Diversity of phytopathogenic polypores and their interaction with host plants in three biotopes in western Burkina Faso

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Abstract

In order to provide data on polypore identification and their taxonomy, survey studies were undertaken in tree biotope of polypore occurrence. The main objective of this study was to provide a scientific database on the diversity of phytopathogenic polypore and interactions with the host plants in their biotope. Transects of 1 km length covering a width of 50 m were selected at each site. Basidiomes were collected along the transects from roots, trunks and/or branches of forest species Sixty-three species of polypore were identified on twenty-three species of host plants belonging to eleven families. The families most prone to polypore infection were Fabaceae, Apocynaceae, Combretaceae, Anacardiaceae and Caesalpiniaceae. These phytopathogenic polypore were annual to perennial. They grow on roots, trunks and branches of trees and shrubs causing crown and root rots, and trunk cankers on the host plants. The genus *Phellinus* was the most represented in the agrosystems and in the classified forest of Kou. Similarly, the terricolous species represented by the genera *Ganoderma, Amauroderma* and *Laetiporus* were found mainly in the classified forest of Niangoloko and gallery forests of Dan.

Keywords: Diversity, Burkina Faso, *Phellinus,* Phytopathogenic polypores.

Introduction

Polypores are one of the most important groups of fungi in the world because they provide a vital function in the decomposition of dead wood, recycling of carbonaceous material, and interactions with plants (Tedersoo *et al.,* 2007). However, forest ecosystems represent the most diverse environments in terms of fungal species due to the several type of vegetation. In fact, each vegetation has its own fungal suite that changes with age, stand health, and site management (Leite, 2008). A given ecosystem is characterized by its biological diversity, which is either due to its geographic location, land use pattern (Yombiyeni, 2014). In a context of climate change, knowledge of pathogenic polypore and their interactions with host plants is necessary for sustainable land management and specific ecological monitoring of forest resources. Indeed, polypore, whether pathogenic or saprotrophic, primarily colonize forest resources at the biotope level and are indicators of ecosystem health (Leite, 2008). Many studies have reported the negative impact of phytopathogenic polypores on plant health in forests and plantations (Pieperbring, 2015, Moussavou, 2021). In addition, they are the cause of wood decay (Moussavou, 2021), brown or white wood rot (Pieperbring, 2015). Some pathogenic polypore grows on tree trunks as a scab or on the ground on the roots of deciduous trees as a console (Peláez *et al.,* 1995; Worrall *et al.,* 1997). These phytopathogenic lignicolous fungi affect the physiology of the tree by attacking the cambium cells and can lead to the death of trees (Dobbertin *et al.,* 2001, Paolo *et al.,* 2002). Indeed, cause host plant responses that are characterized by the appearance or absence of symptoms (Boulet and Bussières, 2018). In Burkina Faso, very few studies have concerned the phytopathogenic polypore of forest resources. In addition, forest phytopathology remains embryonic, unlike that of cultivated plants. Health information on the interactions of phytopathogenic polypore on host plants is still scarce or non-existent. However, this information is important in a process of adaptation of forest species to the effects of climate change, characterized by a variation in rainfall and temperature at the ecological environment level. The main objective of this study was to contribute to the knowledge of the diversity of phytopathogenic polypore and their impact on host plants in Burkina Faso.

Materials and Methods

Study sites

The survey was carried out in the west of Burkina Faso included the region of Haut-bassins and Comoé. Data were collected in the village of Tin, forest gallery of Dan, classified forest of Kou (region of Haut-bassins) and in the classified forest of Niangoloko (region of Comoé).The classified forest of Kou (11°10'54" north latitude and 4°26'04" west longitude) covers 115 ha (Fig. 1). However, the Classified Forest of Niangoloko (latitude 10°17' N and longitude 4°58' W) covers 7295.83 ha. This forest is located between Niangoloko, Temperba and Yendéré. As for the Dan Forest gallery and the Tin village agrosystems are respectively in the Haut-bassins region (Fig. 1). All these sites belong to the South Sudanian phytogeographic sector, characterized by an annual average rainfall 900 to 1100 mm and a low thermal amplitude (20–25 °C). This phytogeographic sector is essentially dominated by wooded savannahs and clear forests with *Isoberlinia doka*, numerous gallery forests with vegetation consisting of Guinean species such as *Berlinia grandiflora* (Sambaré *et al.*, 2010). The forest formations are most often linked to the existence of watercourses. They develop as forest gallery vegetation and riparian strips (Ouédraogo, 2006). The most frequent soil types are vertisols, particularly developed in the south-east and center-west (Sourou valley), which have the same textural relationship as brown soils, but are much less drained (Sambare *et al.*, 2010). The hydrological network of the sites is quite dense and is located in the Comoé basin, which covers 17,000 km^2. It encompasses the sub-basin of the Léraba and Comoé rivers. Agriculture and breeding are the principal activities practice in the site.

Sampling

Stratified sampling method were using looking on biotope characterization (agrosystem, classified forest and forest gallery) as a strate. The survey and collection missions were conducted from July to September between 2018 and 2020. In the study site, 1 km long transects covering a width of 50 m were used in each biotope. Basidiomes were collected along the transects on the roots, trunks and/or branches of forest species using a knife or machete depending on their consistency. The opportunistic sampling approach described by Mueller *et al.* (2004) was used to collected polypore species and in evidence the host plant affected. This method, which took into account the random distribution of fruiting bodies and species, consisted of walking the various collection sites along a specific route (transects) to observe particular indicators, carefully collecting all phytopathogenic polypore encountered. Morphological characteristics of each plant pathogenic polypore encountered were noted before harvested. The sanitary state of each host plant, the height on the trunk where the polypore attaches and the type of decomposition stage of the substrate (trunks, roots) were also noted. Each polypore was carefully labeled, wrapped in aluminum foil and stored in a collection basket. A technical photograph of each sample was taken upon return from the field at the sample drying site. Global Positioning System (GPS) coordinates of each host plant species were recorded (Garming brand, 64S).

The morphological characters of the basidiomes in the fresh state were describing. It considered the growth habit and characteristics of the hymenophore (tubes and pores). This description was done according to the polypore description sheet of Yombiyeni (2014) which was simplified and adapted for the present research. The description of these characters allowed an initial discrimination between species. After this, sample were dried using an electric desiccator (Dorrex brand) for 24 h. Dried basidiomes were placed in sealed mini-grip bags and identified by using polypore identification keys (Ryvarden and Johannsen, 1980; Ryvarden, 2000; Dai, 2010). The identification of plant species from which phytopathogenic polypores were collected was done by using Arbonnier (2002). The exact nomenclatures of fungal species and woody species were made respectively through the Index fungorum (https://www.indexfungorum.org) and International Plant names Index (https://www.ipni.org) (https://www.actaplantarum.org) sites. The evaluation of the polypore-plant-host interaction and the biotopes was done through multiple correspondence analyses (MCA) (Tapsoba *et al.*, 2020). These analyses were done using R 4.1.2 (R core team, 2021).

Results

Diversity of phytopathogenic polypore and host plant species

The survey focusses on opportunist approach allowed collected and identified 120 sample of polypores in all the study site. Base on the morphological characterization, 63 species belonged to 14 genera, 3 families and 2 orders were identified (Table 1). Among the species, 35 were fully identified at the specific level and 28 at the genus level. The family Hymenochaetaceae is the most represented (84%) and the genus *Phellinus* has the highest number of species Phytopathogenic polypore were encountered on 22 woody plant species divided into 11 families (Table 1). The woody plant families most prone to polypore infection were the Fabaceae (*Acacia dudgeonii, Acacia nilotica, Acacia polyacantha, Delonix regia, Parkia biglobosa, Piliostigma thoningii*), Apocynaceae (*Baissea* *multiflora, Holarrhena floribunda, Saba senegalensis, Secamone afzellii, Strophantus sarmentosus*), Combretaceae (*Anogeissus leiocarpus, Combretum micranthum, Terminalia avicennioides*), Anacardiaceae (*Mangifera indica* and *Lannea microcarpa*) and Ceasalpiniaceae (*Berlinia grandifolia, Deutarium microcarpum*).

Affinity between phytopathogenic polypores and host plants

The phytopathogenic polypore had an affinity for three parts of the host plant on which they were harvested. Some polypores were developed preferentially on the roots, others on the trunk and on the branches. These polypores cause brown or white wood rots. Terricolous polypores of the genera *Ganoderma* and *Laetiporus* were encountered here on the roots or crown of *Elaeis guineensis* and *Annona senegalensis* respectively (Fig. 2 B & F). Also, the genera *Phylloporia, Inonotus* and *Phellinus* were respectively collected on the trunks of *Saba senegalensis, Parkia biglobosa* and *Anogeissus leiocarpus* (Fig. 2 D, J & L).

Phytopathogenic polypore and interaction with ecological parameters

Multiple correspondence analysis (MCA) showed a strong correlation for host plants, phytopathogenic polypores and height from ground to the three dimensions (Dim1, Dim2 and Dim3) (Table 2). In fact, all variables were correlated to Dim1, even if the two first Dim, explain 11% of variation (Fig. 3).

The MCA shows the behavior of polypores species according to the substrate in the different biotope. The majority of phytopathogenic polypore species from the Tin agrosystem and the remainder are dispersed between the classified forests and the Dan forest gallery (Table 3, Fig. 2). The behavior of polypores (host plant, height from ground, and type of rot) in the forest gallery (FG) is different from that of polypores in the agrosystems (AG) and classified forests (CF) (Fig. 3). In the FG, phytopathogenics polypore were found on the roots of trees and shrubs, which was not the case in AG and CF where they are located on the trunk and branches.

In the hierarchical classification of variables, four groups appear, two of them being homogeneous, consisting of cluster 1 and cluster 3, that are represented by 83.33% of AG polypores and 100% of CF polypores. Cluster 3 is represented by species of the Apocynaceae family (*B. multiflora, S. senegalensis, S. afzellii and S. strophantus*) and their procession of phytopathogenic polypores, the genus *Phylloporia*.

Discussion

Based on the results, this research on phytopathogenics polypores allowed us to identify 63 species in 3 biotopes (classified forests, forest gallery and agrosystem) in western Burkina Faso. These species belong to three fungi families: Hymenochaetaceae, Ganodermataceae and Laetiporaceae. The predominance of Hymenochaetaceae family could be explained by the climate, the woody species and type management of the site. Indeed, according to Lodge (1997), a large variety of woody resources (botanical diversity, substrate diversity) results in a large number of ecological niches for polypores. Similarly, authors such as Zhou *et al.* (2011) found that tropical and subtropical forest areas harbor the greatest diversity of polypores. In this study, Hymenochaetaceae were collected from the trunk and branches of trees and were responsible for white rot. Similar results were found in Central Africa in Congo and Gabon, respectively, by Balezi (2013) and Yombiyeni (2014). The above research showed that Hymenochaetaceae were infested with hard substrates (wood and living plants). In addition, Ganodermataceae and Laetiporaceae were collected from the roots or crowns of woody species. Thus, the distribution of polypore is thought to reflect the distribution of forest vegetation type (Vaisuanen *et al.*, 1992). Thus, forest vegetation type is one of the factors related to the occurrence of polypore communities in forests (Bujakiewicz, 1992; Perini *et al.*, 1993). According to Ryvarden (1998, 2000, 2004), the wide distribution of lignicolous fungi in the tropical world is due to its high plant diversity. In the Tin agrosystem, nearly half of the phytopathogenic polypores belong to the genera *Phellinus* and *Inonotus*. This could be explained by the presence of old tree stumps (*Parkia biglobosa* and *Mangifera indica*), with anthropization modifying environmental parameters leading to the appearance of lignicolous phytopathogenic polypores. This seems to corroborate the results of Lodge *et al.* (1995), who stated that the diversity of lignicolous decomposer fungi is largely due to habitat and substrate. In addition, according to Selosse *et al.* (2011), host plant was identified as a factor in fruiting body production, due to the need for certain nutrients to form sporophores in the forest. Thus, *Parkia biglobosa, Mangifera indica, Anogeissus leiocarpus* and *Acacia nilotica* would be sensitive and favorable hosts for the development of phytopathogenic polypores of the family Hymenochaetaceae. Regarding the woody species that constitute the hosts of phytopathogenic polypores, a diversity of 22 species in 11 families should be noted. The woody plant families most prone to infection by polypores are respectively Fabaceae with 7 host species, Apocynaceae with 5 species and Combretaceae with 3 species. *Parkia biglobosa, Mangifera indica, Anogeissus leiocarpus* recorded the highest number of polypores in terms of attack frequency, respectively. These woody species were the subject of the development of the genera *Phellinus, Inonotus, Ganoderma* and *Phellinopsis*.

This could be explained by the susceptibility of these woody species to polypore germplasm, by anthropogenic activities that cause wounds that provide a pathway for germplasm, but also by the climate, which is thought to be conducive to polypore establishment. Our results seem to corroborate those of Kiran *et al.* (2012) who showed in India that in a reduced range of *Phellinus* host species, the most frequently attacked host plant genera were *Mangifera*, *Acacia*, *Artocarpus* and *Albizzia*. Substrate specificity was noted for some polypore species. For example, *Amauroderma* spp. and *Phylloporia* spp. were specific to plants of the family Apocynaceae in the gallery forest as well as in the Kou forest. Similar results were obtained in Central Africa in Gabon who showed *Phylloporia* spp. to be parasitic on Melastomataceae and Rubiaceae, *Perenniporia gomezii* parasitic on Caesalpiniaceae, and *Fomitiporia gabonensis* parasitic on Caesalpiniaceae (Yombiyeni, 2014; Yombiyeni and Decock, 2017). In addition, Phylloporia beninensis has been identified on woody species in Benin Olou (2021). It should be noted that polypores often have a wide host range. For example, *Phellinopsis* cf. *pinicola* was also found on *Berlinia grandifolia*, *Piliostigma thoningii*, *Acacia dudgeoni* and *Acacia polyacantha*. This result corroborates that of Balezi (2013) who showed that *Inonotus pachyphloeus* and *Phellinus* cf. *calcitratus* species were parasites of live tree species such as *Bikinia* sp. (Caesalpiniaceae). *Phellinus noxius* has been previously recorded in tropical forest plantations and are known to cause rots (Glen *et al.*, 2009, 2014; Agustini *et al.*, 2014). In West Africa, *Phellinus noxius* species had previously been recorded on *Hevea brasiliensis*, *Tectonia grandis* and *Cedrela odorata* in plantations (Gohet *et al.*, 1991). It is important to note that most of the woody plants parasitized are old stumps; the same observation was made by Wilks and Issembe (2000) who concluded that the genera *Inonotus* and *Phellinus* were indicators of forest aging. Phytopathogenic polypores induced health problem in the agrosystems Tin village. This could be explained by the increased anthropization of the environment, favorable climatic conditions (rainfall) and the aging of woody species.

Conclusion

A total of 63 phytopathogenic species were identified and 84% of these species belong to the family Hymenochaetaceae. Most of the species were collected from living plants in forest ecosystems in the study site. We have noted a large morphological and ecological diversity of these polypores among Classified Forest, Gallery Forest and Agrosystem. In the Gallery Forest, phytopathogenics polypores dominated by the genera *Amauroderma* and *Laetiporus* were found on the ground on the roots of trees and shrubs but in the Agrosystem and Classified Forest these polypores dominated by the genera *Phellinus* and *Inonotus* were found on the trunk and branches Also, it appears that polypores were identified on 22 woody host plant species belonging to 11 families. *Parkia biglobosa*, *Mangifera indica*, *Anogeissus leiocarpus* and *Acacia nilotica* are the woody species most parasitized by polypores in western Burkina Faso. These polypores constitute a phytopathological problem to be taken into account for the preservation of biodiversity. More in-depth studies should be conducted to better characterize mycobiodiversity, especially that of polypores. Finally, the study of the pathogenicity of phytopathogenic polypores would be necessary for the implementation of polypore management methods in orchards as well as in forest formations in Burkina Faso.

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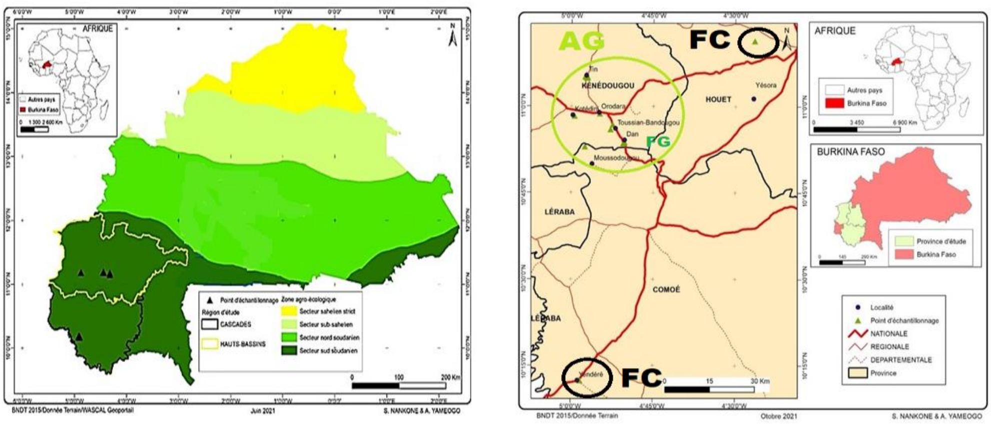

Fig. 1: Position of sampling points on the phytogeographic map of Burkina Faso (Nankoné and Yaméogo, 2021).

Table 1: Diversity of phytopathogenic polypores and their woody hosts.

No.	Hosts plants species	Phytopathogenics polypores	Family	Infected parts
1	*Acacia dudgeoni* Craib ex Holl. **(Fabaceae)**	*Fomitiporia* sp1 *Phellinopsis* cf. *pinicola* (Fr.) Karst. *Fomitiporia* sp2	Hymenochaetaceae	Trunks and branches
2	*Acacia polyacantha* Will subsp. **(Fabaceae)**	*Phellinopsis* sp1 *Phellinopsis* sp2		
3	*Anogeissus leiocarpus* (DC.) Guill. & Perr. **(Combretaceae)**	*Phellinus igniarius* (L., Fr.) Quél. *Phellinus* cf. *tuberculosus* (Baumg.) Niemela *Phellinus* cf. *hippophaecola* (Jahn)		
4	*Annona senegalensis* Pers. **(Annonaceae)**	*Laetiporus sulphureus (Pat.)* *Amauroderma* cf. *albostipitatum* (Gomes- Silva) Ryv. & Gibertoni *Amauroderma fasciculatum* (Pat.) Torr. & Brot. *Amauroderma* sp1 *Amauroderma* sp2 *Amauroderma* sp3	Laetiporaceae Ganodermataceae	Roots Trunks and branches
5	*Baissea multiflora* A. DC. **(Apocynaceae)**	*Phylloporia* cf. *fructica* (Berk. & Curt.) Ryv.	Hymenochaetaceae	Trunks and branches
6	*Berlinia grandiflora* (Vahl) Hutch. Dalz. **(Fabaceae)**	*Phellinopsis* cf. *pinicola* (Fr.) Karst.		
7	*Combretum micranthum* G. Don **(Combretaceae)**	*Phellinopsis* sp3		
8	*Delonix regia* (Bojer ex Hook) Raf. **(Fabaceae)**	*Inonotus* cf. *drayseus* (Pers., Fr.) Murr.		
9	*Elaeis guineensis* Jacq. **(Arecaceae)**	*Ganoderma* cf. *boninense* (Pat.) *Phaeolus* cf. *spadiceus* (Pers. Fr.) Rauschert	Ganodermataceae Laetiporaceae	Roots
10	*Ficus gnaphalocarpa* Steud. Ex Miq. **(Moraceae)**	*Phellinus* cf. *nigricans* (Fr.) P. Karst.	Hymenochaetaceae	Trunks and branches
11	*Holarrhena floribunda D. C.* **(Apocynaceae)**	*Amauroderma* cf. *albostipitatum* (Gomes- Silva) Ryv. & Gibertoni *Amauroderma* cf. *fasciculatum* (Pat.) Torr. & Brot.	Ganodermataceae	Roots
12	*Khaya senegalensis* (Desv.) A. Juss. **(Meliaceae)**	*Phellinus* cf. *ribis* (Schum., Fr.) Karst. *Laetiporus* cf. *baudonii (Pat.) Ryv.*	Hymenochaetaceae Laetiporaceae	Trunks and branches Roots
13	*Lannea microcarpa* Engl. & Krause. **(Anacardiaceae)**	*Laetiporus* sp.	Laetiporaceae	Roots
14	*Mangifera indica* L. **(Anacardiaceae)**	*Inonotus* sp1 *Inonotus* cf. *ochroporus* (Van der Byl.) Pegler *Inonotus pachyphloeus (*Pat.) T. Wag. & Fis) *Laetiporus* cf. *baudonii* (Pat.) Ryv.	Hymenochaetaceae	Trunks and branches Roots
15	*Oxytenanthera abyssinica* (A. Rich.) Munra **(Poaceae)**	*Hymenochaete* cf. *bambusicola* (S. H. He)	Hymenochaetaceae	Trunks and branches
16	*Parkia biglobosa* (Jacq.) Benth **(Fabaceae)**	*Inonotus triqueter* (Lenz) P. Karst. *Inonotus* cf. *leporinus* (Fr.) Gilb.& Ryv.)		Trunks and branches

		Inonotus sp2 *Inonotus* sp3 *Inonotus* sp4		
		Phellinidium cf. *pouzarii* (Kotl.) Fiasson & Niemela		
		Phellinus cf. *cryptarum (Quél.)* *Phellinus* cf. *hartigii* (Allesch & Schnabl.) Pat. *Phellinus* cf. *noxius* (Corner) G. Cunn. *Phellinus* cf. *pachyphloeus* (Pat.) Pat. *Phellinus* cf. *punctatus* (P. Karst.) Pilat. *Phellinus robustus* (Karst.) Bourd. & Galzin *Phellinus* cf. *tremulae* (Bond.) Bond & Borisev *Phellinus leavigatus* (P. Karst.) Bourd. & Galzin *Phellinus* sp1 *Phellinus* sp2 *Phellinus* sp3 *Phellinus* sp4 *Phellinus* sp5 *Phellinus* sp6 *Phellinus* sp7 *Phellinus* sp8 *Phellinus* sp9 *Phellinus* sp10		
		Inonotus cf. *triqueter* (Lenz) P. Karst. *Inonotus* cf. *leporinus* (Fr.) Gilb.& Ryv.) *Inonotus* sp1 *Inonotus* sp2 *Inonotus* sp3		Roots
		Ganoderma carnosum (Pat.)	Ganodermataceae	Trunks and branches
		Navisporus floccosus Ryvard.	Polyporaceae	
17	*Piliostigma thoningii* (Schumach.) Milne Redh. *(***Fabaceae***)*	*Phellinopsis* cf. *pinicola* (Fr.) Karst.	Hymenochaetaceae	
18	*Saba senegalensis* (A.DC.) Pichon. *(***Apocynacea***e)*	*Phylloporia* cf. *oblongospora* (Cui &Dai)		
19	*Secamone afzellii* (Schult.), K. Schum. *(***Apocynaceae)**	*Phylloporia* cf. *oblongospora* (Cui &Dai)		
20	*Strophantus sarmentosus* DC. *(***Apocynaceae***)*	*Phylloporia* cf. *hainaniana* (Cui &Dai)		
21	*Terminalia avicennioides* Guill. & Perr (**Combretaceae***)*	*Kusaghiporia* sp	Laetiporaceae	Roots
22	*Vitellaria paradoxa* C. F. Gaertn. F. **(Sapotaceae**)	*Phellinopsis* sp3 *Fomitiporia* sp2 *Fuscoporia* sp1 *Fuscoporia* sp2 *Fuscoporia* sp3 *Ganoderma* cf *enigmaticum* (Coet. Marinc. & Wingf.)	Hymenochaetaceae	Trunks and branches

Table 2: Correlation of variables in the MCA graphs.

Variables	Dim1	Dim2	Dim3
Height from ground	0.89	0.78	0.84
Roots	0.76	0.17	-
Type of rot	0.74	0.14	-
Branches	0.67	0.17	-
Polypores species	0.99	0.99	0.98
Trunk	0.59	0.21	0.07
Biotope	0.51	0.51	0.14
Host plant	0.68	0.92	0.92

Fig. 2: Some phytopathogenic polypores developing on the roots or trunk of trees in Burkina Faso. **A:** *Ganoderma* cf. *Enigmaticum* in contact with the crown of *P. biglobosa*, **B:** *Ganoderma boninense* on the crown of *E. guineensis*, **C:** *Amauroderma* cf. *fasciculatum*, **D:** *Phylloporia* cf. *hainaniana* on the stem of *S. senegalensis*, **E:** *Phaeolus* cf. *spadiceus*, **F:** *Laetiporus baudonii* on collar of *A. senegalensis*, **G:** *Navisporus floccosus* on root of *P. biglobosa*, **H:** *Phellinus* sp., **I:** *Fomitiporia* sp, **J:** *Inonotus* sp., **K:** *Inonotus* sp. rot, **L:** *Phellinus igniarius* on *A. leiocarpus* trunk.

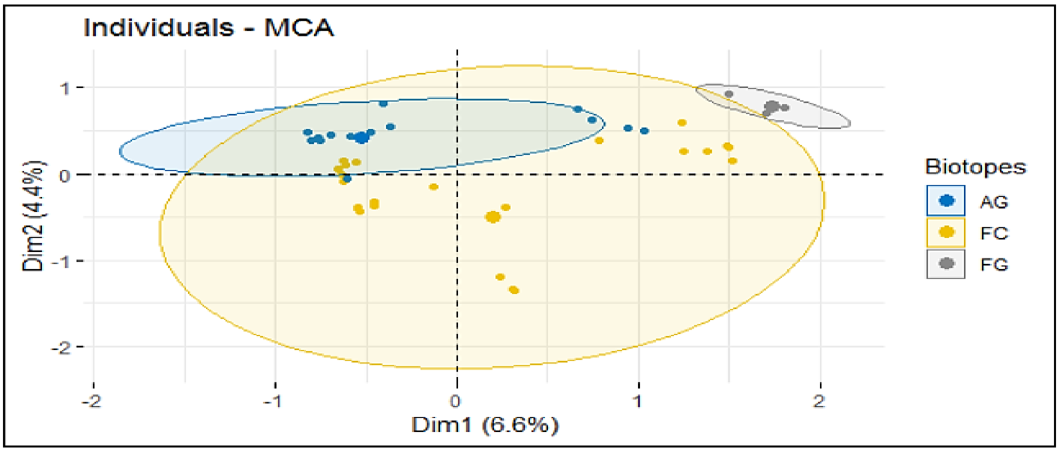

Fig. 3: Two-dimensional distribution showing the dispersion of woody species and their parasitic polypores in different biotopes.

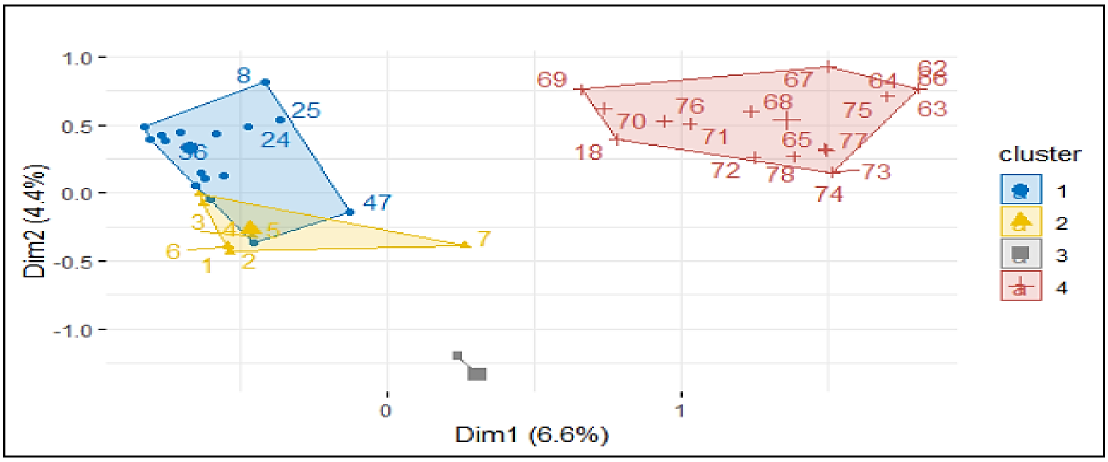

Fig. 4: Hierarchical classification of variables into four groups.

Table 3: Cluster composition of the hierarchical classification.

	Cluster 1		**Cluster 2**		**Cluster 3**		**Cluster 4**	
	Cla/Mod	**Mod/Cla**	**Cla/Mod**	**Mod/Cla**	**Cla/Mod**	**Mod/Cla**	**Cla/Mod**	**Mod/Cla**
AG	88.23	83.33	15.78	16.67	--	--	11.76	22.22
FC	--	--	26.31	100	36.84	100.00	--	--
FG	--	--	--	--	--	--	100	33.33
Acacia dudgeoni	--	--	--	--	--	--	--	--
Anogeissus leiocarpus	--	--	--	--	--	--	83.33	27.78
Baissea multiflora	--	--	--	--	100	21.43	--	--
Elaeis guineensis	--	--	--	--	--	--	100	16.67
Parkia biglobosa	--	--	--	--	--	--	10.34	16.67
Saba senegalensis	--	--	--	--	100	--	--	--
Secamone afzellii	--	--	--	--	100	21.43	--	--
Strophantus sarmentosus	--	--	--	--	100	21.43	--	--
Vitellaria paradoxa								
Fomitiporia sp.1	--	--	100	20	100	28.57	--	--
Phellinopsis cf. *pinicola*	--	--	100	20	--	--	--	--
Phylloporia cf. *fructica*	--	--	--	--	--	--	--	--
Phylloporia cf. *hainaniana*	--	--	--	--	100	35.71	--	--
Phylloporia cf. *oblongospora*	--	--	--	--	100	35.71	--	--

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