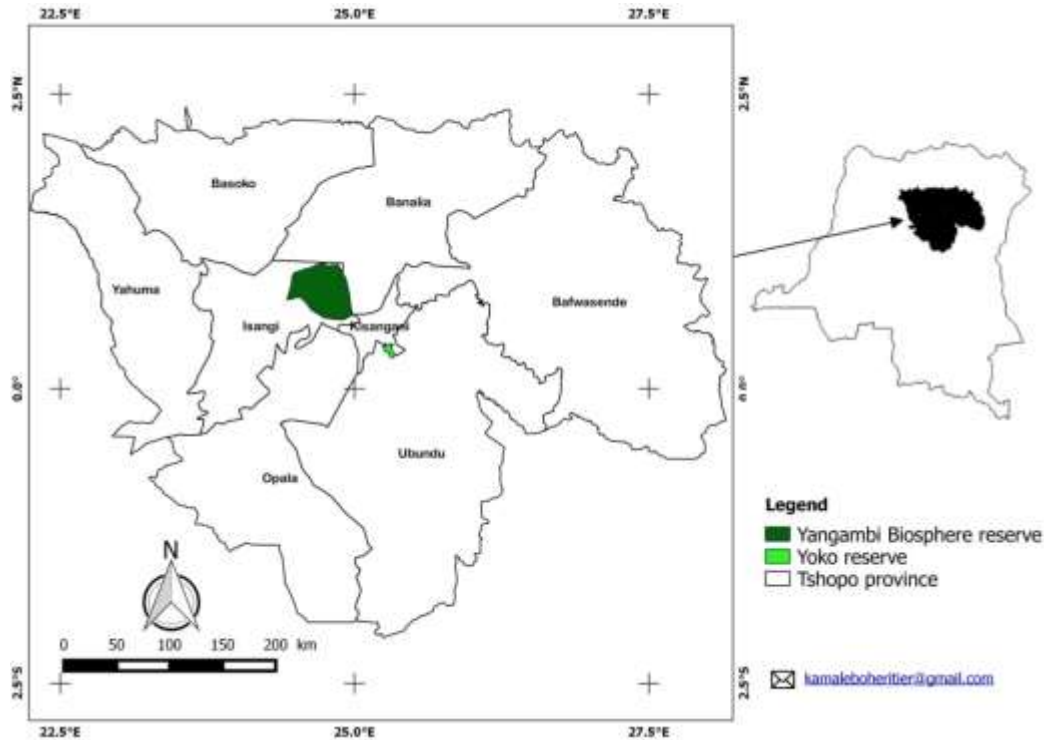


Figure 1. Study site location.

Pegler, 1977; Heinemann and Rammeloo, 1983; Heinemann and Rammeloo, 1987, 1989; Buyck, 1993; Buyck, 1994a, 1997; De Kesel et al., 2002; Verbeken and Walley, 2010; Eyi et al., 2011). Species names and author's abbreviations were annotated using the Index Fungorum site (<http://www.indexfungorum.org/Names/Names.aspx>). All unidentified species but identified to the genus level were noted 'sp.' Before confirming identifications, doubtful records were indicated by the abbreviation 'cf.' or 'aff.' before the epithet. Unidentified taxa (no genus, no species name) were excluded from the analysis.

Analysis of fungal diversity

Species richness was calculated as the number of fungal species collected from each type of forest (Hueck, 1951; Baptista et al., 2010; Caiafa et al., 2017). Based on their mode of nutrition and referring to the studies of Caiafa et al. (2017), all recorded species were classified into trophic groups. Three main trophic groups were defined: saprotrophic fungi (including woody-decaying), parasitic fungi and mutualistic fungi (Read and Perez-Moreno, 2003; Lindahl and Borberg, 2008; Lonsdale et al., 2008; Tedersoo et al., 2010). Saprotrophs are fungi which grow on scraps on organic matter, on dead organisms or on non-living part of a living organism such as animal dung, dead straw, decomposed litter and dead trees or branch. The parasitic fungi constitute a group of fungi which grow either on living plants, animals or on other living fungi and lives totally depending on its host organisms. Furthermore, the mutualistic fungi include the mycorrhizal fungi associated with vascular plants and fungi living in mutualism with termites (Read and Perez-Moreno, 2003; Lindahl and Borberg, 2008; Lonsdale et al., 2008; Tedersoo et al., 2010).

The diversity of macrofungi was determined using the Shannon

(H) index (Fisher et al., 1943). Hierarchical clustering and Correspondence Analysis (CA) among forest types were performed with the packages FactoMineR found in R software (Cornillon et al., 2012). The Chi-squared test ($\alpha=5\%$) permitted to assess the difference between the number of fungi species between different forest types and fungi families.

RESULTS

A total of 341 taxa of macromycetes were recorded in the seven different forest stand types from rainforest of Tshopo. Of all 341 recorded fungi, 193 were determined to species level and 148 to the genus level. The most species-rich group of macromycetes was the class of *Basidiomycetes* (with 310 species), while the class of *Ascomycetes* was only represented by 31 species. Of all *Basidiomycetes*, the *Marasmiaceae* family was the most diverse (with 65 species) followed by the *Russulaceae* (35 species), *Agaricaceae* (23 species), *Cantharellaceae* (18 species), *Polyporaceae* (18 species), *Amanitaceae* (14 species), *Boletaceae* (14 species), *Tricholomataceae* (14 species) and *Pluteaceae* (8 species) (Figure 2). Likewise, the *Xylariaceae* was the most diverse family of *Ascomycetes* (12 species).

Significant difference was observed in number of macromycetes species between forest stand types (p -value<0.001). In all investigated forest stands, the forest dominated by *Gilbertiodendron dewevrei* was reported the most species-rich (total species number = 166,

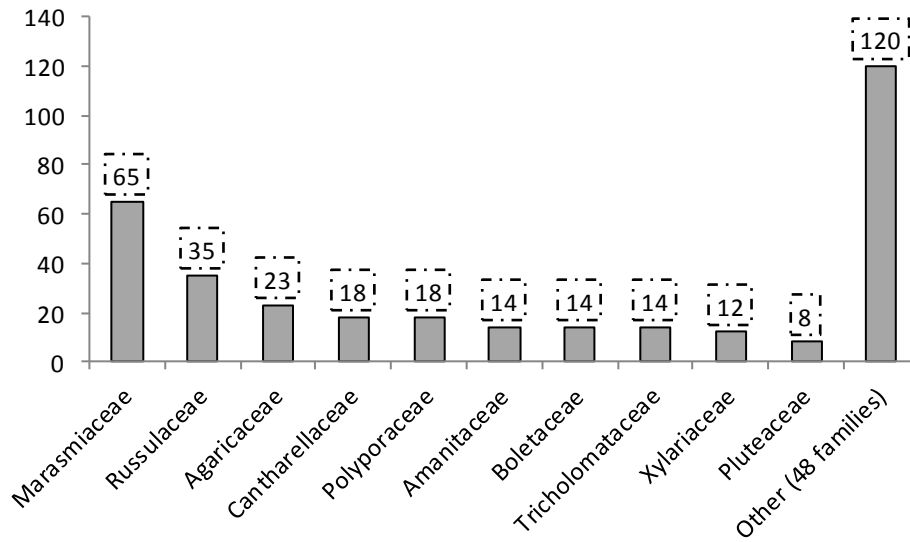


Figure 2. Numbers of macrofungi species in fungal families.

Shannon index value=5,1), followed by the mature mixed forests (total species number=157, Shannon index value=5,1), the disturbed mixed forests (total species number= 101, Shannon index value= 4,6), *Brachystegia laurentii* dominated forest (total species number= 92, Shannon index value= 4,5) and *Julbernardia seretti* dominated forests (total species number= 36, Shannon index value= 3,6). The lowest species richness was observed in *Uapaca heudelotii* dominated forests (with 15 species and 2,7 as value of the Shannon index).

Whereas the numbers of macromycetes significantly differ between forests, several types of forest stands have shown strong variation in the composition of macrofungi (Figure 3). Of all the 166 species of macrofungi recorded in the *Gilbertiodendron dewevrei* dominated forests for example, only an average of 79 ± 3 species was reached per plot. A similar pattern has been observed in the other types of forests. In the mature mixed forests; an average of 54 ± 17 species were reported per plot for a total of 157 species, 60 ± 24 species in *Brachystegia laurentii* dominated forest (with a total of 92 species), 38 ± 19 species in disturbed forests (total species number=101) and 19 ± 3 species in *Julbernardia seretti* dominated forests (total species number=36). The lowest mean number of macromycetes species was reached by the *Uapaca guineensis* dominated forest (8 ± 2 species per plot for a total number of 16 species).

Likewise, significant difference on fungal species numbers was observed in fungal functional groups of each forest stand type (Figure 4). In all forest stand types, the saprotrophic fungi (wood decaying and terrestrial saprotrophic fungi) were the most abundant trophic group represented by 210 species. The following large trophic group was the ectomycorrhizal fungi (93 species), followed by the plant parasitic fungi (7 species)

and the insect parasitic fungi (5 species). The lowest species-rich trophic group was the termites' symbiotic fungi represented by only 4 species. While the highest numbers of wood decaying and terrestrial saprotrophic fungi were found in both mature mixed and disturbed forests, the ectomycorrhizal species were most diverse and abundant in the EcM dominated forests.

Referring to Figure 4, it appears clearly that wood decaying and terrestrial saprotrophic fungi are present in all forest types. Nevertheless, the correspondence analysis (Figure 5) revealed that woody decaying and terrestrial saprotrophic fungi mainly characterize the mature mixed forests and the disturbed mixed forests dominated by many dead woody and fallen trunks to be decomposed. Plant parasitic fungi also occur mostly in mature forests characterized by several fragile old trees. Furthermore, the ordination analysis confirmed the main evidence that ectomycorrhizal fungi are characteristics of ectomycorrhizal trees dominated forests. Figure 5 revealed also that the *Brachystegia laurentii* tree had a prominent influence on the occurrence of insect parasitic fungi. Definitely, strong relationship was observed between fungal trophic groups and vascular plants distribution.

The composition of macromycetes' species is highly correlated with the composition of vascular plants. The hierarchical clustering (Figure 6) revealed that each forest stand type, characterized by a specific floristic composition, has a corresponding and fairly predictable mycological composition. Based on the composition of vascular plants species, all plots of *Gilbertiodendron dewevrei* dominated forests clustered together, while plots of other type of forest stand formed separated groups. Mature mixed stands formed a separate cluster as all plots of disturbed forests highly clustered together

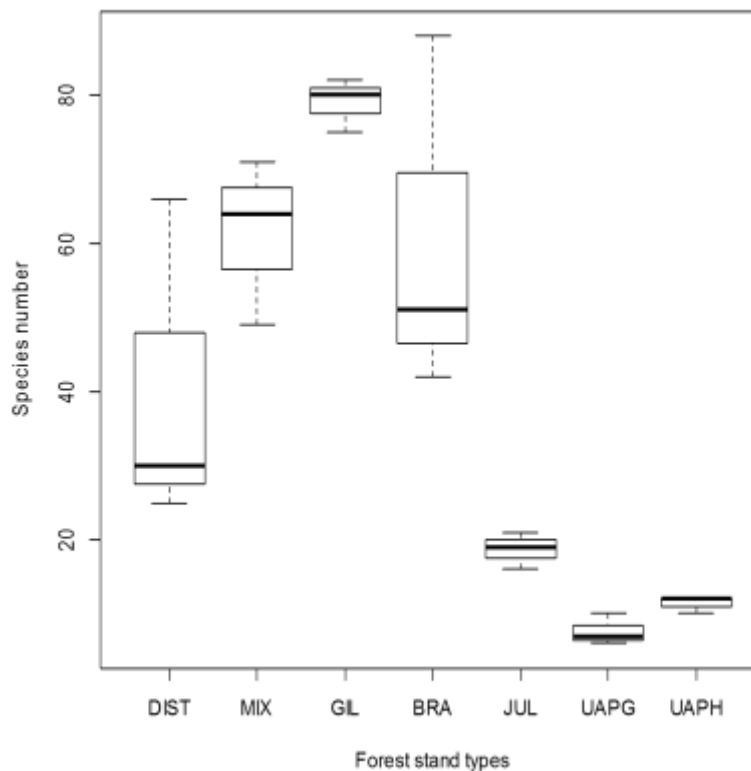


Figure 3. Number of species of macrofungi within studied plots. DIST=Disturbed or degraded mixed forest, MIX= Mature mixed forest; GL= *Gilbertiodendron dewevrei* dominated forest; BRA= *Brachystegia laurentii* dominated forest; JUL= *Julbernardia seretii* dominated forest; UAPG= *Uapaca guineensis* dominated forest; UAPH= *Uapaca heudelotii* dominated forest.

as a whole. A similar pattern was also observed in separate ordinations of plots based on the composition in macrofungi. All plots with same pattern in the composition of vascular plants, present almost same predictable fungal composition. *G. dewevrei* dominated forests plots formed a distinct group which corresponded to the same cluster based on vascular plants composition. Similar pattern was observed in clustering plots of mature mixed forests and disturbed forests based on both floristic and mycological composition.

DISCUSSION

Results from this study showed significant difference of species richness and functional diversity of macrofungi within forest stand types. Species richness and functional diversity are strongly influenced by the occurrence of some particular vascular plants. As reported by several other studies (Hawksworth, 1991; Hawksworth, 1997; Hawksworth, 2001; Mueller and Schmitz, 2007; Schmitz and Mueller, 2007; Caiafa et al., 2017; Dvorack et al.,

2017), the species richness and mycocoenose are affected by the diversity and composition in host plants trees. Munguia et al. (2005) and Gómez-Hernández and Williams-Linera (2011) have also reported that some species of fungi occur on particular substratum or grow in particular type of forest as several other fungal species develop in association with wide range of host plant or colonize diverse types of substrates (Lodge et al., 2004).

The high fungal species richness in *Gilbertiodendron dewevrei* dominated forests suggests that fungal host plant trees in this forest stand have developed mutualistic relationship with wide range of fungal species. In addition, habitats and local environment in the *G. dewevrei* dominated forests are expected to be favorable for the development of numerous species of macrofungi. Several studies (White, 1983; Eyi et al., 2011) have reported that the *G. dewevrei* is the most important ectomycorrhizal tree which develops wide mycorrhizal symbiosis with numerous species of EcM fungi from rainforests of the central Africa. The abundant aboveground litter found in forests dominated by *G. dewevrei* (Bartholomew et al., 1953; White, 1983) should

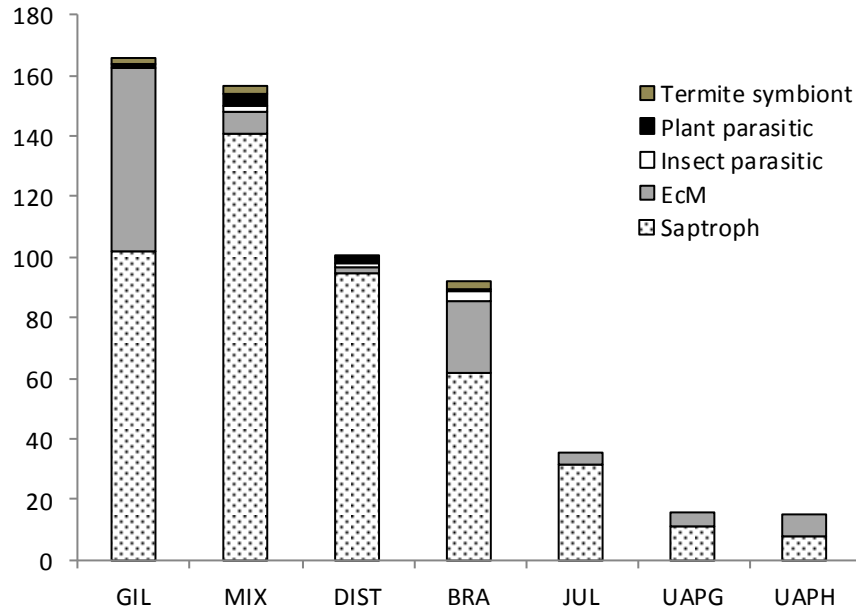


Figure 4. Frequency of fungal trophic groups within forest stands (EcM= Ectomycorrhizal).

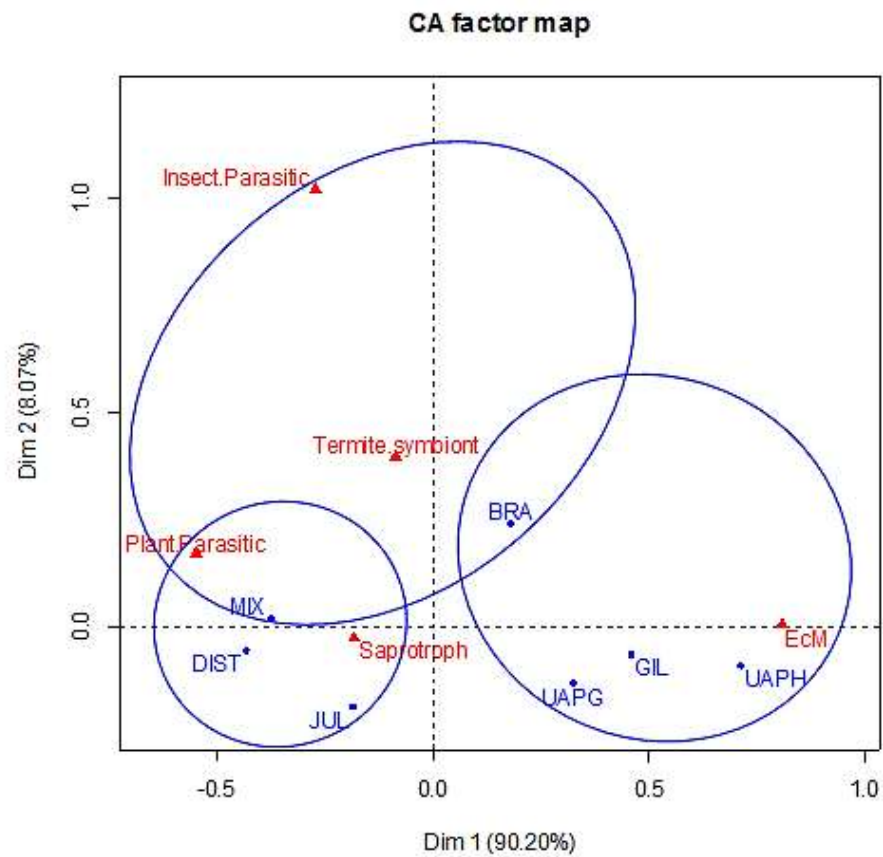


Figure 5. First two axes of the correspondence analysis (CA) showing the ordination of fungal trophic groups (red abbreviated names) within forest stand types (blue abbreviated names). The two axes explain 98.27% of ordination (90.20 % for the first axis and 8.07% for the second axis).

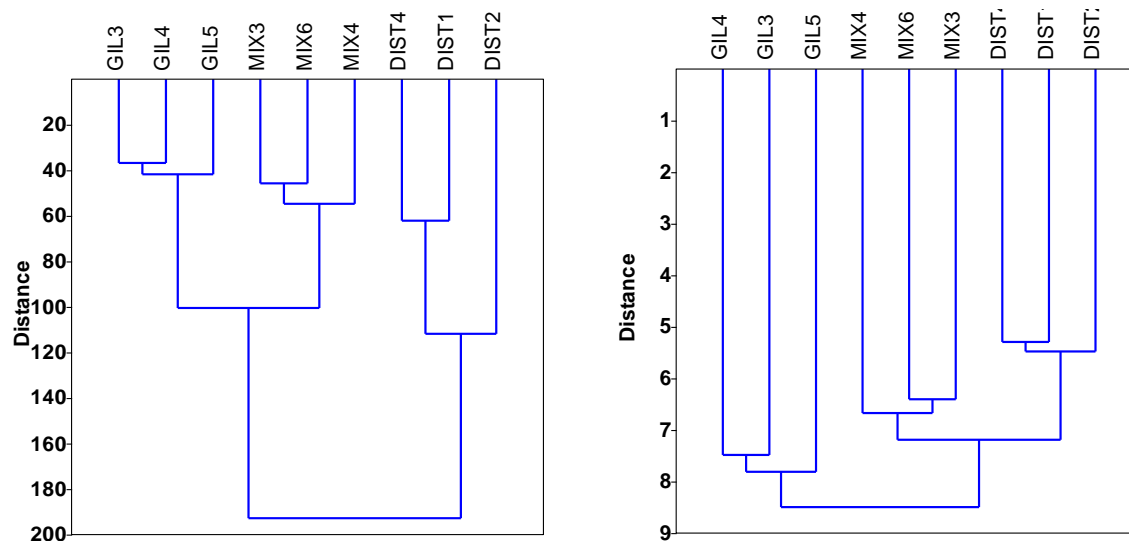


Figure 6. Hierarchical clustering of plots based on fungal composition (on the right side) and the composition in vascular plants (on the left side) of three selected forest stand. GIL= *Gilbertiodendron dewevrei* dominated forest, MIX= Mature mixed forest, DIST= Disturbed young mixed forest.

be normally a favorable habitat for numerous species of saprotrophic fungi (Mayor and Henkel, 2005). However, despite the presence of abundant dried aboveground biomass, high numbers of EcM fungi have been reported than saprotrophic fungi.

The high species richness of ectomycorrhizal fungi compared to saprotrophic fungi reported in the *G. dewevrei* dominated forests can be explain by the fact that the mycelia of some ectomycorrhizal fungi have capacity to inhibit the development of numerous saprotrophic fungi (Gadgil and Gadgil, 1971, 1975; Leake et al., 2002). This presumption is also supported by Torti et al. (2001) who reported that *G. dewevrei* dominated forest is characterized by deep leaf litter with slower decomposition. The slower decomposition of litter is however caused by the alteration of the understory environment by the plant tree physiology (Torti et al., 2001). In addition, the competition for nutrients that occurs between ectomycorrhizal fungi and saprotrophic fungi may retard the decomposition of litter by limiting the activities of the saprotrophs (Gadgil and Gadgil, 1971, 1975; Mayor and Henkel, 2005; Koide and Wu, 2003). However, by inhibiting the development of saprotrophic fungi and because of their capacity to decompose some forms of litter, apart from their role in nutrients uptake, some ectomycorrhizal fungi may supplement the decomposition capacities of saprotrophic fungi (Koide and Wu, 2003). Yet, the *Marasmiaceae* remains the most important and diverse family of litter saprotrophic fungi involved in the decomposition of the aboveground twigs and litter inside this forests.

The analysis of functional diversity allowed also to understand the potential contribution of macromycetes to ecosystem functioning. The insect parasitic fungi for

example are involved in the decomposition and cycling of mineral nutrients from insects and further invertebrates. However, the ecological relationship developed between *Brachystegia laurentii* tree and numerous species insects (Okangola, 2007; Payne et al., 2016) may explain the high occurrence of insect parasitic fungi in this forest stand type. According to these authors, the *B. laurentii* tree constitutes unique favorable habitat and nest for numerous species of insects, especially for numerous larva of *Lepidoptera*. Furthermore, wood-decaying and saprotrophic fungal taxa were abundant in secondary and degraded forests as well as in old dense forests. This observation is in line with several other reports (Eyi et al., 2011; Balezi, 2013) who found that the wood-decaying fungi mostly develop on old and fragile plant trees in mature forests, and on dead wood in degraded forests (Balezi, 2013) while litter saprotrophs mainly occur on the aboveground leaf litter and twigs (Eyi et al., 2011).

The abundance of ectomycorrhizal fungi was also observed in *B. laurentii* dominated forest as in several other ectomycorrhizal trees dominated forests. This observation confirms the main presumption that ectomycorrhizal fungi are characteristics of forests dominated by ectomycorrhizal trees. In addition, the forests dominated by *Uapaca* spp. were reported the lowest species-rich. The lowest species richness in *Uapaca* spp. forests may have been caused by the fact these forests develop on flooded or swamp soil (Beernaert, 1999) which has to inhibit the development of several fungal species. The lowest species richness in *Uapaca heudelotii* can also be explained by the lower sampling intensity in less than 1 ha plots due to the limited distribution of this type of forest. Several studies (White, 1983; Beernaert, 1999; Lejoly et al., 2010) have

reported that species of *Uapaca* develop some limited groves of monodominant dense forest often on soft and spongy soil.

At the plot scale, the *G. dewevrei* dominated forests showed higher pool of species variation. This observation suggests that even small, variation of biotic and abiotic parameters at fine spatial scale has influence on the occurrence of macromycetes. Observed differences in species richness and fungal functional diversity between forest stand indicate that the communities of macromycetes present various ecological niches and a wider variation of their functional traits (Aguilar-Trigueros et al., 2015).

Conclusion

The findings of this study give evidence that species richness and functional diversity of macrofungi are strongly influenced by vascular plants composition. Woody-decaying fungi mostly develop in mature mixed forests to decompose organic matter from fragile old trees and dead wood. Likewise, ectomycorrhizal dominated forests are in particular home for wide range of ectomycorrhizal fungi that inhibit the development of numerous saprotrophic fungi. The results of this study have clearly shown that the different functional groups of fungi play key role in the functioning of natural forests, especially in nutrient cycling. However, their effectiveness depends on the particular functional trait and specific abilities developed by each group. Strategies of fungi nourishment can be also related to some abilities developed in response to various abiotic and biotic factors. Since species of macrofungi play key role in organic matter cycling, describing deeply traits related to their specific performance and abilities is of great importance to understanding the way in which they realize their ecological function and nourishment purpose. Therefore, the establishment of links between species of macrofungi and their functional diversity and traits is of great importance. Hence, wider range of functional traits should be incorporated in future studies to identify the whole range of strategies used by species of macrofungi to maintain ecosystem functioning.

CONFLICT OF INTEREST

The authors declare that they have no competing interests

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Full Length Research Paper

***In vitro* micropropagation of *Rhinacanthus nasutus* (L) Kurz**

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The study was aimed to standardise a protocol for the *in vitro* mass propagation of *Rhinacanthus nasutus* (L) Kurz, an anticancer shrub. Leaf, node and inflorescence explants were inoculated onto the Murashige and Skoog's (MS) medium enriched with different combinations and concentrations of growth regulators. Maximum callusing percentage was achieved in leaf explants in MS medium supplemented with 5 mg/l 2,4-D. Multiple shoots were achieved from leaf, node and inflorescence explants with maximum of 25 ± 0.42 (5 mg/l BAP + 2.5 mg/l IAA), 11 ± 0.87 (5 BAP + 2.5 mg/l IAA) and 8 ± 0.56 (3 mg/l BAP + 1.5 mg/l IAA) shoots, respectively. For *in vitro* rhizogenesis, elongated micro shoots were aseptically transferred to the half strength MS liquid medium with maximum number of 8 ± 0.89 roots per shoot achieved in 1 mg/ml IAA fortified MS medium. The *in vitro* rooted micro shoots were acclimatised under laboratory conditions for two weeks by transferring to polycups containing sterile soil, sand and vermiculite (1:1:1). After two weeks, hardened plantlets were transferred to the green house for two weeks and then finally to the garden with 95% survivability.

Key words: *Rhinacanthus nasutus*, multiple shoots, leaf callus, node, inflorescence, rhizogenesis.

INTRODUCTION

Ever since the the existence of human being, plants have been relied upon for medicinal purposes. In the last few decades, there has been surge in the public interest for the herbal medicine due to the ill effects associated with synthetic medicine. The pressure on pharmaceutical industries to meet the demands has led to the over exploitation of medicinal wealth. Unrestricted harvesting of plants from the wild which is the main source of raw material is the cause of loss of genetic diversity and

habitat destruction. Approximately, there are 50,000 medicinal plant species used and two third of this number is collected from the wild (Edwards, 2004). Growing public interest in herbal medicine, industrial resurgence, growing world population, fast urbanisation and increasing anthropogenic activities has put the natural habitat of medicinal plants in dwindling mode and the wild population of medicinal plants has drastically reduced (Saha et al., 2007). Therefore, the management for the

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conservation of the traditional medicinal plants is the matter of urgency to negate the threat of extinction in future. Hence, *ex situ* conservative measures need to be strategized and standardised for the mass propagation of medicinal plants to cater the rising pharmaceutical demands while simultaneously negating the threat.

Rhinacanthus nasutus is a multipurpose ethnomedicinal shrub, belonging to the family, Acanthaceae. The plant is 1 to 2 m high; leaves are oblong, 3 to 8 cm in length, narrowed and pointed at both ends. The plant is available in India, Taiwan, Thailand, South china, Ceylon and Madagascar. The plant is collected throughout the year for its roots and leaves which are used by tribals for the treatment of various ailments. Traditionally, it is used to treat cancer, rheumatism (Chopra et al., 1956), eczema (Atsusi and Yoshioki, 1993), pulmonary tuberculosis, influenza virus, liver diseases, peptic ulcers, helminthiasis, scurvy, inflammation, hypertension and obesity (Kernan et al., 1997), leprosy, dhobie's itch, ring worm, poison toxicity (Muthukumaraswamy et al., 2003), herpes simplex virus, measles virus, polio virus (Subramaniam, 2006). Pharmacologically, the plant has been reported to possess cytotoxic (Wu et al., 1988); antiviral (Sendl et al., 1996); antitumor (Kongkathip et al., 2003), antiproliferative (Gotoh et al., 2004), anticancer (kupradinun et al. 2009), antimicrobial (Puttarak et al., 2010), anti-inflammatory (Nisarath et al., 2010), antidiabetic (Rao and Naidu, 2010) and antioxidant activities (Upendra et al., 2010). Natural resurgence of *R. nasutus* is through stem cuttings which is plagued with low rooting percentage and seeds are non-viable (Rao and Naidu, 2010). From last few years, *R. nasutus* seldom appears in its natural habitat of low hills of Nilgiri of Western Ghats of Tamil Nadu. At this point, micropropagation through plant tissue culture holds a significant promise for true to type and mass propagation of medicinally important plants. It is a potent biotechnological tool which has opened a vast area of research for biodiversity conservation. Owing to the alarming rate at which the *R. nasutus* is harvested and high pharmaceutical demands, a study was taken up to standardize a protocol for the mass propagations of *R. nasutus* using leaf, node and inflorescence explants.

MATERIALS AND METHODS

Rhinacanthus nasutus plants were collected from Nilgiri Hills of Western Ghats of Tamil Nadu and maintained in the botanical garden of Department of Botany, University of Mysore, Mysuru, India. Explants like leaf, node and inflorescence were collected from the garden and washed under running tap water for 10 min to remove the soil and dust particles. The explants were then treated with bavistin (5% w/v) for 5 min followed by dipping in 70% alcohol for 30 s and were then washed with sterile double distilled water. Inside the laminar air flow explants were treated with 0.01% HgCl₂ for 5 min followed by washing thrice with sterile double distilled water. The surface sterilised explants were cut into small pieces (1 to 2 cm) and inoculated on the MS medium fortified with different combinations and concentrations of growth regulators (Tables 1 and 2). The pH of the medium was adjusted by using 1 N

NaoH/HCL to 5.8 prior to autoclaving at 121°C for 15 min. The cultures were incubated at 22±2°C with 16 h photoperiod under light florescent tubes with light intensity of 25 µmol/s²/m² for 4 weeks. *In vitro* regenerated shoots were excised aseptically after attaining a height of 3 to 5 cm and transferred to half strength MS liquid medium fortified with different concentrations of auxins (Table 4) for *in vitro* rhizogenesis. The data was collected after 4 weeks, measuring root lengths and number of roots per shoot. After 4 weeks, well rooted micro shoots were hardened in laboratory for 2 weeks by transferring to the polycups containing sterile soil, sand and vermicompost in the ratio of 1:1:1. The hardened plantlets were then transferred to the green house for two weeks and then to the garden. Statistical analysis was carried out by using SPSS 16 version (DMRT).

RESULTS

Callus was initiated from all the explants tested (leaf, node and inflorescence) on MS medium enriched with different concentrations and combinations of auxins alone and in combination with BAP (Table 1). Callus was initiated from the cut edges of leaf and from the basal portions of nodal and inflorescence explants within three weeks of inoculation. Out of the auxins used, 2,4-D (2 to 5 mg/l) was found to be the best for callus induction. Leaf explants almost transformed into complete callus within 3 to 4 weeks of inoculation (Figure 1a). On combination of auxins with BAP (Table 2), BAP + 2,4-D (5 mg/l+2.5 mg/l) was found to be effective in callus induction. Differences in callus appearances and morphology were observed among the three explants with callus from leaf discs was soft creamy whitish, node with nodular light brown callus and inflorescence with light creamy and nodular callus. The calli in some leaf cultures turned dark brown and developed roots. The formation of roots was least found in nodal and inflorescence calli. After 5 weeks, calli derived from explants were subcultured for proliferation on suitable callus inducing growth regulator supplemented MS medium. Post subculture, most of the calli cultures of node and inflorescence turned brown, hard and eventually stopped proliferation; however, leaf callus proliferated well and appeared creamy and soft. Callus with creamy and soft appearance from leaf explants was further subcultured (Figure 1b) on suitable regeneration MS medium supplemented with BAP alone and in combination with IAA, IBA and NAA (Table 3). BAP+IAA (7 +3.5 mg/l) was found to be the best combination to induce indirect multiple shoots with maximum of (25±0.54) shoots per culture (Figure 1c). The regenerated shoots from callus were allowed to grow on regeneration medium for better growth. Axillary bud elongation was achieved in BAP alone and in combination with different auxins (Table 2); however, bud proliferation was achieved with maximum number of 11±0.87 shoots per node in BAP+IAA (5+2.5 mg/l) combination (Figure 1d). This concentration was found to be very specific for the proliferation of axillary buds, as no other combinations like BAP+IAA, BAP+NAA, BAP+IBA induced axillary bud proliferation although bud elongation was achieved in all

Table 1. Effect of different auxins on callus induction of leaf, stem and inflorescence of *R. nasutus*.

Growth regulator	Concentration (mg/l)	Callusing percentage		
		Leaf	Node	Inflorescence
2,4-D	0.5	40	20	--
	1	50	27	--
	1.5	68	35	20
	2	70	60	25
	2.5	80	66	28
	3	88	73	35
	3.5	94	80	30
	4	90	85	52
	4.5	90	88	63
	5	88	80	71
IAA	0.5	20	10	--
	1	22	15	--
	1.5	30	24	14
	2	46	30	35
	2.5	53	37	43
	3	64	38	48
	3.5	70	46	50
	4	68	50	53
	4.5	70	58	60
	5	78	60	58
IBA	0.5	10	--	--
	1	18	14	10
	1.5	20	17	23
	2	32	24	20
	2.5	35	28	30
	3	40	40	51
	3.5	52	48	49
	4	54	50	57
	4.5	63	48	48
	5	65	58	60
NAA	0.5	15	--	--
	1	10	18	13
	1.5	23	20	16
	2	27	17	25
	2.5	35	28	28
	3	35	37	47
	3.5	47	42	51
	4	53	48	50
	4.5	58	50	48
	5	60	53	50

*All treatments with six replicates and were treated thrice (no. of explants callused/total no. of explants inoculated) x 100.

in clusters, multiple shoots (8 ± 0.56) were achieved in BAP+IAA (3 +1.5 mg/l) combination with profuse basal nodular callusing (Figure 1e). In the fourth week of

incubation, vegetative buds started emerging from flower buds which was later confirmed when well-developed shoots emerged out in most of the cases (Figure 1f). The

Table 2. Effect of BAP alone and in combination with auxins on callusing and multiple shoot induction on leaf, stem and inflorescence explants of *R. nasutus*.

PGR	Concentration (mg/l)	Leaf		Node		Inflorescence	
		Callus culture response (%)	Multiple Shoot	Callus culture response (%)	Multiple shoots	Callus culture response (%)	Multiple shoots
BAP	0.5	10	--	--	--	--	--
	1	10	--	10	--	10	--
	3	25	--	20	--	10	--
	5	50	--	40	--	20	--
	7	45	--	60	--	20	--
BAP+2,4-D	1+0.5	30	--	15	--	15	--
	3+1.5	85	--	25	--	25	--
	5+2.5	100	--	90	--	40	--
	7+3.5	95	--	85	--	40	--
BAP+ NAA	1+0.5	20	--	15	--	--	--
	3+1.5	25	--	55	2.00±0.00	15	--
	5+2.5	55	--	75	2.00±0.00	50	--
	7+3.5	70	--	75	--	45	--
BAP+IAA	1+0.5	25	--	10	--	--	--
	3+1.5	40	--	35	4.00±0.66	30	8.00±0.56
	5+2.5	65	--	80	11.00±0.87	60	5.00±0.56
	7+3.5	60	--	75	7.38±0.57	50	5.33±0.67

*All the treatments with 6 replicates and repeated thrice. Each value represents Mean±S.D. Statistical analysis by DMRT ($P \leq 0.5$).

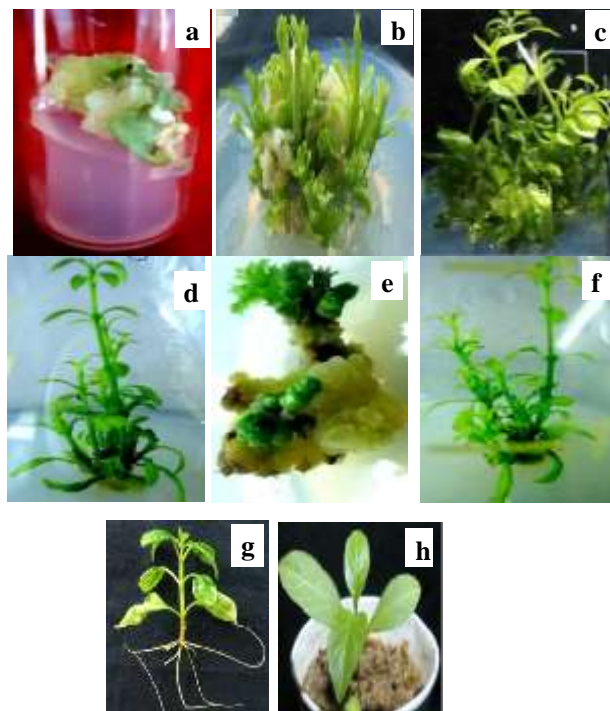


Figure 1. a- Leaf callus, b- multiple shoot in leaf callus, c- shoot proliferation in leaf callus, d- axillary bud proliferation from nodal explant, e- Shoot emergence and basal callusing in inflorescence explants, f- multiple shoot proliferation in inflorescence explants, g- *in vitro* rooted micro shoot, h- acclimatized plantlet

Table 3. Effect of subculture on multiple shoot induction on leaf callus in BAP alone and in combination with auxins supplemented MS medium.

PGR	Concentration (mg/l)	Mean no. of shoots
BAP	0.5	--
	1	--
	3	6±0.34
	5	8±0.64
	7	11±0.23
BAP+2,4-D	1+0.5	--
	3+1.5	6±0.34
	5+2.5	8±0.54
	7+3.5	11±0.28
BAP+ NAA	1+0.5	--
	3+1.5	14±0.65
	5+2.5	17±0.54
BAP+IAA	7+3.5	21±0.42
	1+0.5	--
	3+1.5	15±0.43
	5+2.5	25±0.42
	7+3.5	22±0.54

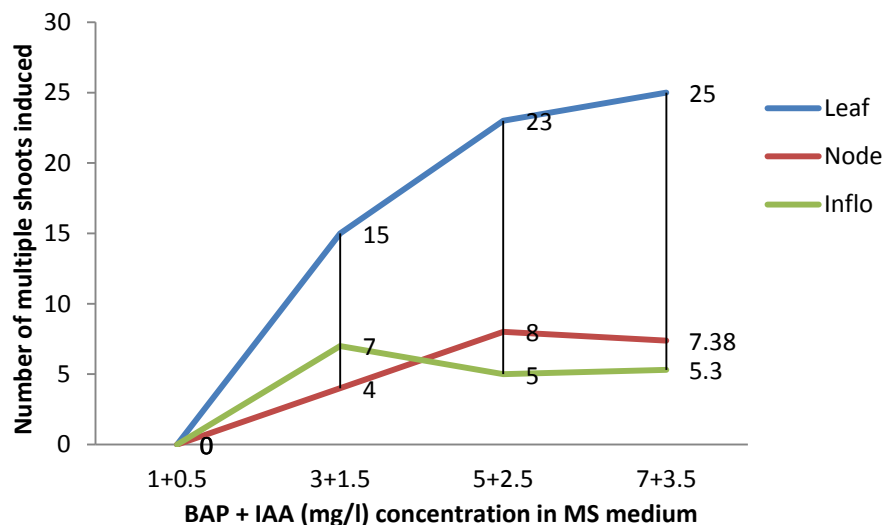
*All treatments with 3 replicates and treated five times, statistical analysis by DMRT, Mean±S.D (P≤0.5).

effect of BAP in combination with IAA on the multiple shoot induction in leaf, nodal and inflorescence explants is represented in Graph 1. For *in vitro* rhizogenesis, the well-developed elongated shoots (3 to 5 cm) derived from leaf callus, node and inflorescence explants were aseptically excised and transferred to half strength liquid MS medium fortified with different auxins (Table 4). Data were collected for days to root initiation, percent of shoots forming roots, number of roots per shoot and root length. Roots were induced in 3 weeks of time with maximum root induction (85%, Figure 1g) in half strength MS liquid medium supplemented with IAA at 1 mg/l concentration followed by IBA at 2 mg/l (62%). At higher auxin concentration basal callusing was reported with stunted shoot growth. Fully developed rooted plantlets were hardened in the laboratory for 2 weeks by transferring to the polycups containing autoclaved mixture of garden soil, sand and vermiculite (1:1:1) (Figure 1h). After two weeks of hardening, plantlets were transferred to greenhouse conditions and finally to the garden with maximum survivability (95%).

DISCUSSION

The overall aim of the present investigation was to standardise an *in vitro* system for the establishment of high frequency callusing and regeneration from different

explants of *R. nasutus*. Explants showed different callus responses at various concentrations and combinations of auxins and cytokinin BAP, when used alone and in combinations. Best callus induction was reported in leaf explants with 2,4-D at 4 mg/l as compared to other explants tested. Similar responses of higher callus induction from leaf explants have been reported in other plant species such as *Cichorium intybus* (Nandagopal and Ranjitha, 2006) and *Clematis gouriana* (Raja and Krishna, 2007). In contrary, other investigations carried out by Perera and Ozias (1991) have shown that stem explants callused more than leaf explants. During the callus formation, some replicates of leaf explant formed roots and the same is in confirmation with the results of Chuhan and Singh (1995). The combination of BAP with 2,4-D produced high percentage of callus than other combinations tested. The results are in concurrence with the studies carried out by Davendra et al. (2009) and Tola et al. (2015), whereas contradicts the one carried out by Chaitali et al. (2014), who reported BAP+IBA as best combination for callus induction. Callus induction at the proximal ends of the nodal and inflorescence explants in the present study is in confirmation with the results of Beena et al. (2003). According to Marks and Simpson (1994), basal callus formation might result from auxin accumulation in the tissues that stimulate cell proliferation. Different explants responded differently to



Graph 1. Effect of BAP in combination with IAA on multiple shoot induction of different explants of *R. nasutus*.

Table 4. Effect of different auxins on *in vitro* rooting of *R. nasutus* micro shoots regenerated from different explants.

Growth regulator (mg/l)	Mean root length (cm)	Mean no. of roots	Percent shoots forming roots
IAA			
0.5	6±0.45	7±0.65	74
1.00	8±0.34	9±0.34	85
2.00	5±0.21	5±0.65	65
3.00	4±0.45	3±0.55	42
IBA			
0.5	--	--	--
1.00	4±0.21	5±0.43	61
2.00	7±0.65	7±0.61	62
3.00	3±0.32	3±0.21	42
NAA			
0.5	--	--	--
1.00	4±0.35	4±0.31	65
2.00	5±0.48	4±0.65	68
3.00	3±0.43	4±0.23	46

multiple shoot induction against different concentrations and combinations of growth regulators tested. There was a significant difference in multiple shoot induction when different auxins were used in combination with BAP. In this study, IAA in combination with BAP induced maximum multiple shoots in leaf callus followed by BAP+NAA and BAP+IBA. However, in nodal and inflorescence explants, only BAP+IAA induced multiple shoots. These studies contradict the studies carried on *Rotula aquatica* (Martin, 2003) where addition of different

auxins to the medium containing BAP produced same number of multiple shoots in nodal explants. The synergistic effect between BAP and auxins have been reported in many medicinal plants like *Santolina canescens* (Casodo et al., 2002), *Bupleurum fruticosum* (Fraternali et al., 2002) and *Curcuma* species (Salvi et al., 2002). The main observation of their investigation was that low auxin concentration with high cytokinin modifies the frequency of shoot induction and growth and auxins at higher concentrations facilitates the more callus

formation, which is in line with the current investigations. However, contrasting results have also been reported by Nair and Seeni (2003) where addition of auxins in combination with BAP decreased the percentage of shoot induction and proliferation.

Several researchers (Bairu et al., 2008; Venkatachalam et al., 2007; Vuylsteke and Lanhe, 1985) observed that BAP at 3 to 5 mg/l is the most efficient concentration for *in vitro* shoot proliferation and the same is in line with the current results. In our study, BAP at higher concentration; beyond 5 mg/l did not enhance fresh weight or number of shoots in nodal explants. At concentration of 6-8 mg/l, the number of shoots produced was less when compared with concentration of 5 mg/l. Higher concentrations of cytokinin tend to have an adverse effect on the multiplication rate and morphology of the culture in nodal explants (Jafari et al., 2011; Strosse et al., 2004).

The success of *in vitro* micropropagation depends on rooting percentage and survival of hardened plantlets in natural conditions. In the current study, IAA at 1 mg/l was found effective for *in vitro* rooting followed by IBA and NAA. IBA and NAA showed poor shoot quality with intervening callus. Auxins at lower concentrations (2 mg/l and below) have been reported to be effective in *in vitro* rooting in earlier studies by Turker et al. (2001) and Mandal and Gupta (2001). de-Klerk et al. (1997) reported in their studies that rate of auxin uptake varies from species to species. The current study results are in concurrence with the studies carried out by Van der Krieken et al. (1993) who reported in their study that IAA is taken four times faster than IBA. Subsequently, the efficacy of rooting in the presence of IAA may be due to its faster intake. The superiority of IAA over other auxins for root induction has also been reported in *Cajanus cajan* (Dayal et al., 2003), *Murraya konini* (Rout, 2005) and *Quill resiliencies* (Fleck et al., 2009). Of the *in vitro* rooted shoots transferred to small cups, 95% survived in the natural habitat.

Conclusion

The present study describes the standardised protocol for callus induction and mass propagation of *R. nasutus* from leaf derived callus, nodal and inflorescence explants. Wild population depletion due to reckless anthropogenic approach can be neutralised by adopting *in vitro* techniques of mass propagation. Callus cell lines can be established for the mass production of biologically viable secondary metabolites and hence the near future threat to such medicinal plants could be kept at bay and thus could conserve the valuable taxa.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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ABBREVIATIONS

MS, Murashige and Skoog; **BAP**, 6-benzylaminopurine; **2,4-D**, 2,4-dichlorophenoxyacetic acid; **IAA**, indole-3 acetic acid; **IBA**, indole butyric acid; **NAA**:- naphthalene acetic acid; **Kn**, kinetin.

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Full Length Research Paper

Study on community perception of termite expansion and control in Borana plateau: Case study of Southern Oromia, Ethiopia

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Ecologically termites can be divided into damp wood dwellers, dry wood dwellers under and above ground dwellers in Dire, Miyo and Moyale districts. The combination of methods and tools such as stakeholder, key informant interview, group discussions, timelines, transect walk, community sketches were used. About 90 pastoralists were interviewed formally on its expansion and control techniques. The cause of termite expansion in the study area is diverse and complex. Mound-less termites take the advantages of camel population growth in the Borana rangelands as reproduction ground to quickly reproduce and expanded in the grasslands. Participatory rural appraisal was also conducted to assess the trend of termite expansion in the past 50 years. It was found that the expansion of termite has been increasing linearly. Pastoralists expect the coming 20 years termites may forage human beings due to the extent of its abundance. According to the respondents mound-less termites prefer the *Adoolleessa* (cool dry season) and the onset of rain at the end of dry season (*Bona-Hagayyaa*). Termite invasion is a new phenomenon which becomes a threat to rangeland management. The termite fauna of Ethiopia is not well known. At present 62 species belonging to 25 genera and four families have been recorded and 10 of the species are endemic. Currently, 100% of interviewers' in responses of no traditional and modern termite control techniques. Accordingly after the bun of traditional prescribed burning techniques, termite infestation becomes serious. There are termite predators such as *ant*, different bird species and poultry but worth less in termite control. The only plant species that is resistant to termite species in the study locally called *Annannoo* which is foraged by camel.

Key words: Borana lowland, termite expansion, termite mound, community perception.

INTRODUCTION

The problem of termites from a broader systems perspective is complex. Various factors in the Borana rangelands might have contribution for the expansions of

termites. The recent expansion and intensification of termites' damage is not well understood and documented. The past research and extension intervention did not

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Figure 1. Impacts of termite mounds on maize production.

focus on the identifying the root causes of termite expansion. The approach to manage termite damage in the study area is not well understood and therefore, needs of analyzing the situation of termite damage and infestation. This study also identifies potential social *species* and informal institutions that are responsible for the termite control. Pastoralists' access to resources, technology support and other sources of information were gathered in the area. Furthermore, assessment of the termite damage, community indigenous knowledge, trend analysis, and ecological impact of termite in the rangelands has been identified. Ecologically termites can be divided into damp wood dwellers, dry wood dwellers, underground and the aboveground dwellers (Evans et al., 2013). Termites are important in many ways. Good maize color around termite mound than the mound adjacent could be taken as an example (Figure 1). The reason is that termite excretes nutrients rich in solid wastes from their body that are essential for vegetation around the mound.

On the other hand, a large number of termite workers are responsible for the seriousness of the damage they cause on grasses (Figure 2) and different crops at maturity time. This may have a relation with that of soil infiltration capacity due to soil compaction. Accompanied by the problem of bush encroachment, opportunistic cultivation, and recurrent drought, in the study area of Borana rangelands, a large portion of the rangelands has been attacked by termites.

MATERIALS AND METHODS

Descriptions of the study area

The study was conducted in three districts of the Borana range lands. These are the Dire, Miyo and the Moyale District (Figure 3). These districts cover extensive areas in Borana pastoral system as well as the heart of Borana production system. Some crop production and animal rearing are the major pastoral community production system. These areas were under termite invasion for a long time. The study was conducted on two pastoral associations for each of the three districts; namely, Haralo and Dambala Badana in Dire district, Melbana and Boku-Luboma in Miyo district and

Tilemedo and Dembi in Moyale district. The data collection comprises different techniques. Combination of methods and tools such as stakeholder, key informant interview, group discussions, timelines, transect walk, were used to collect data.

Questionnaires

Face-to-face or directly interviews used open-ended and closed-ended questions, individual interviews were carried out by the administration of a questionnaire to the respondents.

Direct observation

The research team has been interested in observing the termite situations in some areas. The status of termite expansion and trends, timelines has been considered in depth.

Key informants

The key informants were among the following; local chiefs, elders, corporal and program coordinators such as program coordinator of rangelands in different offices. The aim was to solicit additional data on local peoples' perception towards conflict and its management. Informal discussions have been held with the key informants.

Data management and statistical analysis

Both quantitative as well as qualitative statistical analyses were applied in the data analysis. Computer based data coding, storage and retrieval mechanisms were used. The collected data were analyzed using Statistical Package for Social Science (SPSS) software.

RESULTS AND DISCUSSION

History and spread of termite in Borana

All of the respondents agree that there is a termite problem in their area. The problem that 46% of the respondents indicated that termite induced damage on everything they encounter; while 54% listed that termites



Figure 2. Impact of termite mounds on grasses and vegetation around the mounds.

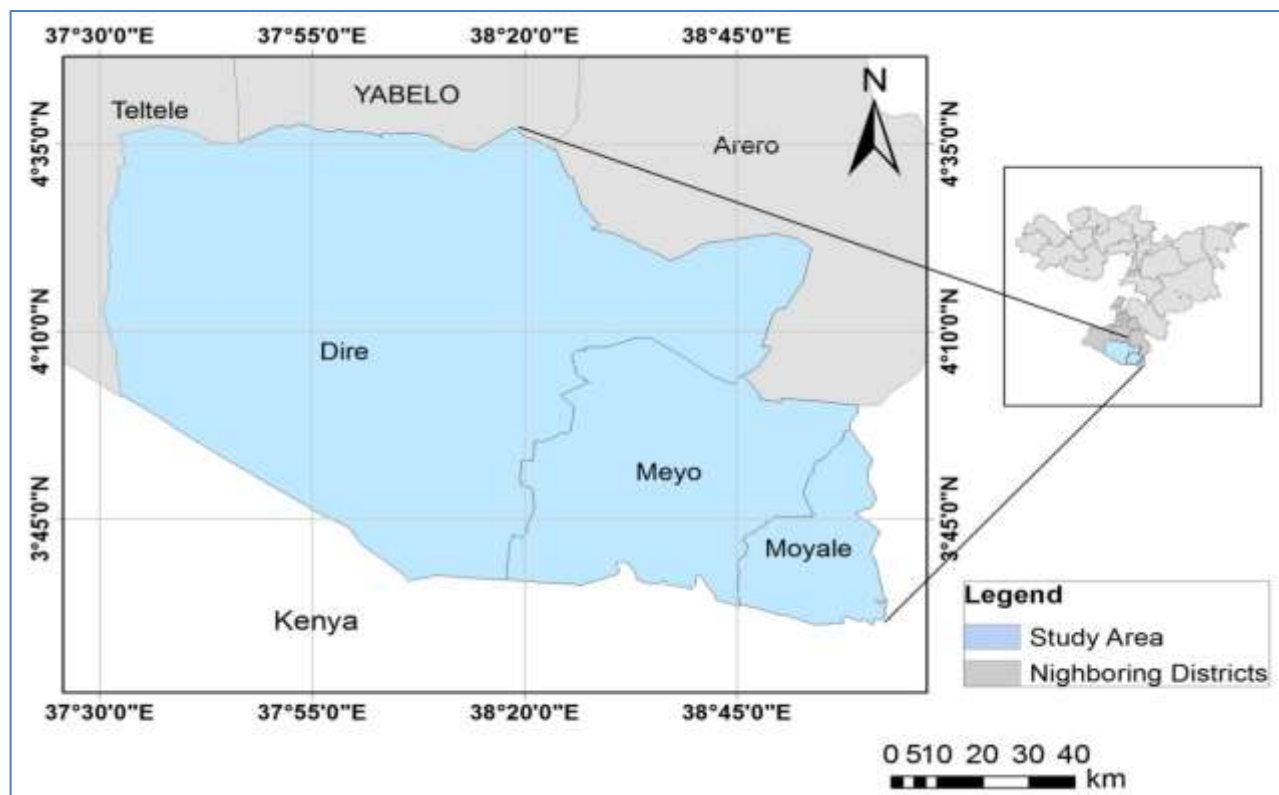


Figure 3. Map of the study area, showing the specific site in Dire, Miyo and Moyale district.

are damaging grass, crops and buildings. About 40% of the respondents know or presume that termite invasion was first seen around thirty to forty years ago, but not 60%. Locally, the communities identify the common species of termites as mound builder and non-mound builder; and in terms of size small, medium or large. 71% of respondents indicate that both mound-builder and mound-less termites are available in the Borana rangeland; while 16% had seen only termites which build mounds; and 13% classify the presence of termites in to different body size categories namely small, medium and large. When respondents compare the recent condition of termites in relation to the past 25 years ago their estimates were as follows: good (31%), fair (49%) and worst (20%). Among mechanisms of termite spread to new un-infested areas, underground tunnels, camel urine, cattle dug and spreading over surface by building tunnels are listed as a top system. According to the respondents the main causes of termite intensification are climate change and overgrazing.

Community perception about termites' damage in the rangelands

More than half of respondents think that mound building termites affect rangeland and crops by eating both grass and crops, while the others are not. According to 87% of the respondents eating grass, destruction of crops and degradation of rangeland are the main damage induced by mound-less termites. According to the respondents severity of termite intensification is higher in communal grazing land use type followed by degraded rangeland. When compared destroyed mounds soil with normal soil or adjacent soil around the mound area, the production is lower because of the bad nature of soil according to 44% of the respondent but 32% while argue that the dead or destroyed mound give high production due to its high level of fertility and the rest understood that there was no change on production.

Crop types that are more affected by termite intensification according to the respondents were ranked as *teff*, wheat and maize respectively. Due to this effect, around 32% of the respondents have changed their crops, while the other 68% have not changed the crop type. Sever damage to crops is reported to occur mostly during flowering followed by immediately after germination or the seedling stage, and the roots are the part of crop that are more affected as mentioned by the respondents. The types of fodders and trees susceptible and resist to termite effect are identified by the respondents (Table 1).

High crop damage in maize confirms the findings of Umeh and Ivbijara (1997), obtained from farm interviews with famers in south western Nigeria. Termites feed on roots of grasses, grasses, soil seed banks and barks of tree; and thereby damage valuable tree species.

Termites damage fences and crops in the study area. Pastoralists of Haralo PA reported that termites damaged eucalyptus stands including its seedlings. Termites have the potential to completely damage big trees over a long period. Termites' mounds are reported to be one of the problems in the rangelands. No grasses grow near the mounds. According to the pastoralists, this could be due to pulverization of the soils and some termite secretions. In Moyale district termite mounds are viewed as equivalent to bush encroachment. Some termite species are reported to damage the rangeland more than the others. In the study area the whitish grey termite with big abdomen causes more than the other kinds of termites. This species feeds more on grasses and thereby damage the rangeland. The reported information is in line with study conducted in Ghana by Akutse et al. (2012).

Causes of termite expansion

The cause of termite expansion in the study area is diverse and complex. According to the key- informants, it is directly related to the shortage of rainfall, recurrent drought, ecological change, and increased settlement. Termites prefer long dry seasons accompanied by shortage of rainfall for their reproduction. Big showers wash away the routs and feeding holes of the mound-less termites. Therefore, their damage and reproduction is reduced sharply during the rainy season. Mound-less termites take the advantages of camel population growth in the Borana rangelands. They use camel dung as reproduction ground to quickly reproduce and expand in the grass lands. Also, mound-less termites use some bush species (*acacia melifera* and to some extent *acacia drepanolobium*) as host for their reproduction. Pastoralists stress about the expansion of termites that the ecological change is responsible particularly after the ban of traditional rangeland management. Termites' mounds are more serious on red soils than on whitish (Calcic) soils. No termite mound is observed on the black soils (Vertisols) in the study area. This could be due to the compacted nature of the soils and the soil temperature which is cold during the night time. Increased human and livestock population accompanied by ban of traditional rangeland management (that is, ban of prescribed burning), overgrazing, and restriction of livestock mobility due to rangeland shrinkage and conflict have contributed to rangeland degradation and intensification of the termite problems in Borana lowlands. The damages caused by termites have forced pastoralists to abandon their pasture and thus create a threat for livestock production. Termite damages are serious where the ecosystems have been much disturbed as is currently still observed in pastoral areas in Dire, Miyo and Moyale districts. Our findings confirmed the previous reports by Grace and Yamamoto (2009) who concluded that termites are capable of ingesting and utilizing virtually all of the cellulose in the

Table 1. List of species of fodder and of trees and shrubs most affected in the area of study and those deemed to be resistant.

Susceptible /most affected fodder	
Scientific name	Local name
<i>Cenchrus ciliaris</i>	Matagudessa
<i>Plectranthus cosmosus</i>	Barbaarersa
<i>Bidens hilderrandi</i>	Abune
<i>Digitaria milanjana</i>	Hiddoo
<i>Themedatriandra</i>	Gaaguroo
<i>Cynodon dactylon</i>	Sardoo/qarcaa
<i>Bothriochloa insculpta</i>	Luucolee
Susceptible /most affected trees and shrubs	
Scientific name	Local name
<i>Combretum molle</i>	Rukeessaa
<i>Acacia bussei</i>	Halloo
<i>Commiphora</i> spp.	Hameessaa
<i>Commiphora kua vollensen</i>	Calanqaa
<i>Dodonea angastifoli</i>	Dhitacha
<i>Ehretia cymosa</i>	ulaagaa
<i>Acacia nilotica</i>	Burquqgee
Resistant tree/shrubs	
Scientific name	Local name
<i>Olea europaea</i>	Ejersaa
<i>Grewia bicolor</i>	Haroressa
<i>Boscia mossambicensis</i>	Qalqalchaa
<i>Croton macrostachyus</i>	Makkanisaa
<i>Juniperus procera</i>	Hindheensaa
<i>Cordia gharaf</i>	Madheeraa
<i>Acacia tortilis</i>	Dhadachaa

wood upon which they feed, and therefore seriously disturb the ecosystem.

Trend analysis

Participatory rural appraisal was conducted to study the trend of termite expansion in the past 50 years in the study area. It was found that the expansion of termite has been increasing linearly. It has been said by the Borana key informants that in each Gada system, the existence of termite increases sharply. Termite mounds appeared in the Borana land in the mid-1960s in sparse manner. Then after, the expansion progressed linearly and eventually, nowadays, has covered most of the rangeland in the study area. The mound-less termites species, which are relatively new to the study area, are the most serious types in destroying everything of the rangelands. If the termite invasion continues, it would be hard to find productive rangeland in the coming few decades in or

around the study area. Pastoralists were asked about the termite situation in the past 20 years and responded that it was good in terms of its expansion. However, these days the situation seems worse; termites have invaded much of the rangelands. According to the key informants, the situation of invading termites continuously increases and most of their lands will likely be taken by termites in the study area. This will end up with the collapse of the total production systems. Pastoralists expect that in the coming 20 years, termites may forage human beings due to the extent of its abundance.

Seasonal occurrence of termites

Mound-less termites prefer the *Adoolleessa* (cool dry season) and the onset of rain at the end of dry season (*Bona-Hagayyaa*). After the first rain showers, mound-less termites invade the ground immediately. Long showers wash the roots and feeding holes of termites

thereby eliminating them from the ground.

Livestock production constraints and termite expansion

Pastoralism is under stress due to constraints in the study area. These include shortage of adequate rains, bush encroachment, conflict, recurrent droughts, livestock diseases, cultivation of valley bottoms and termite invasion. Termite invasion is a new phenomenon, which becomes a threat to rangeland management. The mound-less termites which are of two types in the study region destroy grasses and other useful rangeland resources. Termites have infested grazing areas in the study sites during the dry season as well as wet season. Fall-back sites including Melbana, Golbo, Wayama, and Borbor are under severe termite infestation.

Distribution of termites and species composition

Termites are abundant and widely distributed throughout the study area and pose a threat to crops, rangeland and domestic houses in the study area. The termite fauna of Ethiopia is not well known. At present 62 species belonging to 25 genera and four families have been recorded and 10 of the species are endemic (Cowie et al., 1990). Among termite species recorded by Cowie et al. (1990), about 25% of these species are pests of agricultural crops, forestry, seedlings and grazing lands. The four families that contain the pest species are *Kalotermitidae*, *Hodotermitidae*, *Rhinotermitidae*, and *Termitidae* (Amsalu, 2009). Most species *Macrotermes*, *Odontotermes*, *Pseudacanthotermes*, *Ansistrotermes*, and *Microtermes* are found throughout the savannah and wooded steppe of tropical Africa (Homann, 2008). It is expected that most of the above-mentioned species are found in the study area where the vegetation is characterized by acacia-dominated savannah grass land. Pastoralists of the study area classify termites in three groups based on color, size and shape. Locally termites are classified into two types which are mound-less and mound-forming ones. The mound-forming ones are red and big-headed termites.

Association of termites with environmental factors

More than 98% of the respondents agreed upon that there were no termite resistance fodder species introduced. But 88% reported that there was no relation between termite invasion and livestock disease. However, around Dugda dawa district some of them indicate that a host for certain diseases like Awarsa (snake disease), or 'luxa' (body weight loss), which come from shortage of feed. Physical destruction and snake disease are among the other

problems induced by mound-building termites and mound-less termites. Among major problems which are induced by termites some respondents indicated in rank order from first to fourth as follows: 1) crop damage (before and after harvesting), 2) impact on buildings, 3) reduced feed sources (in terms of space occupied by mound, eating grasses and land degradation) and 4) physical damages on livestock and children.

More than 70% of the respondents agreed that termites have impact on coping strategies of drought by destroying conserved feeds. Mounds did not have mineral lick in Borana rangelands. Instead according to 65% of the interviewed community respondents, locally mounds give a benefit to construct houses and "naniga" which are water canals for livestock watering at water points throughout the rangeland.

Environmental relationship of termites

More than 55% of the respondents indicate that there was no impact due to bush encroachment on termite infestation and spread; and about 40% of the respondents justified that due to the fact that the bush serves as a feed source for termites. In relation with the effect of bush clearing on termite infestation, more than 60% of the respondents elaborated that it has an effect in the way that disturbance reduces termite spread, and the bush serves termites as feed source; as well as there was no indication of the ban on rangeland burning as a cause of termite infestation. Cultivation reduces mound building by physical destruction and flooding according to half of the participants responses. The severity of damage and infestation of termite is higher in flat lands than of hilly and valley bottoms. The season for termites to spread on new or uninfested areas is greater in long rainy seasons and cool dry seasons. Furthermore, "wayama" red deep soil is the soil type where termite infestation and damage is severe. Cool dry season is the favorable condition for termite damage pronounced on grass, building and crops than the other season. Mound building takes place also in the cool dry season, than short rainy season. 45% of the respondents agree that drought and the presence of termites are related.

Traditional termite management, research, policy and extension

Currently, 100% of the interviewed pastoralists said that they have no traditional as well as modern termite management techniques. According to the informants, after the ban of traditional prescribed burning techniques, termite infestation has become serious in the study area. There are termite predators in the study area, including ant species, different bird species and poultry. However, the reality is that the predators are worthless in termite

control. This agrees with the findings of Sekamatte and Okwako (2007) that, Ugandan elders linked the increasing termite problem and low abundance of predatory ant species to aerial sprays intended to control tsetse flies (*Glossina* sp.) during the 1960s and 1970s.

Resistant fodder species in the study area

The only plant species that is resistant to termite species in the study area is locally called *Annannoo* or *Kinchib*. This plant is foraged by camel and it is drought tolerant.

CONCLUSION AND RECOMMENDATIONS

Borana rangeland has been under stress starting from the past few decades. Termite intensification in this area has been increasing from time-to-time. Even if termites are believed to be ecological engineers, the destruction of crop and fodder needs to be minimized at an optimum level. This has to be considered and to enhance the indigenous people's knowledge of termite control mechanisms which include organic methods that must be used. Introduction of termite-resistant fodder species to the region is mandatory. The rate of termite intensification must be quantified using remote sensing techniques. The fertility status of termite mound needs to be assessed in further studies for the area.

The termite invasion poses a great problem for pastoral livelihoods in the study area. Therefore, the following socioeconomic and policy considerations should be practiced.

Increase livestock off take

The study area has a high number of livestock, though the rangeland has been shrinking both in quality and quantity; yet the number of livestock population is increasing over time. This has resulted in overgrazing, intensification of termite problems and finally rangeland degradation and land abandonment. Livestock off take should be increased to relieve pressure on the rangelands in the study area of Dire, Moyale and Miyo districts.

Reduce human population

Pastoral communities have been increasing significantly in the past decades. This has resulted in denser settlement, limited livestock mobility, and competition for individualizing the commons, and settlement in wet as well as dry season grazing sites. The combined effects of these situations have created ecological imbalances and caused the problem of rangeland deterioration and

aggravated termite problems. Therefore, population control policy and strategy should be practiced in the study area by direction of the government as well as the consensus of concerned stakeholders in the region.

Community participation

To tackle termite problems there is a need to develop participatory community based approaches to matters of rangeland management. The need for pastoralists' education on this aspect needs to be addressed with emphasis. Overall, a more vigorous research and development agenda should focus on community interests in relation to the issue of termites. Appropriate policy on environmental issues is essential to sustainability of the system.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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Full Length Research Paper

Diversity, distribution and habitat association of birds in Menze-Guassa Community Conservation Area, Central Ethiopia

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A study was conducted in Menz-Guassa Community Conservation Area (MGCCA) from November 2016 to March 2017, to assess the diversity, distribution and habitat association of birds. Three habitat types including forest, grassland, and moorland habitats were identified based on their vegetation composition. Point count method in *Eucalyptus* and *Juniperus* forest, and line transect technique in grassland and moorland habitats were used to study avian diversity. Data were collected in the early morning (6:30 to 9:30 a.m.) and late afternoon (4:30 to 7:00 p.m.) when the activities of birds were prominent. Species diversity and evenness was given in terms of Shannon-Weaver diversity Index. A total of 86 avian species belonging to 14 orders and 35 families were identified. The identified areas are rich with seven (8.14%) endemic bird species namely; abyssinian catbird (*Parophasma galinieri*), abyssinian longclaw (*Macronyx flavicollis*), ankober serin (*Crithagra ankoberensis*), black-headed siskin (*Serinus nigriceps*), blue-winged goose (*Cyanochen cyanoptera*), moorland francolin (*Scleroptilia psilolaema*), spot-breasted plover (*Vanellus melanocephalus*), and five (5.81%) near-endemic bird species including rouget's rail (*Rougetius rougetii*), wattled ibis (*Bostrychia carunculata*), white-collared pigeon (*Columba albitorques*), thick-billed raven (*Corvus crassirostris*), and white-winged cliff chat (*Myrmecocichla semirufa*). Avian diversity was high in moorland ($H'=4.57$) and low in grassland ($H'=3.42$) habitats. The highest even distribution of birds was recorded in the forest habitats and the lowest in grassland habitats with $E=0.75$ and $E=0.59$ values respectively. Families Accipitridae, Apodidae, Columbidae, Corvidae, Fringillidae, Motacillidae, Muscicapidae and Turdidae were commonly distributed in all habitats, however the highest number of avian family was encountered in Moorland (15 families) and lowest (9 families) in Forest habitats. The area supported variety of avian species with high endemics and habitat specific. Conservation of the area is vital for habitat restricted and endemic birds. Further ecological investigation is suggested in the seasonal abundance of birds, and population dynamics of wildlife for biodiversity conservation and ecotourism.

Key words: Afro-alpine, community conservation area, diversity, habitat association, Guassa.

INTRODUCTION

Ethiopia is one of the richest and incredible ornithological destinations in Africa with more than 926 bird species identified so far (Yalden, 1983). The astonishing avian

richness can be attributed to its rich and diverse climatic zones, topography, and habitats. Thus, the various lush and green forests, woodlands, moist and arid savannah,

lakes, rugged terrain and wetlands are home of Ethiopian birds (Urban and Brown, 1971).

Birds are considered as the most easily recognized categories of vertebrate animals. Among the key characteristic categories of such birds that allow their easy recognition include:

- (1) The presence of feathers which are unique to them,
- (2) The development of forelimbs as wings used mostly for flight;
- (3) Feathered tail for balancing, steering and lifting;
- (4) Toothless horny beak and skeleton exhibiting unique adaptations, mainly for flight and bipedal locomotion (Wallace, 1955; Padian and Chiappe, 1998).

Worldwide, there are about 10,000 known avian species and they are considered as part of the global ecosystem. They are known as good indicators of habitats quality and environmental degradation (Jarvis, 1993). Since they serve as good indicators to monitor environmental changes like the level of contamination and environmental impacts as a result the conservation of such bird species could contribute to ensure the survival of their environment and the conservation of a correspondingly large number of other taxa (Stattersfield et al., 1998).

Patterns of abundance and distribution of birds are strongly related to environmental factors. According to Pomeroy (1992), the areas with non-uniform topography and variable climatic conditions tend to support more species than uniform ones. On the contrary, small geographical range tends to be associated with habitat specialization (Reif et al., 2010). As a result, the diversity of avifauna represents one of the most important ecological indicators to evaluate the quality of habitats. Although avifaunal diversity has been decreasing due to the destruction of natural habitats and human disturbances (Bhadja and Vaghela, 2013) while area occupancy by bird species in disturbed or strongly seasonal habitat types tend to be larger. Factors affecting bird species distribution include bird body size and birds' abundance. According to Allen (1961), large species in size usually occur at lower densities than small bird species. The power of flight allows them to move easily allowing them to adapt perfectly to every environment, conditions for successful reproduction and birds survival (Estrella, 2007).

Protected areas, known as specific and unique natural habitats, are essential for biodiversity conservation because they often provide habitats protection and conservation from hunting, especially for threatened and endangered species. However, such conservation areas

represent only a small proportion of the total land mass and only a few of the diverse ecosystems available in eastern Africa. This is the case of Afroalpine habitat in eastern Africa. Afroalpine areas are found at altitudes over 3,200 m above sea level in Africa and they consist of grasslands, shrub lands and moorlands. In Ethiopia for example, only 2% of the total land area belongs to Afroalpine habitat type but covers 80% of land above 3,000m sea level in the Afrotropical realm (Ashenafi et al., 2012).

Menz-Guassa Community Conservation Area (MGCCA) is one of Ethiopian highlands' most pristine and sheltered natural (Ashenafi et al., 2012). The area is known as a home to important Afroalpine biodiversity including endemic and rare species (Biniyam and Tefera, 2011). The vegetation composition of the Guassa area is characterized by high altitude Afro-alpine vegetation with different habitat types which consist of three groups of bird species; namely, globally threatened species, biome-restricted assemblage and congregations of populations, as such the area is listed as important bird areas of Ethiopia (EWNHS, 1996).

The area is also part of the Conservation International's Ethiopian Highland Biodiversity Hotspot and an Endemic Bird Area (EWNHS, 1996). Thus, the present study was designed to investigate the diversity, distribution and habitat association of Birds in Menze-Guassa community conservation area.

MATERIALS AND METHODS

Description of the study area

The study was conducted in the Menz-Guassa Community Conservation Area (MGCCA) of Menz-Gera Midir Woreda, North Shewa Zone, Amhara National Regional State. It is located in the central highlands of Ethiopia at about 20km from Mehal Meda, the capital of Menz Gera-Midir district (Biniyam Admassu and Ashenafi et al., 2012). The area lies between 10° 15' to 10° 27'N latitudes and 39° 45' to 39° 49'E longitudes. The total area is estimated to be 100Km². Its altitude ranges from 3,200 to 3,700 masl (Admassu and Tefera, 2011). The area forms part of the high-altitude plateau of the central Ethiopian highlands at the edge of the Rift Valley escarpment, and comprises hills and valleys interspersed with swamps and open areas of Afro-montane and Alpine grassland (Ashenafi et al., 2012) (Figures 1 and 2).

Materials

The materials used during the study period includes binoculars, Global Positioning System (GARMIN, tRex-30), digital camera, field guide books, data sheets and notebooks.

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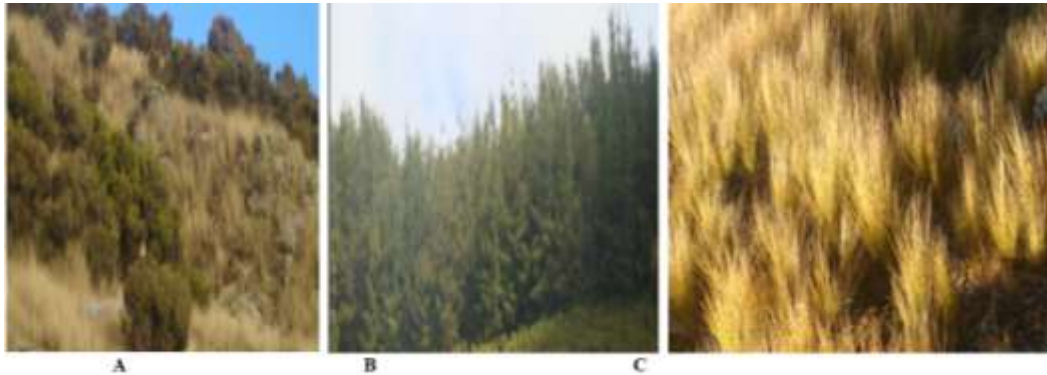


Figure 1. Habitat types of the study area; A= Moorland, B= Plantation, C= Festuca grassland. Source: Aynalem (2016).

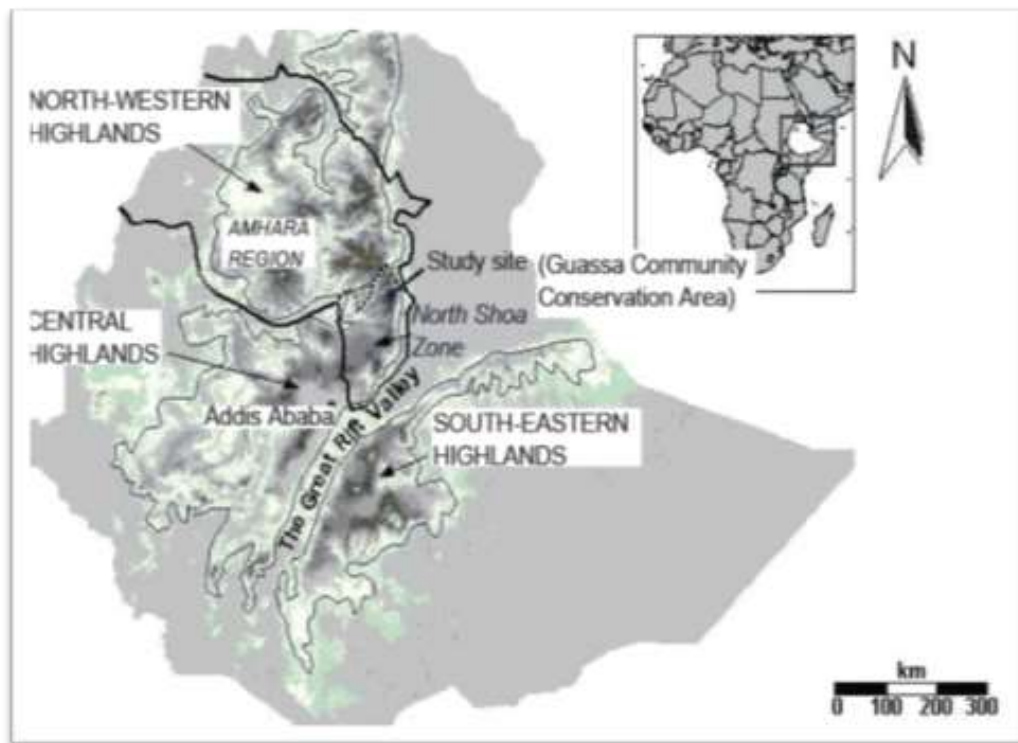


Figure 2. Topographic map of the study area (Source: Zelalem Tefera et al., 2012).

Preliminary survey

Ecological survey, focusing on avian species, was carried out during the month of December 2016 to assess parameters such as: habitat types and distribution, topographic features and vegetation area cover.

Sampling design

Ecological investigation based on ornithological survey and habitat assessment were all undertaken to study the avian diversity, especially the avian species coupled with their activities, and

habitats distribution. Random sample sites were selected based on the bird type of habitats mostly. A stratified random sampling was used to select sample units represented by each habitat type. In order for the ecological survey to be represented, at least 20 to 25% of the study area was covered in each sample site or location (Bibby et al., 1992). The identified sample site consists of blocks that were laid down randomly around selected habitats in the study area, and on a basis of random numbers (Sutherland, 1996).

Data collection

Three habitat types; forest, moorland and grassland areas were

identified and avian species observed in each of the selected habitats were recorded. For each of the selected habitat, line transects were used for open grassland habitats only while points count techniques were used for collecting data in both dense forest and moorland habitats. Data were collected from 6:30 to 9:30 a.m. and 4:30 to 7:00 p.m when the activities of birds were prominent. During such range time, birds observed in each observation point were recorded on 500 meters on either sides of the transect. To minimize disturbance, a waiting period of 3 to 5 minutes were applied prior to counting (Bibby et al., 1992). For identification of species in the field, plumage pattern, size, shape, color, songs and calls were used as key parameters (Bekele and Aynalem, 2009). However, in case of poor identification of species in the field, samples of birds' plumage pattern, size, shape, color, songs and calls were taken into the laboratory for future identification. Thus, the avian species were identified and their taxonomic groups were categorized based on field guide books (Pol, 2001; Redman et al., 2011).

Data analysis

Avian species diversity and evenness of the area were analyzed in terms of Shannon-Weaver diversity Index and Evenness (Shannon and Wiener, 1949). Shannon-Weaver diversity Index is calculated as follows:

$H' = -\sum (P_i \cdot \ln P_i)$ where:

H' = Shannon-Weaver Diversity Index

P_i = Fraction of the entire population made up of species i

\ln = Natural logarithm

\sum = Sum from species 1 to species S

The species evenness was evaluated using Shannon-Wiener evenness Index (E) as:

$E = H' / H_{max}$ where:

E = Shannon-Wiener Evenness Index

H' = Shannon-Wiener Diversity Index

$H_{max} = \ln S =$ natural logarithm of the total number of species (S) in each habitat.

RESULTS

Avian species composition and diversity

A total of 86 species of birds were identified. The identified bird species were grouped into 14 orders and they belong to 35 families. Family Accipitridae (13.09%) had the highest number of species followed by Fringillidae (9.52) and Motacillidae families (8.33%). The lowest number of family species accounts for 1.19% and it belongs to the following species: Alaudidae, Bucerotidae, Charadriidae, Cisticolidae, Coliidae, Cuculidae, Hirundinidae, Indicatoridae, Laniidae, Malaconotidae, Nectariniidae, Oriolidae, Psittacidae, Pycnonotidae, Rallidae, Scopidae and Zosteropidae with one representative species each (Table 1).

Regarding the bird species protection status, the

results of table 1 showed that out of the observed bird species, seven (8.14%) were endemic and five (5.81%) were near-endemic to the county. In the study area, the endemic bird species were mostly Abyssinian catbird (*Parophasma galinieri*), Abyssinian long claw (*Macronyx flavicollis*), Ankober serin (*Crithagra ankoberensis*), Black-headed siskin (*Serinus nigriceps*), Blue-winged goose (*Cyanochen cyanoptera*), Moorland francolin (*Scleroptilia psilolaema*), and Spot-breasted plover (*Vanellus melanocephalus*). On the contrary, the near endemic bird species include, Rouget's rail (*Rougetius rougetii*), Wattled ibis (*Bostrychia carunculata*), White-collared pigeon (*Columba albitorques*), Thick-billed raven (*Corvus crassirostris*), and White-winged cliff chat (*Myrmecocichla semirufa*) (Table 1).

Besides, the endemic and the near endemic species of the bird species, 26 (30.23%) recorded birds belong to restricted highland biome while only 6 (6.97%) of them belong to both the endemic and restricted highland biome.

Overall and specific diversity and evenness of bird species in Menz-Guassa community conservation area

The highest and lowest diversity of birds were recorded in the moorland ($H' = 4.57$) and grassland habitats ($H' = 3.42$). On the contrary, the relatively even distribution of birds was high in forest ($E = 0.75$) and low in grassland habitats ($E = 0.59$) (Table 2).

Overall and specific distribution of avian species in the Menz-Guassa community conservation area

The distribution of avian family showed variation among habitats. Highest number of bird families were recorded in moorland (15 families) and lowest number of families were recorded in forest habitats (9 families) (Table 3). In all habitats, the families of the following bird species Accipitridae, Apodidae, Columbidae, Corvidae, Fringillidae, Motacillidae, Muscicapidae and Turdidae were the most abundant and they were commonly distributed.

DISCUSSION

Avian species composition and diversity in the Guassa-Menze community conservation area

Guassa-Menze Community Conservation Area supports a variety of avian species and it consists of high diversity and abundance of endemics and highland biome restricted bird species. The diversity in habitat characteristics of the Afro-montane area coupled with

Table 1. Avian species composition and diversity in Menz-Guassa community conservation area.

Common name	Scientific name	Order	Family
Abyssinian Catbird	<i>Parophasma galinieri</i>	Passeriformes	Sylviidae
Abyssinian Ground Thrush	<i>Zoother piaggie</i>	Passeriformes	Turdidae
Abyssinian Longclaw	<i>Macronyx flavicollis</i>	Passeriformes	Motacillidae
Abyssinian Oriole	<i>Oriolus larvatus</i>	Passeriformes	Oriolidae
African Citril	<i>Crithagra citrinelloides</i>	Passeriformes	Fringillidae
African Dusky Flycatcher	<i>Muscicapa adusta</i>	Passeriformes	Muscicapidae
African Hobby	<i>Gypohierax angolensis</i>	Accipitriformes	Accipitridae
African stone Chat	<i>Saxicola torquatus</i>	Passeriformes	Muscicapidae
Ankober Serin	<i>Crithagra ankoberensis</i>	Passeriformes	Fringillidae
Augur Buzard	<i>Buteo augur</i>	Accipitriformes	Accipitridae
Baglafaecht Weaver	<i>Loceus baglafaecht</i>	Passeriformes	Ploceidae
Black Kite	<i>Milvus migrans</i>	Accipitriformes	Accipitridae
Barbary Falcon	<i>Falco peregrines</i>	Falconiformes	Falconidae
Black-headed Siskin	<i>Serinus nigriceps</i>	Passeriformes	Fringillidae
Black Kite	<i>Milvus migrans</i>	Accipitriformes	Accipitridae
Black-winged Lovebird	<i>Agapornis taranta</i>	Psittaciformes	Psittacidae
Blue-winged Goose	<i>Cyanochen cyanoptera</i>	Anseriformes	Anatidae
Booted Eagle	<i>Hieraaetus pennatus</i>	Accipitriformes	Accipitridae
Brown-rumped Seedeater	<i>Crithagra tristriata</i>	Passeriformes	Fringillidae
Brown Woodland-warbler	<i>Phylloscopus umbrovirens</i>	Passeriformes	Sylviidae
Cape crow	<i>Corvus capensis</i>	Passeriformes	Corvidae
Cattle Egret	<i>Bubulcus ibis</i>	Pelecaniformes	Ardeidae
Common Bulbul	<i>Pycnonotus barbatus</i>	Passeriformes	Pycnonotidae
Common Buzzard	<i>Buteo buteo</i>	Accipitriformes	Accipitridae
Common Fiscal	<i>Lanius collaris</i>	Passeriformes	Laniidae
Common Kestrel	<i>Falco tinnuculus</i>	Falconiformes	Falconidae
Dusky Turtle Dove	<i>Streptopelia lugens</i>	Columbiformes	Columbidae
Egyptian Goose	<i>Alopochen aegyptiaca</i>	Anseriformes	Anatidae
Erckel's Francolin	<i>Pternistis erckelii</i>	Passeriformes	Phasianidae
Ethiopian Boubou	<i>Laniarius aethiopicus</i>	Passeriformes	Malaconotidae
Fan-tailed Raven	<i>Corvus rhipidurus</i>	Passeriformes	Corvidae
Grassland Pipit	<i>Anthus spragueii</i>	Passeriformes	Motacillidae
Great Sparrowhawk	<i>Accipiter nisus</i>	Accipitriformes	Accipitridae
Grey Wagtail	<i>Motacilla cinerea</i>	Passeriformes	Motacillidae
Ground scraper Thrush	<i>Psophocichla litsitsirupa</i>	Passeriformes	Turdidae
Hadada Ibis	<i>Bostrychia hagedash</i>	Pelecaniformes	Threskiornithidae
Hamerkop	<i>Scopus umbretta</i>	Pelecaniformes	Scopidae
Hooded Vulture	<i>Necrosyrtes monachus</i>	Accipitriformes	Accipitridae
House Finch	<i>Haemorhous mexicanus</i>	Passeriformes	Fringillidae
Lammergeier	<i>Gypaetus barbatus</i>	Accipitriformes	Accipitridae
Lanner Falcon	<i>Falco biarmicus</i>	Falconiformes	Falconidae
Lesser Kestrel	<i>Falco naumanni</i>	Falconiformes	Falconidae
Little Egret	<i>Egretta garzetta</i>	Pelecaniformes	Ardeidae
Little Swift	<i>Apus affinis</i>	Caprimulgiformes	Apodidae
Long-billed Pipit	<i>Anthus similis</i>	Passeriformes	Motacillidae
Montane White-eye	<i>Zosterops poliogastrus</i>	Passeriformes	Zosteropidae
Moorland Chat	<i>Cercomela sordid</i>	Passeriformes	Muscicapidae
Moorland Franolin	<i>Scleroptila psilolaema</i>	Passeriformes	Phasianidae
Nyanza Swift	<i>Apus niansae</i>	Caprimulgiformes	Apodidae
Pied crow	<i>Corvus albus</i>	Passeriformes	Corvidae
Red-billed Firefinch	<i>Lagonosticta senegala</i>	Passeriformes	Estrilidae

Table 1. Contd.

Red-cheeked Corden-bleu	<i>Uraeginthus bengalus</i>	Passeriformes	Estrildidae
Red-collared Widowbird	<i>Euplectes ardens</i>	Passeriformes	Ploceidae
Red-throated Pipit	<i>Anthus cervinus</i>	Passeriformes	Motacillidae
Rock Martin	<i>Ptyonoprogne obsoleta</i>	Passeriformes	Hirundinidae
Rouget's Rail♠▶	<i>Rougetius rougetii</i>	Gruiformes	Rallidae
Ruppell's Robin Chat▶	<i>Cossypha semirufa</i>	Passeriformes	Muscicapidae
Sacred Ibis	<i>Threskiornis aethiopicus</i>	Pelecaniformes	Threskiornithidae
Shikra	<i>Accipiter badius</i>	Accipitriformes	Accipitridae
Silvery-cheeked Hornbill	<i>Bycanistes brevis</i>	Bucerotiformes	Bucerotidae
Speckled Pigeon	<i>Columba guinea</i>	Columbiformes	Columbidae
Slender-billed Starling▶	<i>Onychognathus tenuirostris</i>	Passeriformes	Sturnidae
Speckled Mouthbird	<i>Colius striatus</i>	Coliiformes	Coliidae
Spot-breasted Plover□▶	<i>Vanellus melanocephalus</i>	Charadriiformes	Charadriidae
Streaky Seedeater▶	<i>Serinus striolatus</i>	Passeriformes	Fringillidae
Stripe-breasted Seedeater	<i>Crithagra striatipectus</i>	Passeriformes	Fringillidae
Swainson's Sparrow	<i>Passer swainsonii</i>	Passeriformes	Passeridae
Tacazze Sunbird▶	<i>Nectarinia tacazze</i>	Passeriformes	Nectariniidae
Tawny-flanked Prinia	<i>Prinia subflava</i>	Passeriformes	Cisticolidae
Thekla Lark	<i>Galerida theklae</i>	Passeriformes	Alaudidae
Thick-billed Raven♠▶	<i>Corvus crassirostris</i>	Passeriformes	Corvidae
Tree Pipit	<i>Anthus trivialis</i>	Passeriformes	Motacillidae
Verreaux's eagle	<i>Aquila verreauxii</i>	Accipitriformes	Accipitridae
Wahlberg's Honey bird	<i>Prodotiscus regulus</i>	Piciformes	Indicatoridae
Wattled Ibis♠▶	<i>Bostrychia carunculata</i>	Pelecaniformes	Threskiornithidae
White-backed Vulture	<i>Gyps rueppellii</i>	Accipitriformes	Accipitridae
White-billed Starling♠▶	<i>Onychognathus albirostris</i>	Passeriformes	Sturnidae
White-collared Pigeon♠▶	<i>Columba albitorques</i>	Columbiformes	Columbidae
White-winged Cliff Chat▶	<i>Monticola semirufus</i>	Passeriformes	Muscicapidae
Yellow-Billed Kite	<i>Milvus aegyptius</i>	Accipitriformes	Accipitridae
Yellow Bishop	<i>Euplectes capensis</i>	Passeriformes	Ploceidae
Yellow Wagtail♯	<i>Motacilla flava</i>	Passeriformes	Motacillidae
Yellow-billed Kit	<i>Milvus aegyptius</i>	Cuculiformes	Cuculidae
Yellow-crowned Bishop	<i>Euplectes afer</i>	Passeriformes	Ploceidae
Yellow-crowned Canary	<i>Serinus flavivertex</i>	Passeriformes	Fringillidae
Yellow-spotted Petronia	<i>Gymnoris pyrgita</i>	Passeriformes	Passeridae

NB: □= Endemic, ♠ = near endemic, ▶ Highland Biome bird species, ♯ = Migrant.

less human disturbance are certainly among the key reasons explaining the richness of bird species (including restricted-range bird species) in the conservation area.

According to MacArthur (1961), habitat disturbance and poor environmental quality tend to drive avian fauna decline or loss. On the contrary, the richness of the environment in adequate food supply can increase the abundance of avian species at a given area. However, in the case of this study, the diversity of avian species was distributed differently among habitats. The highest number of bird species was observed in the moorland and grassland habitats and the lowest was encountered in forest habitat. This is probably due to the diversity of

vegetation that provides heterogeneous habitats and the availability of food resources from which birds can feed into. In avian ecology, the relationship between habitat heterogeneity and bird species diversity is a well-documented patterns (Tews et al., 2004). Available literature tends to show that changes driving habitat disturbances (that is, forest stratification) influence the richness and avian diversity. In that regards, Asmare (2009) has reported that birds tend to be more diverse and abundant in lower stratum shrub communities (small plants and trees) than in complex forests (taller trees).

Similarly, a study by Mamo et al. (2016) carried out in Bale mountains National Park revealed that bird diversity

Table 2. Species diversity of birds by habitat types in Menze - Guassa community Conservation area.

Habitat types	Number of species	H'	Hmax.	Evenness (E)
Forest	23	3.53	4.77	0.75
Grassland	29	3.42	5.77	0.59
Moorland	34	4.57	6.25	0.73

Table 3. Overall distribution of birds by habitat types in the Menze-Guassa community conservation area.

Habitat type	Total no. of families	Percentage
Forest	9	25.71
Grassland	11	31.43
Moorland	15	42.485

and abundance significantly differed between habitat types but they were positively correlated with shrub and grass height. Menze-Guassa Community Conservation Area is a raptor-watcher's paradise where Augur Buzzard (*Buteo augur*) and Bearded Vulture (*Gypaetus barbatus*) are common and frequent. Admassu and Tefera (2011) noted that Guassa-Menze plateau is an ideal place to observe Augur Buzzard than anywhere else in the country.

Avian species habitat preferences in Guassa-Menze community conservation area

Similarly, among habitats, the number of avian species was the highest in moorland and grassland habitats than in forest habitat. The results of field observations tend to showed the highest number of different seeds producing shrubs and grasses in moorland and grassland habitats than in forest habitat. It can be pointed out that the presence of seeds producing shrubs might drive the abundance of avian species in moorland and grassland habitats than in forests. Habitat heterogeneity is a measure of the diversity and evenness of variation in land cover. However, habitat diversity is dependent, in part, on the scale of observation and the corresponding landscape scale.

Avian species distribution in Guassa-Menze community conservation area

The distribution of avian families showed variation among habitats. The highest numbers of bird families was observed in moorland and grassland habitats while the least number of families was in the forest habitat due certainty in the richness, the complexity of the vegetation

and the floristic composition of its habitats in those habitats. Tellaria (1992) pointed out that habitat structure tend to affect the distribution of individual avian species. Similarly, habitat size, foraging modes and floristic composition are also among the other driving factors that tend also to influence the distribution of birds species (Manley et al., 2006). Menz-Guassa Conservation Area is known as a conservation area of high Endemism and restricted-range bird species that are commonly associated with Afro-Alpine ecosystems while serving as a wintering ground for many palearctic migrant birds. Therefore, there is need to reinforce measure for protection of the area that will likely contribute to safeguard bird specific habitats while acting as an ideal place for avian species watching in the highlands of Ethiopia since it supported variety of avian species with high endemics and habitat specific bird species.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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