

# 14 Termitomyces/Termite Interactions

Corinne Rouland-Lefèvre, Tetsushi Inoue, Toru Johjima

## 14.1 Introduction

The first observation of brain like formations inside termite nests were made by the German naturalist, J. D. König (1799), in the East Indies. These formations were several centimeters in diameter and were later given the name of fungus combs. A fungus was developing on these plant structures in the form of mycelium with small white nodules (mycotetes) which are characteristic of the group. More than half a century later, the English cryptogamist, G. Gardner (cited by Petch 1913), collected a large carpophore-bearing fungus of the Agaricales order from a termite nest in Ceylon. However, it was only in 1906 that Petch (1906) pointed out the relationship between the mycotetes and carpophore fungal formations and showed that these large mushrooms were cultivated by the termites inside their nests. Heim (1941) created a new genus for these fungi, *Termitomyces*, which contains all the "termitophilic Agaricales".

*Termitomyces* have since been studied by entomologists seeking to clarify the relationship between termites and fungi. Grassé (1959) was the first to show that *Termitomyces* were associated with only a single subfamily of termites, the Macrotermitinae, and that this is a real symbiosis as neither of the two symbionts can exist without the other. Other more recent works have shown the details of this symbiosis: on the one hand, because termite nests are both temperature and humidity regulated (Matsumoto 1977; Johnson 1981; Thomas 1987a), they provide ideal conditions for the growth of these *Termitomyces* and, on the other hand, the fungus helps the termites to degrade the plant matter (e.g. wood, dry grass, leaf litter) on which they live. It grows on a special structure in the nest, the fungus comb, which is actively maintained by the termites, by continuously adding plant matter and consuming the comb.

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The precise nature of the relationship between termites and the associated fungus, as well as its specificity, have provoked considerable controversy which has been largely resolved by new biochemical and molecular biology techniques. In this chapter, we shall present the results obtained using molecular biology to study termite/*Termitomyces* co-evolution. We shall then look at recent scientific advances regarding the contribution of the termite and its symbiotic fungus to the degradation of major plant components (cellulose, hemicellulose, lignin).

## 14.2 Phylogeny and Co-Evolution of Fungus-Growing Termites and *Termitomyces*

Symbiotic relationships have played an essential role in termite evolution, involving a range of symbionts including protists, methanogenic archaea and bacteria (Bignell 2000). Only one Termitidae subfamily, the Macrotermitinae, has evolved an external mutualistic symbiosis with fungi of the *Termitomyces* genus.

### 14.2.1 The Symbionts

**Macrotermitinae or “Fungus-Growing” Termites.** Macrotermitinae belong to the family of higher termites (Termitidae), which accounts for 70% of known species of termite. They are organized in complex societies with a number of well-defined castes and do not have symbiotic protists in their digestive tract. These characteristics are specific to the Termitidae family which encompasses 235 of the 281 currently recognized genera in the order Isoptera. Termitidae are divided into four subfamilies, one of which is the Macrotermitinae.

Macrotermitinae are only found on the African and Asian continents where they are the dominant group in tropical areas (Abe and Watanabe 1983; Wood and Thomas 1989). The Macrotermitinae have been divided into 11 taxonomically distinct genera and approximately 330 species (Khambhampati and Eggleton 2000). Most of the diversity occurs in Africa, where 10 of the 11 genera are found. Genera are also found in Asia and Madagascar, and one genus is exclusively Asian (Khambhampati and Eggleton 2000).

**Termitomyces Fungi or “Termitophilic” Fungi.** *Termitomyces* are Basidiomycotina fungi from the order Agaricales, the Tricholomataceae Roze family and

the Termitomycetaceae (Jülich) Singer tribe. Approximately 40 *Termitomyces* species have been described. However, their taxonomy was based on the fruit structures (Heim 1977) and, as some *Termitomyces* never fruit, their taxonomy is thus difficult to determine. However, since Heim, no other mycologist has been interested in the composition of the *Termitomyces* genus, even though it contains fungi of extremely diverse form, origin and biology. The common denominator of the *Termitomyces* fungi is that all species in the genus are cultivated by termites in their nests. Furthermore, all the fungi cultivated by Macrotermitinae termites belong to this genus.

Although additional varieties have been identified using molecular biology (Rouland et al. 2002; Aanen et al. 2002), the small number of fungal species compared with the number of Macrotermitinae species (40/330) suggests that many of these fungi are shared by different termite species.

### 14.2.2

#### Evolution of Fungus-Growing Termites and *Termitomyces*

There has recently been a resurgence in interest in phylogeny of *Termitomyces*, phylogeny of Macrotermitinae and co-evolutionary dynamics. The first study by Rouland et al. (2002) on 15 African *Termitomyces* species sequenced their internal transcriber spacer region (ITS1–5.8S–ITS2) and showed that *Termitomyces* was clearly a monophyletic group belonging to the family Tricholomataceae. The hypothesis that "each species of termite is associated with a separate species of fungal symbiont" (Heim 1942; Grassé 1982) seems unlikely since identical ITS sequences were obtained from fungi cultivated by three species of termites in different genera. On the other hand, Katoh et al. (2002) demonstrated, by sequencing ITS and 18S rDNA, that the symbiotic fungi cultivated by several colonies of the same termite species, *Odontotermes formosanus*, belonged to two different *Termitomyces* species. The work of Taprab et al. (2002) on the molecular phylogeny of symbiotic *Termitomyces* of several species of Asian Macrotermitinae also indicates that the relationships of symbiotic fungi with host termites and their locality were apparently complex.

The most comprehensive study on termite/*Termitomyces* evolution was conducted by Aanen et al. (2002) who created phylogenetic trees of the two symbionts in this mutualism across several genera and reconstructed both the origin and a number of key aspects of the co-evolutionary dynamics of the symbiosis. They studied 38 colonies of 32 species, covering 9 of the 11 genera of fungus-growing termites from three locations in Africa (Cameroon, Senegal and Gabon) and 3 in Asia (Sumatra, Kalimantan (Indonesia) and Sri Lanka), spanning most of the distribution of the Macrotermitinae. Maximum likelihood and Bayesian analyses of DNA

sequences were used to reconstruct the phylogenetic trees of both symbionts. This study confirmed that the fungus-growing termites are monophyletic within the Isoptera order and the fungi cultivated by these fungus-growing termites are monophyletic within the Basidiomycotina order, as has been described in other papers (Rouland et al. 2002; Monçalvo et al. 2002). Moreover, these authors demonstrated that the symbiosis has a single African origin and that the secondary domestication of other fungi or reversion of mutualistic fungi to a free-living state has not occurred. According to the papers mentioned above (Taprab et al. 2002; Katoh et al. 2002), host switching has been frequent especially at lower taxonomic levels, and different nests of a particular termite species can have different symbionts. These observations are consistent with horizontal transmission of fungal symbionts. But, in spite of frequent host switching, there is a very high correlation between the termite and fungal phylogenetic trees because the mutualistic interactions at higher taxonomic levels are highly specific. If horizontal transmission is the main transmission mode, the symbiont specificity at higher taxonomic levels is surprising. The question arises how this specificity has evolved. One possibility is that termites select their fungal symbionts indirectly (i.e. by supplying substrates suitable only for particular groups of fungi). If this is the case, we must consider that not all *Termitomyces* have the same capacity to degrade plant matter and therefore their importance in the digestive symbiosis with termites varies. This will be discussed in the following section.

## 14.3

### The Role of *Termitomyces* in Mutualistic Symbiosis

#### 14.3.1

##### Nature, Structure and Dynamics of the Fungus Comb

Fungus combs are sponge-like structures enclosed in specially constructed chambers inside a termite mound and the soil. The structure provides a large surface area, allowing air circulation and access by the termites. The fungus comb is the culture medium for *Termitomyces* as well as food for the termites and it is constructed with the undigested feces of termite workers (Josens 1991; Grassé 1978; Sieber and Leuthold 1981; Johjima et al. 2003). In most *Macrotermes*, the fecal material is deposited on the top rim of the fungus comb. There is an age gradient within the fungus comb, such that the upper part of the fungus comb is newer than the lower part. The termites eat the fungus comb from the lower rim (Josens 1971; Sieber and Leuthold 1981). The termites, therefore, eat the mature part of the fungus comb which creates a highly efficient method of digesting plant matter. The fungus

comb has a cycle time of approximately 40 days (Traniello and Leuthold 2000). An exception has been reported for *Macrotermes carbonarius* where gradient exists among individual combs (Hyodo et al. 1999). Other fungus comb structural forms have been observed in Macrotermitinae other than *Macrotermes*, and were described in detail in the review by Rouland (2000). Some species of fungus-growing termites have a food store in addition to the fungus comb. This comprises small particles cut from plant litter and looks like moist sawdust (Wood 1978; Darlington 1994). This food store is also ingested by the termites and then excreted on the fungus comb without obvious digestion. The function of this food store is not well understood. Lower concentrations of plant secondary metabolites have been detected in *Macrotermes gilvus* food stores than in the leaf litter around the mound (Johjima et al. 2003). The food store may well help in detoxification or improve the palatability of the litter.

*Termitomyces* have only been found in association with fungus-growing termites in the form of mycelium with aggregations of asexual spores which have been called various names such as mycotetes, synnemata, conidia, nodules. Mycotetes are also consumed by the termites. The sexual stage of the fungus, the basidiocarps with a long pseudorhiza extended from fungus comb (Singer 1986), is developed at specific times in the rainy seasons. However, as they last no more than few days, they are easily overlooked. *Termitomyces* is absent everywhere else in the nest structure including the food store and the internal walls of the nest. Outside the fungus comb it only occurs in the guts of workers (Thomas 1987a,b). Although the fungus comb seems to have a pure culture of *Termitomyces* when it is in the termite nest, other fungi such as *Xylaria* proliferate on the fungus comb within a few days if the comb is removed from the nest. It is not fully understood how the growth of contaminants is controlled in the termite nest. If there are still live termites on the comb after it has been removed from the nest, the growth of non-symbiotic fungi is suppressed for a few days (Grassé and Noirot 1958; Thomas 1987b). In a study of *Macrotermes bellicosus*, very little evidence of germination of fungal spores in the food store was observed despite the presence of various fungal spores (Thomas 1987b). The food store consists of comminuted food mixed with saliva. Furthermore, extracts of the food store, whole termites and the termite gut showed fungistatic activity, suggesting that termite secretions inhibit fungal spore germination and growth. Recently, antimicrobial peptides were identified in the fungus-growing termite *Pseudacanthotermes spiniger* (Lamberty et al. 2001). Termicin is present in hemocyte granules and salivary glands of the termite which has an activity against several fungi. However, the antimicrobial activity against *Termitomyces* and the typical contaminant fungus *Xylaria* has not been studied. The fungistatic activity of termite secretions, especially saliva, appears to be a major part of fungus comb

maintenance. Other possible factors that control fungal activities have also been discussed by Thomas (1987b).

### 14.3.2

#### Role of *Termitomyces* in the Digestive Metabolism of Termites

Sands (1956) showed that *Odontotermes badius* workers supplied with fresh fungus comb survived much longer than workers supplied with wood chips and filter paper containing starch or sugars. Workers supplied with fungus comb from which the mycotetes had been removed survived only slightly longer than starved workers. These observations indicate that fungus comb, especially mycotetes, is important for termite nutrition. Four roles in the symbiotic relationship with host termites have been proposed for *Termitomyces*: (1) enrichment in nitrogen (Matsumoto 1976; Collins 1983); (2) a source of metabolic water and heat (Lüscher 1951); (3) provision of glycosyl hydrolases which work synergistically with enzymes from the host termites (Martin and Martin 1978; Rouland et al. 1988b,c); (4) the degradation of lignin to improve cellulose digestibility (Grassé and Noirot 1958). Termites feed mainly on plant debris that is poor in nitrogen. The nitrogen content of the mycotetes was reported to be much higher (6–8%) than in the fungus comb (0.8–2.0%) and, therefore, the mycotetes are a nitrogen-rich food for the termites (Matsumoto 1976; Rohrmann 1978, Wood and Thomas 1989). The roles suggested in (1) and (2) will be more or less significant for all fungus-growing termites, while the roles suggested in (3) and (4) are controversial and would depend on the host as discussed below.

**Provision of Polysaccharide-Degrading Enzymes.** The role of *Termitomyces* in plant polysaccharide degradation was first clarified by determining the enzyme activities of the various parts of termite workers digestive tract as well as of the fungal nodules (Abo-Khatwa 1978; Martin and Martin 1979; Rouland et al. 1988a–d, 1991; Sengupta and Sengupta 1990). To define the respective role of each partner of the symbiosis, a multi-variance analysis of 19 enzymatic activities detected in 5 termites and fungal species was made. The first two axes of the PCA (Fig. 14.1a) accounted for 74% of the total variance (41% on axis 1, 33% on axis 2). Discriminant analysis carried out on 10,000 permutations showed that the PCA was highly significant ( $P < 0.00001$ ). On axis 1, the correlation circle showed the separation of samples having polysaccharidase activity and those with oligosaccharidase activity. On axis 2, samples with  $\beta$ -xylosidase activity were separated from those with heterosidase activity. The projection of sample classes (termites and associated fungal species) on the first two PCA axes (Fig. 14.1b), on the one hand, clearly differentiate the low level of oligosaccharidasic and heterosidasic activity of the fungi from the higher level of activity of the

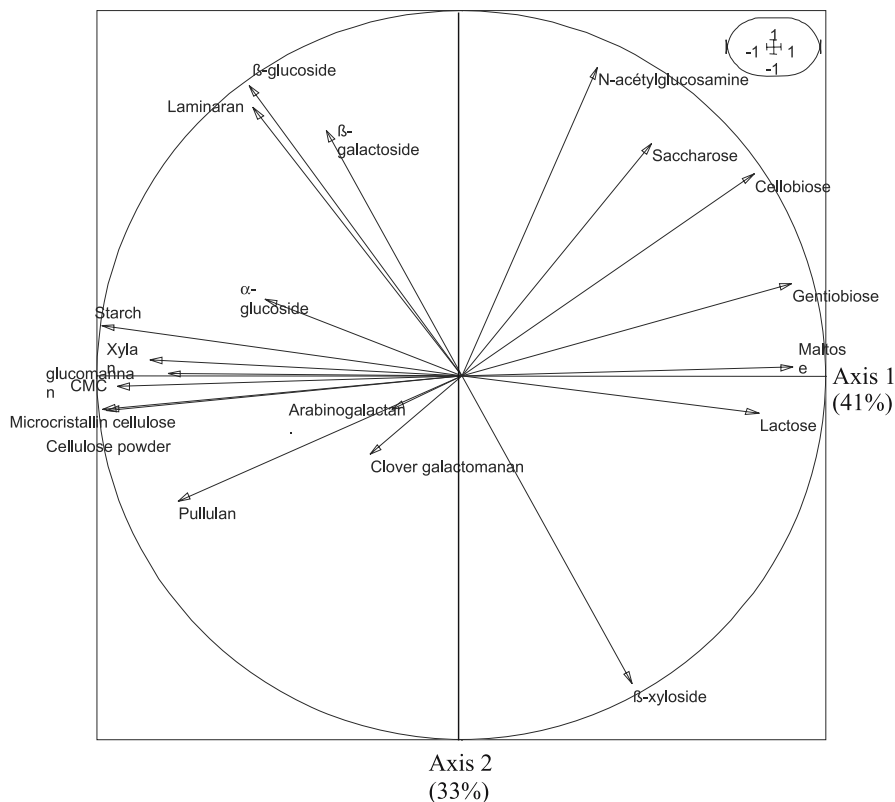


Fig. 14.1. Results of principal components analysis (PCA). a Correlation circle; Results of principal components analysis (PCA).

termites and, on the other hand, clearly differentiate the fungi/termite associations of the species *A. cavithorax* and *M. toumodiensis* from the other species of termites. The differentiation between these termite/fungus associations is principally due to a greater degradation of polysaccharides by *A. cavithorax* and *M. toumodiensis* workers than by their associated fungi whereas, in the other species studied, the two symbionts (termite/fungus) degrade polysaccharides to the same extent. Furthermore, for some associations, the substrate most degraded by the termites' digestive tract is also the substrate most degraded by the symbiotic fungus. In this case, the enzymes produced by the symbionts are not complementary unlike the enzymes produced by fungus-cultivating ants (D'Ettore et al. 2002). To explain this anomaly, several authors have proposed an acquired enzyme hypothesis (Martin 1991; Martin and Martin 1978, 1979; Kukor and Martin 1983). This hypothesis suggests that some fungi can produce polysaccharidases which act synergistically with the enzymes produced by the termites.

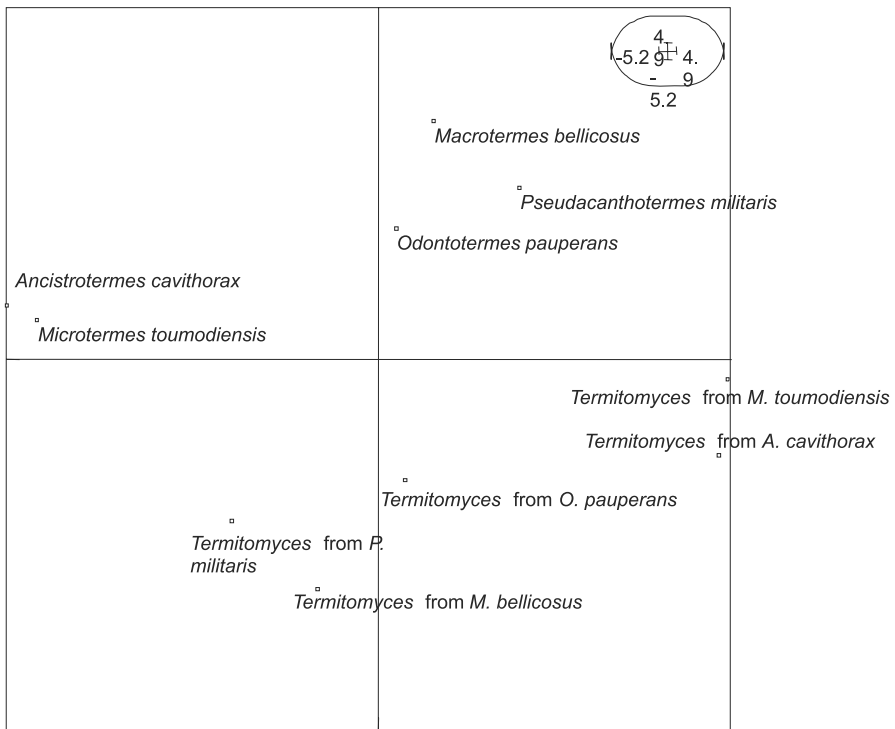


Fig. 14.1. (continued) **b** ordination of the samples in the plane defined by axes 1 (41%) and 2 (33%) of the PCA

Degradation of polysaccharides could, therefore, be achieved in the worker termite guts by the combined action of fungal and termite enzymes. Fungal cellulases and xylanases have been found in the digestive tract of two species of *Macrotermes* (Rouland et al. 1988a–c; Matoub and Rouland 1995), but without any equivalent recent work on other species, this hypothesis is still contested by some authors (see Rouland 2000).

For polysaccharide degradation, symbiotic fungi exhibit different enzyme activities. For example, *T. eurhizus*, associated with the termite *P. spiniger*, is highly amylolytic, whereas *Termitomyces*, associated with *Macrotermes bellicosus*, is both xylanolytic and cellulolytic (Rouland et al. 1991; Ikhouane 1995). The differences in enzyme activities could be due to different genetic patterns in the fungi or to different environmental conditions. In order to distinguish between these factors, the enzyme production of several species of *Termitomyces* cultivated under the same conditions has been examined (Table 14.1). It is, therefore, possible to distinguish two groups of *Termitomyces*: in the first group (*Termitomyces* sp., *T. eurhizus* and *T. medius*), the fungi can produce enzymes which vary ac-



**Table 14.1.** Production of several osidasic enzymes on fungus comb extracts from *Anistrotermes guineensis*, *Macrotermes bellicosus*, *Microtermes subhyalinus* and *Pseudacanthotermes spiniger*

	Cellobiase	CMCase	Maltase	Amylase	$\beta$ -Xylosidase	Xylanase
<i>T. eurhizus</i> from <i>P. spiniger</i>						
<i>A. guineensis</i> comb	12 $\pm$ 3	84 $\pm$ 8	12 $\pm$ 2.5	18 $\pm$ 4	24 $\pm$ 3	112 $\pm$ 5
<i>M. bellicosus</i> comb	0	270 $\pm$ 36	11 $\pm$ 1.3	0	48 $\pm$ 5	1385 $\pm$ 59
<i>P. spiniger</i> comb	14.6 $\pm$ 1.3	5.2 $\pm$ 0.3	2.3 $\pm$ 0.1	10.6 $\pm$ 0.5	12.8 $\pm$ 1.2	18.2 $\pm$ 2.4
<i>T. medius</i> from <i>A. guineensis</i>						
<i>A. guineensis</i> comb	15.4 $\pm$ 1.1	76.05 $\pm$ 8.6	12.4 $\pm$ 2	278 $\pm$ 25	25.3 $\pm$ 1.6	824 $\pm$ 56
<i>M. bellicosus</i> comb	0	0	0	17.9 $\pm$ 2.4	22.7 $\pm$ 3.6	821 $\pm$ 47
<i>P. spiniger</i> comb	12.3 $\pm$ 0.6	76 $\pm$ 5.2	74.8 $\pm$ 8.3	75.2 $\pm$ 6	18.4 $\pm$ 2	992 $\pm$ 36
<i>T. sp bellicosus</i> from <i>M. bellicosus</i>						
<i>A. guineensis</i> comb	0	0	0	0	14.5 $\pm$ 2.3	672 $\pm$ 42
<i>M. bellicosus</i> comb	0	198 $\pm$ 36	28 $\pm$ 6.4	0	48 $\pm$ 9	986 $\pm$ 51
<i>P. spiniger</i> comb	0	0	0	0	10.9 $\pm$ 3	550 $\pm$ 37
<i>T. sp subhyalinus</i> from <i>M. subhyalinus</i>						
<i>M. subhyalinus</i> comb	4.5 $\pm$ 0.3	2.05 $\pm$ 0.2	5.3 $\pm$ 0.8	3.4 $\pm$ 0.6	14.6 $\pm$ 1.2	14.6 $\pm$ 1.6
<i>P. spiniger</i> comb	4.1 $\pm$ 0.5	2.0 $\pm$ 0.6	3.8 $\pm$ 0.8	2.5 $\pm$ 0.4	3.7 $\pm$ 0.9	12.3 $\pm$ 1

Activities are expressed in  $\mu\text{mol permn per mg protein}$  (Mora and Rouland 1994; Ikhouane 1995)

ording to the substrate and thus enzymatic production is correlated with environmental factors. These fungi are generalists and can be cultivated by several species of termite. In the second group, however, the variety of substrates that induce enzyme production is more limited. The enzymes produced in culture media are constitutive. This type of fungus appears to be more specialized in that it is found only in association with a single termite species. The group includes the symbiotic fungus associated with *M. bellicosus* (Ikhouane 1995) and *T. clypeatus* which produces several constitutive enzymes in vitro (Ghosh and Sengupta 1987; Sengupta and Sengupta 1990; Roy et al. 1994; Sinha and Sengupta 1995; Mukherjee et al.

1995). This classification of *Termitomyces* according to their metabolism seems to be correlate strongly with the co-evolution conclusions discussed above. *T. medius* has been found as a cultivated fungus associated with three species of *Microtermes*, two species of *Ancistrotermes* and with *Synacanthotermes heterodon*, whereas the symbiotic fungi associated with *M. bellicosus* have only been cultivated in the nests of this species (Aanen et al. 2002; Rouland et al. 2002).

**Lignin Degradation in the Fungus Comb.** Lignin is a heterogeneous random phenylpropanoid polymer that constitutes 15–30% of woody plant cell walls. Free-radical condensation of lignin precursors (coniferyl, sinapyl and *p*-coumaryl alcohols) results in the formation of an amorphous and highly branched polymer with at least 12 different types of linkage (Monties and Fukushima 2001). Since lignin forms a matrix surrounding the cellulose microfibrils, cellulose-depolymerizing enzymes are locked out and the decomposition of the cellulose will be retarded. Experimental evidence of lignin degradation in fungus combs was reported by Rohrmann (1978), and later by Hyodo et al. (2000). They determined proximate fractions for parts of the fungus comb differing in age, showing that lignin concentrations in the older parts of the combs were lower than those in the newer parts (Table 14.2). The structural changes of the lignin as the comb aged were analyzed using solid-state  $^{13}\text{C}$  nuclear magnetic resonance (NMR) spectroscopy of the molecules (Hyodo et al. 2000). Compared with the NMR spectrum of newer comb, the relative peak intensities at 56 and 154 ppm were clearly lower in the older comb. The peaks at 56 and 154 ppm were assigned to methoxyl and aromatic carbon in lignin, respectively. Further

**Table 14.2.** Chemical composition of various fungus combs (as dry weight %)

	Part of comb	Cellulose	Lignin	Ash
<i>M. ukuxii</i> <sup>a</sup>	Newer	20.82 <sup>c</sup>	14.30	8.00
	Older	27.18 <sup>c</sup>	2.43	7.45
<i>M. natalensis</i> <sup>a</sup>	Newer	17.78 <sup>c</sup>	9.80	16.22
	Older	21.82 <sup>c</sup>	5.67	15.47
<i>M. gilvus</i> <sup>b</sup> colony 1	Newer	17.1 <sup>d</sup>	32.6	14.0
	Older	26.3 <sup>d</sup>	15.0	15.5
<i>M. gilvus</i> <sup>b</sup> colony 2	Newer	21.5 <sup>d</sup>	34.6	5.7
	Older	33.8 <sup>d</sup>	53.4	11.2

<sup>a</sup> Data from Rohrmann (1987)

<sup>b</sup> Data from Hyodo (2000)

<sup>c</sup> Cellulose + chitin

<sup>d</sup> Calculated from glucose content

studies for precise peak assignment will be required because fungus comb consists of a variety of plant material so that the spectrum must be very complex.

There have been extensive biochemical studies of lignin degradation by basidiomycetes which have revealed that extracellular peroxidases are responsible for the depolymerization of lignin (see reviews by Kirk and Farrell 1987; Gold and Alic 1993; Hatakka 2001). Laccase is one of main components of ligninolytic enzymes in some basidiomycete (e.g. *Pycnoporus cinnabarinus*, Eggert et al. 1997). However, many fungi that are not able to degrade lignin also produce laccase (e.g. *Neurospora crassa*). Lignin peroxidase (EC 1.11.1.14) catalyzes the oxidation of various aromatic compounds to form aryl cation radicals that are unstable and undergo a variety of nonenzymatic (chemical) reactions such as ring-opening and side-chain cleavages (Kirk and Farrell 1987). The substrate of manganese peroxidase (EC 1.11.1.13) is  $Mn^{II}$ . The enzyme oxidizes  $Mn^{II}$  to  $Mn^{III}$ , which diffuses from the enzyme surface and oxidizes a variety of phenolic compounds (Gold and Alic 1993). Thus  $Mn^{III}$  acts as a diffusible oxidant and attacks macromolecular lignin. In the case of lignin peroxidase, substrate oxidation site is located on the surface of the enzyme (Doyle et al. 1998). Direct interaction and electron transfer between lignin peroxidase and lignin were observed (Johjima et al. 1999). Both enzymes show broad substrate specificities and are suitable for degradation of lignin because lignin structure is a random, highly branched polymer with various linkages.

The understanding of the lignin degradation mechanism in fungus comb is limited. Rohrmann and Rossman (1980) detected pigmentation in *Macrotermes ukuzii* and *Termitomyces* combs grown on comb agar in the presence of syringaldazine (4-hydroxy-3,5-dimethoxybenzaldehyde). This suggests that *Termitomyces* produces extracellular phenol oxidase(s) such as peroxidase and laccase in the fungus comb. However, this does not show that *Termitomyces* can degrade lignin because laccase and peroxidase are secreted by non-ligninolytic fungi.

The work discussed above was based on *Macrotermes*. Hyodo et al. (2003) analyzed chemical composition of the fungus combs from *Odontotermes*, *Hypotermes makhamsensis*, *Ancistrotermes pakistanicus* and *Pseudacanthotermes militaris* in addition to four species of *Macrotermes*. In all *Macrotermes* species, the carbohydrate:lignin ratio increased progressively with comb age, whereas it decreased or remained constant in three species of *Odontotermes*, *H. makhamsensis*, *A. pakistanicus* and *P. militaris*. This indicates that, in *Macrotermes*, lignin is preferentially degraded in the combs, whereas in the other four genera carbohydrate is preferentially degraded. The authors also conducted a stable carbon isotope analysis and suggested that *Macrotermes* depend more on plant matter for nutrition than the other four genera. It is uncertain whether the differences are accounted for by the

different sources of the fungus combs or by the phylogenetic differences between the symbiotic fungi. The authors mentioned that the *Macrotermes* species examined in the study, where lignin content in fungus combs decreased with age, seem to tend to feed on leaf litter, while the other genera appear to feed predominantly on wood with the exception of *P. militaris*. *M. gilvus*, in which the lignin degradation was analyzed by solid-state NMR as described above, also mainly uses leaf, grass and stalks as a source of the fungus comb (Roonwall 1970). It has been observed that grass lignin is more easily degraded by fungi than wood lignin (Rodriguez et al. 1996). It is possible that *Termitomyces* can degrade grass and leaf lignin but not wood lignin. Molecular biological studies covering the cloning of ligninolytic enzymes and the distribution of the genes within the symbiotic fungi from various host termites will resolve the question.

The existence of plant secondary metabolites as well as lignin will interfere with carbohydrate utilization by termites because these compounds are apparently key components of plant defence against pests and pathogens and are, therefore, considered to be an important controlling factor for litter decomposition in soils (Swift et al. 1979; Bennett and Wallsgrave 1994). Phenolics such as tannins and flavonoids are one of major classes of plant secondary metabolites. The concentration of phenolics in the fungus comb of *M. gilvus* is much lower than in the fallen leaves around the termite mound (Johjima 2003). The concentration of water-soluble phenolics in extractable compounds from older comb is lower (40%) than that in newer comb, suggesting that phenolics are degraded in the fungus comb. Phenol oxidase activity has been detected in the fungus comb as mentioned above. This enzyme might be responsible for the degradation of phenolics in the fungus comb.

Chemical analyses of fungus comb at molecular level will provide further insights into the function of fungus comb. However, it is nearly impossible to determine the fungus comb compositions in molecular level using degradative chemical methods since the fungus comb consists of a variety of plant debris and microorganisms. For example, the Klason lignin method has been shown to overestimate lignin content in litter, where the residue contains cutin, suberin and tannins as well as lignin (Kögel 2003 and references therein). The results obtained by Rohrmann (1978) and Hyodo et al. (2000) may be due to degradation of cutin, suberin and tannins rather than lignin being degraded in the fungus comb. New analytical approaches such as solid-state NMR spectroscopy and analytical pyrolysis/gas chromatography/mass spectrometry combined with conventional methods will allow a detailed analysis of fungus comb components and help the understanding of the detailed mechanism of lignin degradation and the tracing the fate of lignin and plant secondary metabolites such as tannin in Macrotermitinae colonies.

## 14.4 Conclusions

The efficiency of degradation of lignocellulose by fungus-growing termites is largely attributed to their symbiotic *Termitomyces*. These fungi provide a variety of functions that termites do not possess. Recently, the application of new technologies and molecular methods has greatly improved our knowledge of lignin degradation by both Macrotermitinae termites and *Termitomyces* fungi and on the co-evolution of the symbionts. However, there are still gaps in our knowledge on the adoption of a particular species of fungus by termites. As described above, the same fungus can be cultivated by several different termite species. A crucial and as-yet-unanswered question is: to what extent do the Macrotermitinae manage to reduce the genetic diversity of horizontally acquired symbionts to a single strain to prevent the evolution and appearance of non-cooperative symbiont traits?

The other important unsolved questions concern the acquired enzymes: do these enzymes exist in genera of Macrotermitinae other than *Macrotermes*? Can lignin-degrading enzymes also be acquired by termites? New biochemical and molecular studies are required to answer these questions.

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