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THE AMYLOSTEREUM SYMBIONT OF SIREX NOCTILIO IN SOUTH AFRICA

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DECLARATION

I, the undersigned, hereby declare that the thesis submitted herewith for the degree *Magister Scientiae* to the University of the Orange Free State, contains my own independent work and has hitherto not been submitted for any degree at any other University.

Bernard Slippers

December 1998

I dedicate this thesis to my loving father and mother.

Your supporting hands, loving hearts and guiding words will always carry me.

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PREFACE

Sirex noctilio and its symbiotic fungus, Amylostereum areolatum, were first reported from New Zealand at the turn of the century. Since then it has spread to most Southern Hemisphere areas were pine is grown commercially. Unlike the situation in the Northern Hemisphere, where it is native, this insect-fungus complex has been responsible for great economic losses to the softwood industries of the Southern Hemisphere. These losses have prompted considerable research into controlling this pest complex, especially through the use of biological agents. The fungal symbiont has, however, received less attention, despite its important role in the symbiosis. The aim of this study was to investigate more closely, the fungal symbiont of a recently introduced population of S. noctilio in South Africa.

The literature concerning the *Sirex-Amylostereum* complex is reviewed in Chapter 1. The review focuses on *Sirex* in the Southern Hemisphere, but compares this to the Northern Hemisphere where applicable. Firstly, the distribution and spread of *Sirex* is considered. Furthermore, various aspects of the taxonomy and biology of the insect and the fungus are analysed separately, after which these features are combined in the disease cycle. Similarly, different hosts and the factors that predispose them to attack by *Sirex*, are investigated. Lastly, the management of *Sirex* in the Southern Hemisphere is reviewed.

In April 1994, S. noctilio was reported for the first time from standing pine trees in South Africa. In Chapter 2, the population structure of isolates of A. areolatum associated with this recently introduced Sirex population, is investigated. The possible origin of Sirex in South Africa is also considered by comparing the fungal population associated with it, with isolates and populations of A. areolatum from other regions of the world.

In 1958, Boidin described the genus Amylostereum and included the species A. chailletii, A. areolatum and A. laevigatum. In 1984, Boidin and Lanquetin added a fourth species, namely A. ferreum. Although mating studies in this last study indicated possible relationships among the species of this genus, their relationships to each

other was not clearly defined. In Chapter 3, the phylogenetic relationship between the species of *Amylostereum* is investigated using sequence analysis of the mitochondrial small-sub-unit of the rDNA complex. The relationship of *Amylostereum* with other Basidiomycetes is also unclear. This question is also addressed in the chapter by comparing sequence of the mt-SSU-rDNA of *Amylostereum* spp. with that of various other genera and species of Basidiomycetes.

Amylostereum areolatum reproduces asexually in its life cycle associated with Sirex. This effectively separates populations of this fungus associated with the different wasp species. In Chapter 4, the relationship between isolates of A. areolatum from different parts of the world and associated with different wasp species is investigated. This is achieved using sequence analysis of variable part of the rDNA complex, namely the nuclear intergenic spacer region. The usefulness of RFLP analyses of this region to delineate the various species of Amylostereum, is also assessed.

Renewed interest in *Amylostereum* as a symbiont of woodwasps in recent years, has led to exciting progress in this field. A summary of the recent findings regarding the taxonomy, phylogeny and ecology of *Amylostereum* spp., is given in Chapter 5. New questions and the future direction of research on *Amylostereum* and its symbiosis with woodwasps, are also discussed.



THE SIREX-AMYLOSTEREUM COMPLEX, WITH SPECIAL REFERENCE TO ITS INFLUENCE ON PINE SILVICULTURE IN THE SOUTHERN HEMISPHERE

1.0 INTRODUCTION

Sirex noctilio Fabricius is a member the Siricidae, a family of insects with a woodboring larval state (Chamberlin, 1960; Morgan, 1968). A common characteristic of these insects is a highly specialised mutualism with members of wood rotting Basidiomycetes (Cartwright, 1929; Francke-Grosmann, 1939; Morgan, 1968). In combination, through a phytotoxic mucus secreted by the wasp and the subsequent rotting of the wood by the fungus, these insect-fungal associations have the ability to kill a living tree (Coutts, 1969a & b). S. noctilio and its symbiotic fungus, Amylostereum areolatum Boidin, are, however, the only members of the Siricidae that regularly attack living trees (Hanson, 1939; Spradbery & Kirk, 1978).

In the Northern Hemisphere, where the *Sirex noctilio – Amylostereum areolatum* complex is native, it is considered to be a secondary pest of little economic importance (Hall, 1978; Hanson, 1939; Spradbery & Kirk, 1978). In these regions, trees are rarely killed and a tree may support a colony of woodwasps for more than one season (Spradbery, 1973; Spradbery & Kirk, 1978). This is in contrast to the Southern Hemisphere, were the *Sirex-Amylostereum* complex has caused extensive damage in the exotic pine plantations (Neumann & Marks, 1990; Chou, 1991)

Sirex noctilio was first reported from the Southern Hemisphere at the turn of the century from New Zealand and it subsequently spread to the other countries of Australasia (Tasmania and Australia) in the 1950's and 1960's (Madden, 1988; Neumann & Marks, 1990; Chou, 1991). More recently in the 1980's and 1990's Sirex was also reported from South America (Uruguay, Brazil and Argentina) and South Africa (Tribe, 1995a; Reardon, Eav, & Wetterberg, 1995). Damage in the exotic softwood plantations of these regions of the Southern Hemisphere has generally been at low levels, except for some major outbreaks where millions of trees were killed (Neumann, Morey & McKimm, 1987; Madden, 1988 & 1998b; Haugen, 1990; Neumann & Marks, 1990; Chou, 1991). These outbreaks were always associated with stress conditions on the trees that were attributable to either environmental stress (e.g. droughts) or stress caused by poor silvicultural management (Neumann & Marks, 1990; Chou, 1991). Outbreaks of Sirex have the potential of causing

losses of A\$1-4 billion to the softwood industries of Australasia over a 30 year rotation period (Bedding, 1995). The *Sirex-Amylostereum* complex is, therefore, of considerable economic importance in the Southern Hemisphere.

Through a national *Sirex* control programme in Australia, millions of A\$ have been spent on research and survey programmes to combat this pest (Neumann *et al.*, 1987; Madden, 1988). Mainly through this programme, control strategies have been devised that are used throughout affected countries of the Southern Hemisphere (Neumann *et al.*, 1987; Anonymous, 1991; Bedding, 1995). Today, control of *Sirex* is through a combination of silvicultural practises to ensure forest health and the use of a series of biocontrol agents (Neumann *et al.*, 1987; Anonymous, 1991). Where implicated thoroughly, these control strategies have been used to great effect. The importance of these principles of sound silviculture, thorough surveys and timely, adequate implementation of biocontrol programmes has, however, been obvious in areas were they were not enforced properly. In such regions, *Sirex* numbers steadily increased and eventually serious outbreaks followed (Neumann *et al.*, 1987; Madden, 1988 & 1998b; Haugen, 1990; Neumann & Marks, 1990; Chou, 1991).

The largest majority of the agents used in the biological control programmes of *S. noctilio* are parasitic wasps that attack the larvae of *Sirex* (Neumann *et al.*, 1987). The most effective and widely used biocontrol agent is, however, the nematode *Deladenus siricidicola* Bedding (Neumann *et al.*, 1987; Anonymous, 1991; Bedding, 1995). This nematode has a bicyclic life-cycle, that during the one stage, feeds and reproduces on the fungus, *A. areolatum*. During another phase it infects the larvae of *S. noctilio* and eventually sterilise the adult females of the wasp (Bedding, 1995).

Despite the amount of research that the *Sirex-Amylostereum* association has stimulated in the past many misconceptions have been and are still sometimes encountered, as pointed out by Thomsen (1996) in a review of the literature. In the light of the importance of this pest complex to the softwood industries in the Southern Hemisphere and the prevailing misconceptions regarding this pest complex, the aim of this review was to summarise all relevant information about the above mentioned fungus and insect. Specific attention is

given to the occurrence and ecology of the *Sirex-Amylostereum* complex in the Southern Hemisphere. The review also considers the influences that this pest complex has had, especially in the Southern Hemisphere, and the control strategies that have been used to combat it.

2.0 DISTRIBUTION AND PEST STATUS

2.1 SIREX IN THE NORTHERN HEMISPHERE

Sirex noctilio is found throughout the temperate regions of the Northern Hemisphere and is thought to be native to Eurasia (Benson, 1943; Morgan, 1968; Spradbery & Kirk, 1978). In its native range S. noctilio is considered a secondary pest that mainly affects felled or severely stressed and damaged trees (Chrystal, 1928; Hanson, 1939; Hall, 1978). Levels of infestation by Sirex are in general kept low by natural parasites of the wasp, except in cases were other factors severely damage and stress the trees (Hall, 1978). Of all the siricid species in Europe and North Africa, only S. noctilio regularly attacks living trees and then only severely physiologically stressed, damaged or over mature dying trees (Hanson, 1939; Spradbery & Kirk, 1978). These trees often recover and may support a colony of woodwasps for an extended period of time (Spradbery & Kirk, 1978). The few severe attacks recorded from Germany and Italy, followed serious primary epidemics of defoliating insects (Spradbery & Kirk, 1978). In their native range woodwasps are, thus, viewed as natural thinning agents and as the indicators of pathological conditions, rather than primary factors in causing them (Chrystal, 1928; Cartwright, 1929).

2.2 SIREX IN THE SOUTHERN HEMISPHERE

2.2.1 New Zealand and Australia

Different species of wood wasps have occasionally been recorded from the Southern Hemisphere on imported timber or timber products (Chrystal, 1928; Morgan, 1968). Of these, only *Sirex noctilio* has successfully established itself in Australasia where it has become an economically serious pest (Neumann & Marks, 1990; Chou, 1991). *Sirex noctilio* was first reported from standing trees in New Zealand around 1900. It was found

in Tasmania in the early 1950's and on the mainland of Australia in 1961 (Neumann et al., 1987, Madden, 1988).

Sirex noctilio did not cause serious losses in New Zealand until the drought of 1946 - 1948 (Hanson, 1939; Chou, 1991). During this period, it was responsible for the devastation of many stands of *Pinus radiata* D. Don, killing approximately 30% of the trees before 1951 (Chou, 1991). Apart from this outbreak, however, New Zealand escaped further serious outbreaks.

Despite considerable investment in research, the steady spread and occasional serious outbreaks of *S. noctilio* have not been curtailed in Australia (Neumann *et al.*, 1987; Madden, 1988 & 1998b; Haugen, 1990). The ever present, but moderate damage in Australia, has frequently been interspersed with serious to very severe outbreaks. The latest of these occurred in the Green Triangle (mainland Australia), despite an established control programme. This outbreak resulted in the death of approximately 4.8 million trees before 1990 (Haugen & Underdown, 1990a; Haugen, 1990). According to Bedding (1995) *Sirex* has the potential to cause a loss A\$1-4 billion over a 30-year rotation period in Australia.

2.2.2 South America and South Africa

More recently, the softwood industries of South America and South Africa have also fallen victim to *S. noctilio* (Tribe & Cillié, 1994; Tribe, 1995a; Reardon *et al.*, 1995). Despite attempts to control the pest, *S. noctilio* spread steadily through South America from the initially point of introduction in Uruguay in 1980 (Maderni, 1998) to Argentina in 1985 (Klasmer *et al.*, 1998) and Brazil in the late 1980s (Iede, Do Rocio Chiarello Penteado & Schaitza, 1998; Reardon *et al.*, 1995). Although *S. noctilio* has not been detected in other pine growing countries in South America, it is considered the greatest threat facing the millions of hectares of exotic pine plantations, throughout this region. Countries such as Chile that grow large stands of *P. radiata*, have already implemented thorough detection and exclusion procedures (Aguilar, 1998; Poisson, 1998).

Sirex noctilio was first reported in imported wood in South Africa in 1962 (Taylor, 1962; Morgan, 1968). At this time the wasp apparently did not escape or become established in

pine plantations. In April 1994, *S. noctilio* and its fungal associate, *A. areolatum*, were reported from *P. radiata* trees in the Cape Province in South Africa (Tribe & Cillié, 1994, Tribe, 1995a; Baxter, Rong, & Schutte, 1995). It is supposed that the wasp entered the country in infected wood crates. Based on the number of exit holes in infected trees, it has been estimated that the initial introduction was at least 2 years before this report (Tribe, 1995a). During the first three seasons after the initial report, the wasp spread in a 90 km arc through the pine plantations of this region (Hinze, 1998; Tribe, 1996). Early biological control and the mountainous surroundings seemed to constrain *Sirex* to this region. Surveys in the 1997/1998 season, however, established that the woodwasp had spread to plantations more than 200km from the initial site of occurrence from were it was reported, along both the west and south coast of the Cape province (Tribe, 1997 & 1998). Currently the damage caused by the wasp is moderate. It is, however, evident that the *Sirex* woodwasp has become firmly established in South Africa. Furthermore, it is spreading at a steady rate, threatening the pine plantations of the country as a whole (Tribe, 1998).

3.0 THE INSECT-FUNGUS-TREE ASSOCIATION

Sirex noctilio and Amylostereum areolatum form an inseparable relationship in their quest for survival, which is also true for their association with Pinus spp. Their separate discussion in this review is thus artificial, but necessary to fully understand the biology of the system.

3.1 TAXONOMY AND MORPHOLOGY

3.1.1 The woodwasp

The taxonomic classification of S. noctilio as given by Neumann et al. (1987) is as follows:

Order:

Hymenoptera

Sub-order:

Sympata

Family:

Siricidae

Sub-family:

Siricinae

Genus:

Sirex Linnaeus, 1761

Species:

Sirex noctilio Fabricius, 1793

The order Hymenoptera includes amongst others, bees, wasps, ants and horntails (Chamberlin, 1960). These insects are characterised by having four membranous wings (clipped together in flight); various forms of an ovipositor (borer, saw, sting, etc.); biting, rasping or sucking mouthparts; as well as having a complete metamorphic life cycle. Included in this order is the family Siricidae under which the genera *Sirex*, *Xeris*, *Urocerus* and *Tremex* are grouped (Benson, 1943).

Certain members of the family Siricidae are easily distinguished by the distinct colour of their legs, antennae and thorax, as well as the differences in size ratios of certain body parts (Chrystal, 1928; Benson, 1943; Chamberlin, 1960). Others, like *S. noctilio, S. cyaneus* Fabr. and *S. juvencus* Linn. are, however, very similar in general appearance and are often mistaken for one another (Benson, 1943; Talbot, 1977; Thomsen, 1996). Differentiation due to geographical separation has also contributed to the confusion in classifying some of the members of the Siricidae (Benson, 1943; Cameron, 1967). The characteristics of *S. noctilio* are given in Table 1 and Figure 1.

3.1.2 The fungus

The taxonomic classification of *A. areolatum* as taken from Breitenbach & Kränzlin (1986) and Kendrick (1992) is as follows:

Kingdom:

Eumycota

Phylum:

Dikaryomycota

Sub-phylum:

Basidiomycotina

Class:

Holobasidiomycetes

Sub-class:

Hymenomycetae

Order:

Aphyllophorales

Family:

Corticiaceae

Sub-family:

Stereaceae

Genus:

Amylostereum Boidin 1958

Species:

Amylostereum areolatum (Fr.) Boidin 1958

The genus Amylostereum includes four species. Boidin described the first three, A. chailletii (Pers. ex Fr.) Boid., A. areolatum (Fr.) Boid. and A. laevigatum (Fr.) Boid. and transferred them from Stereum species in 1958 (Boidin, 1958). A fourth species thought to be associated with Podocarpaceae, A. ferreum (Berk. ex Curt.) Boid., was only described in 1984 from a collection of S. ferreum isolates (Boidin & Lanquetin, 1984) from South America.

The work of Boidin and Lanquetin (1984) is the only phylogenetic study on the genus Amylostereum. In the mating studies used by Boidin and Lanquetin (1984), A. ferreum formed hybrid mycelia with A. chailletii and A. laevigatum, but not with A. areolatum. No mating was observed in any of the other crosses. This indicates an older evolutionary delineation between A. areolatum and the A. chailletii/A. laevigatum group, with A. ferreum forming a link between the two last species, that would presumably have speciated later.

As with the Siricidae, the taxonomy of the fungi associated with these insects has been controversial. This is evident from numerous incorrect classifications in the past (Talbot, 1977; Thomsen, 1996). The fungal symbiont of *S. noctilio* in the Southern Hemisphere was first thought to be *Stereum sanguinolentum* (Albertini & Schwein.:Fr.) Fr. or at least a species of *Stereum* (Cartwright, 1929; Parkin, 1941). Later Talbot (1964) showed that the symbiont of *Sirex* in Australia is a species of *Amylostereum*, but thought that it was *A. chailletii* or a strain of this species, as did King (1966). Gaut (1969) showed that *A. chailletii* does not produce arthrospores in culture, which the *S. noctilio* fungus constantly does. By using the biological species concept and the formation of clamps in successful matings (as described by Buller, 1931) in combination with polymorphisms in protein banding patterns, Gaut (1969) could show that the fungus associated with *S. noctilio* in Australia was *A. areolatum*.

Natural fructifications of A. areolatum are rare and do not occur naturally in Australia or New Zealand (Talbot, 1964). In those countries the fungus has had to be studied entirely in culture and from intersegmental sacs of the wasp, that contains arthrospores (Talbot, 1964; King, 1966). Reasonably mature fructifications could, however, be obtained by using the

wood block culture method of Tamblyn and Da Costa (1958). This wood block method is also used by other researchers to overcome the problem of the rarity of the fruit bodies in combination with cultural studies of *Amylostereum* (Siepmann & Zycha, 1968). Studies of fructifications from wood blocks and natural fructifications, should, however, be approached with great caution as considerable differences exist between immature and mature stages (Talbot, 1964). Furthermore, the morphological characteristics of *A. areolatum* and *A. chailletii* mycelium and fruiting bodies are very similar and subject to some variation (Breitenbach & Kränzlin, 1986). The morphological characteristics of *A. areolatum* are presented in Table 2 and Figure 2, while the principal differences between *A. areolatum* and *A. chailletii* are summarised in Table 3.

Studies on the taxonomy and phylogeny of the fungal symbionts of siricids and the genus *Amylostereum* as a whole, rely on morphological characters, the biological species concept and polymorphisms in protein patterns (Boidin, 1958; Talbot 1964; King, 1966; Gaut, 1969; Gaut, 1970; Boidin & Lanquetin, 1984). It is curious, however, that despite numerous novel and powerful molecular techniques that have become available recently, no attempt has been made to substantiate the hypotheses raised by these researchers. Techniques such as PCR based sequencing and RFLP analysis have, for example, been useful in providing quick, reliable means of distinguishing different species of Basidiomycetes, as well as clarifying the phylogenetic relationships between them (Hibbett & Vilgalys, 1991; Harrington & Wingfield, 1995; Hibbett *et al.*, 1997).

3.2 ECOLOGY AND BIOLOGY

3.2.1 The woodwasp vector

Members of the family Siricidae are all characterised by a larval state which either lives in the stems of plants or are woodborers (Chamberlin, 1960; Morgan, 1968). Members of the genera Sirex, Urocerus and Xeris attack softwoods (especially conifers), while Tremex spp. attack hardwoods. Tremex is considered to be more highly evolved, due to its greater morphological reduction and the fact that it exhibits a higher form of specialisation by boring through the harder bark (Benson, 1943).

Common among the Siricidae are associations with specific wood destroying Basidiomycetes (Cartwright, 1929; Francke-Grosmann, 1939; Stillwell, 1964; Morgan, 1968). The only exception is the genus *Xeris* which is thought to parasitise wood already infected by other wasps and their associated fungi (Francke-Grosmann, 1939; Morgan, 1968; Spradbery, 1977). Conidia (oidia) or bundles of fungal mycelium are carried in a pair of special intersegmental pouches (mycangia) near the base of the ovipositor of the adult female and in external hypopleural organs by the female larvae (Buchner, 1928; Francke-Grosmann, 1939; Parkin, 1941). The fungus is then inoculated into the wood together with the eggs during oviposition. It is hypothesised that this fungal inoculation is instrumental in the subsequent development of the larvae (Madden & Coutts, 1979; Madden, 1981).

Gaut (1970) showed conclusively that the symbiosis between certain siricid and fungal species are always species specific. Certain fungal species are, however, carried by more than one siricid species. He found *A. areolatum* to be the symbiont of *S. noctilio*, *S. juvencus* and *S. nitobei*, while *A. chailletii* is carried by *S. cyaneus*, *S. imperiales* Kirby, *S. areolatus* Cress., *S. californicus* Ashmead, *Urocerus gigas* Linn., *U. augur augur* Klug. and *U. augur sah* Mocs. With the difficulties in the taxonomy of the Siricidae, this specific symbiosis can serve as a useful taxonomic character (Talbot, 1977).

Life cycles of siricid woodwasps vary from one to three years in length. In the cooler Northern Hemisphere, life cycles commonly span over two to three years (Hanson, 1939; Morgan, 1968; Spradbery & Kirk, 1978). In Australasia, however, the majority of *S. noctilio* wasps complete their life cycle in one year (Taylor, 1978; Neumann & Minko, 1981). Some even emerge after two and a half to three months, while it is reported that less than 10% undergo two-year cycles (Taylor, 1978; Neumann & Minko, 1981).

In the Southern Hemisphere adult *S. noctilio* wasps emerge between mid-summer and mid-autumn after which mating takes place, trees are attacked and eggs are laid (Neumann *et al.*, 1987; Neumann & Minko, 1981). It is reported that males tend to emerge before females and to also outnumber them in natural populations (Morgan, 1968). The life span of adult wasps vary with climatic conditions, being shorter in summer and longer (± two weeks) in the cooler autumn (Neumann *et al.*, 1987). The average life span for a female is

five days and approximately 12 days for male wasps (Neumann *et al.*, 1987). Emerging adults are sexually mature and mating directly follows emergence in the upper branches of trees after a mating ritual (Chrystal, 1928; Morgan, 1968).

Mating appears to be enhanced by sunny conditions, temperatures above 21°C and the greater ratio of males to females (Neumann *et al.*, 1987). The *S. noctilio* female is also facultatively parthenogenic and capable of ovipositing before mating. The eggs produced in this manner will develop into haploid male wasps. This phenomenon was first observed by Peacock & Gresson (1931) for *S. cyaneus* and for *S. noctilio* by Rawlings (1953) and is thought to be common among Siricidae (Morgan, 1968). It is possible that this may in part explain the predominance of males in the natural populations.

Siricids have a very complex oviposition behaviour that is specific to each genus (Spradbery, 1977). Sirex noctilio has a short ovipositor (average of 12.4 mm) compared to other Siricids and spends a shorter time drilling (average 9.4 min), which accounts for the shallower drill that just reaches the xylem (Spradbery, 1977). The number of eggs carried by a female depends on her size and varies from 30 to 450 (Madden, 1974). This will influence the amount of oviposition drills made by the female wasp (Madden, 1974). Neumann et al. (1987) calculated that the average annual reproductive potential of one fertilised female is ± 53 females.

A number of drills are made by a female as she moves up the stem from base to top and back down again. Each drill is evaluated on an individual basis for its potential of sustaining the eggs and larvae (Madden, 1974). In regions of high osmotic pressure only the first hole is made. This is filled with mucus and oidia of the fungus, possibly conditioning the tree for later attack (Madden, 1974; Madden & Coutts, 1979). As the osmotic pressure in the phloem decreases, more holes are drilled through the same entry (up to five), each containing fungal material and eggs, except the last hole of the site that contains only mucus and fungal spores (Coutts & Dolezal, 1969 cited in Madden, 1974).

The eggs that have been laid will generally hatch within two weeks of oviposition, but this period could be longer in cooler weather and shorter in warmer weather (Madden, 1981).

Given suitable conditions (intimately related to successful establishment of its fungal symbiont) the larvae develop and start burrowing principally along the grain of the wood, later turning inwards towards the heartwood (Hanson, 1939, Madden, 1981). During this time (in a one year life cycle) the larvae go through six or seven instar phases, turning to the outer sapwood, just under the bark before pupation in late Spring or Summer (Neumann *et al.*, 1987). The total length of the burrows from where the eggs were laid to the pupation site, could eventually range from five to 26 cm in length.

The female larvae from the second instar onwards acquires the fungus by scraping against it on the walls of its borrow (Parkin, 1941). The fungal arthrospores are stored in a waxy matrix in deep skin folds (hypopleural organs) on both sides, between the first and second abdominal segments (Parkin, 1941). The waxy pockets will preserve the fungal spores, should the fungus in the wood die prematurely (Gilmour, 1965). These hypopleural organs are shed during molting to the pupal form which, therefore, does not contain any fungal spores. Francke-Grosmann (1957) hypothesised that abdominal movements made while boring out of the wood, moves the waxy pockets containing fungal spores up the outside of the ovipositor and through the vaginal openings to the internal mycangia. Here, proliferation of the fungus is stimulated by special glandular secretions within the mycangial walls, until the mycangium is filled with short hyphal filaments and arthrospores (Gilmour, 1965).

3.2.2 The fungal symbiont

In a review by Gilmour (1965) the life cycle of A. areolatum and its association with S. noctilio has been divided into three sections and will be discussed as such here.

Adult female - tree stage The main means of dissemination of this fungus and its infection of the host tree is by inoculation by *S. noctilio* females (Gilmour, 1965). As noted earlier, oidia or small mycelial fragments are carried in paired intersegmental sacs at the base of the ovipositor (Buchner, 1928; Francke-Grosmann, 1939; Parkin, 1941). These mycangia are connected via a duct to the tube down which the egg moves during oviposition. Eggs are never laid without also introducing these fungal cells, while arthrospores and mucus are introduced alone in unsuitable hosts (Madden, 1974; Madden & Coutts, 1979). The reason for this becomes evident from the fact that the larvae of the wasp do not develop if the

fungus does not become established in the wood (Francke-Grosmann, 1939, Gilmour, 1965). Resistance of the tree to attack, which is correlated to resinosis, fungistatic volatiles and moisture content of the wood, therefore, centres around inhibition of fungal growth (Madden & Coutts, 1979). The benefit to the fungus is evident in that it is placed deep in the wood of suitable hosts where these factors are impaired (Madden, 1974). It is also speculated that growth of the fungus in the wood might also be stimulated by the glandular secretions of the insects (Talbot, 1977).

Amylostereum areolatum mainly reproduces by asexually formed arthrospores that are spread by the woodwasp vector. This results in large clones or vegetative compatibility groups that are maintained in the fungal population (Vasiliauskas, Stenlid & Thomsen, 1998; Slippers, 1998; Thomsen & Koch 1999; Vasiliauskas & Stenlid, 1999) (Chapter 2). These clonal lines have been shown to be spread over considerable distances and to be preserved over long time spans (Slippers, 1998, Thomsen & Koch, 1999; Vasiliauskas & Stenlid, 1999). This property could be very useful in tracing the origin and spread of S. noctilio throughout the world by comparing the VCG's of its associated fungus from different geographical regions.

Tree - larval stage It is at this stage that the fungus plays its most critical role in the mutualism. Larvae of *S. cyaneus* have been shown to live for three months on fungal cultures (Cartwright, 1929). This showed that they are at least partly mycetophagous, with the mycelium presumably being digested extra-intestinally (Morgan, 1968). The sparseness of the mycelium in the wood, however, suggests that both the fungus and the wood (after decomposition) contribute essential nutrients to the larval diet (Francke-Grosmann, 1939; Cooke, 1977; Madden & Coutts, 1979). Indigestible cellulose and lignin is converted into more readily digestible forms for the insect. The rotting of the wood at the same time facilitates burrowing of the larvae (Madden & Coutts, 1979). Kukor and Martin (1983) and Martin (1987) showed that the larvae of *S. cyaneus* acquire essential digestive enzymes, such as cellulases and xylanases, by ingesting the fungal mycelium. The activity of the fungus is also essential in creating a suitable developmental microniche for the eggs by drying out the sapwood, thus reducing the intensity of the tree's response to attack (Madden & Coutts, 1979).

The female larval stage of *S. noctilio* possess fungus-carrying organs in the form of paired hypopleural sacs (Parkin, 1941). These organs are situated on the outside of the body and are quickly filled with scrapes of mycelium and arthrospores. Here the fungal spores are coated in a protective wax like material (Gilmour, 1965). This serves to preserve the fungus, and is important should the fungal mycelium in the wood die due to desiccation or other factors.

The larval - pupal - adult stage The pupae do not appear to have any special organ for carrying the fungus (Parkin, 1941). Francke-Grosmann (1957) suggested that the adult only acquired the fungus when the pupal skin is shed and the female starts to leave the wood. The shrivelled larval and pupal skins remain attached to the ovipositor of the adult until emergence. The ritual movement of the abdomen as the wasp starts boring out, breaks up the wax pockets containing the fungal spores. The alternating movement of the two halves of the ovipositor causes these sticky wax pockets to move up the outside of the ovipositor, through the genital opening and into the intersegmental sacs. Here, glandular secretions stimulate growth of the fungal cells (Gilmour, 1965; Talbot, 1977). The mycangia subsequently become packed with arthrospores as the growing cells become pressed for space and nutrients (Gilmour, 1965).

As a saprophyte remaining in the tree after emergence of the wasp, *A. areolatum* can fruit and theoretically also spread by means of basidiospores. In the Southern Hemisphere this has, however, not been observed and despite some persistence, it is eventually replaced by other colonisers and decomposers (Vaartaja & King, 1964b). In the Northern Hemisphere fruiting does occur, although (especially in the case of *A. areolatum*) not very frequently (Thomsen 1993; Thomsen & Koch, 1993; Thomsen, 1998). *Amylostereum chailletii* (referred to as *S. chailletii*) has also been reported as an early colonist of cut or damaged ends of stumps or wood blocks (Basham, 1959; Etheridge & Morin, 1963). The influence of insects in these cases is, however, difficult to rule out entirely.

3.3 PATHOGENICITY

As stated earlier *Sirex* is considered to be a secondary pest of little economic importance in the Northern Hemisphere, while it has caused extensive tree mortality and economic loss in the Southern Hemisphere. This higher aggressiveness, and reason why only *S. noctilio* has become established, has been ascribed to a combination of factors. Firstly, *S. noctilio* is almost always confined to *Pimus* spp. that are present in millions of hectares of exotic monocultured plantations in the Southern Hemisphere, while other siricids rarely infest pines (Spradbery & Kirk, 1978 & 1981). Furthermore the annual life cycle and bioclimatic preferences of *S. noctilio* provide a greater potential for population increases in the Southern Hemisphere, than other siricid species (Hanson, 1939; Kirk, 1974). *Sirex noctilio* is, for example, most commonly found as a native in Mediterranean climates that are also common in the Southern Hemisphere (Kirk, 1974). In the Southern Hemisphere, periods of prolonged drought are also much more frequent than in the Northern Hemisphere. This provides more drought-stressed trees that are especially susceptible to attack by *S. noctilio* (Kirk, 1974; Spradbery & Kirk, 1978).

In Europe, *S. noctilio* emerges latest of all the siricid species (during autumn and early winter) (Spradbery, 1973; Spradbery & Kirk, 1978). In Australia, emergence peaks are from January - March (summer months) and also over a shorter period than in the Northern Hemisphere (Neumann *et al.*, 1987). This results in a higher number of adult wasps, and thus the number of attacks, per time section. Furthermore, it has been shown that the susceptibility of *P. radiata* is subject to seasonal variation, being greatest in summer and least in autumn and winter (Spradbery, 1973; Kile *et al.*, 1974) (see 1.3.4.2). These factors, together with the general absence of natural parasites of *Sirex* probably enabled *S. noctilio* to adapt to its new environment more effectively.

Of all the siricid species, only *S. noctilio* regularly attacks living trees (Spradbery, 1973; Spradbery & Kirk, 1978). The *S. noctilio* mucus also induces a drastic physiological change in the stem and foliage of trees. The mucus of other siricids, however, only induces a mild or absent reaction in the plants (Spradbery, 1973). The mucus reservoir, which is

connected via a duct to the ovipositor, is also markedly larger in S. noctilio than those found in other siricid species (Spradbery, 1977).

Inoculation of *S. noctilio* mucus into *P. radiata*, induces drastic change in the physiology of the stem and foliage within weeks and thus accounts for the early symptoms of attack. This includes a dramatic reduction in radial growth, serious chlorosis and loss of needles, increased respiration and a reduction in leaf pressure (Coutts, 1969b; Spradbery, 1973; Fong & Crowden, 1973 & 1976) (Figure 3). This activity of the mucus conditions trees for fungal growth, while presumably at the same time stimulating the fungal growth in the wood (Gilmour, 1965, Talbot, 1977). No differences were found in physiological activity of mucus from female wasps from Europe and Australia (Spradbery & Kirk, 1978). When the mucus was inoculated in trees together with *A. areolatum*, however, only one tree died in the trial in England, whereas all the trees in a similar experiment in Australia died (Coutts, 1969a & b; Spradbery, 1973). The only difference between these experiments was that the seasons differed.

Amylostereum areolatum is considered to be a weak facultative pathogen unable to establish itself and kill living trees. It is probably best described as a saprophyte and wood rot fungus (Vaartaja & King, 1964a & b; Gilmour, 1965; Coutts, 1969a). However, once the resistance of trees is broken down by the action of the mucus, A. areolatum grows slowly through the wood, in the end killing and drying out the sapwood (by causing a firm dry white rot) enough locally as to render it non-conducting (King, 1966; Coutts, 1969a). Multiple attack all around the stem thus amounts to many overlapping dry sapwood zones, which cause a girdling effect (restricting sap supply to the crown) that will eventually kill the tree (Coutts, 1969a) (Figure 3). This is similar to the way that certain blue-stain fungi (Ophiostoma spp. and Ceratocystis spp.) carried by bark beetles are thought to kill trees (Caird, 1935). Trees often die within two months of attack, but this period is determined by the season and the number of attacks recorded (King, 1966). In such a killed tree the combination of the advancing dry white rot and the boring activity of the larvae could then render the wood worthless within six months (Neumann & Marks, 1990).

3.4 THE HOSTS

3.4.1 Different hosts

The hosts of S. noctilio and A. areolatum include all species of Pinus, as well as species of Abies, Larix, Picea and Pseudotsuga menziesii (Mirb.) Franco (Browne, 1968; Spradbery & Kirk, 1978; Gibson, 1979). In its native range the wasp prefers Pinus spp., and also standing rather than felled timber (Spradbery & Kirk, 1978 & 1981). Pinus pinaster Aiton appears to be the most attacked host tree in the native range of the wasp, but in New Zealand and Australia S. noctilio has successfully colonised P. radiata as the main host (Spradbery & Kirk, 1978). This is probably due to the overwhelming abundance of stands of this pine species in Australasia (Ray et al., 1979; Anonymous, 1991; Chou, 1991).

South America (except Chile) and South Africa both have large *P. radiata* plantations, but this species is planted less commonly as main softwood source than in Australasia. In South America and South Africa other species of pine planted are also affected by the pest complex (Poynten, 1977; Anonymous, 1993; Aguilar, 1998; Iede *et al.*, 1998, Maderni, 1998). In South America *P. taeda* appears most affected by *S. noctilio*, while *P. pinaster*, *P. patula* Schlechtend. & Cham., *P. radiata*, *P. elliottii* Engelm., *P. echinata* Mill., *P. palustris* Mill., *P. halepensis* Mill. are also attacked, albeit at various levels of intensity (Iede *et al.*, 1998; Maderni, 1998). Species such as *P. elliottii*, for example, appears more resistant to attack (Maderni, 1998). In South Africa, *P. canariensis* Chr. Sweet ex Spreng, *P. elliottii*, *P. patula*, *P. pinaster*, *P. pinea* L. and *P. radiata* have all been confirmed as hosts of *S. noctilio* (Tribe, 1995a & 1996).

3.4 2 Host selection and susceptibility

There is evidence that *S. noctilio* is, as is the case with other phytophagous insects, attracted to suppressed, drought-stressed or nutritionally deprived trees. (Chrystal, 1928; Stillwell, 1960; Thorsteinson, 1960; Madden, 1968b & 1971; Spradbery, 1973; Hall, 1978; Spradbery & Kirk, 1978 & 1981; Moeck, Wood & Lindahl, 1981). The timing and duration of attractiveness of the trees largely depends on the extent and persistence of the stress condition (Madden, 1968b & 1971; Spradbery & Kirk, 1978 & 1981).

Damage due to man-made forces, for example volatiles from freshly felled logs or wounds, encourage attack (Madden, 1968b & 1971; Simpson & McQuilkin, 1976a & b). Biological damage to the tree often plays a role in attracting *S. noctilio* wasps to a specific tree (Chrystal, 1928; Hanson, 1939; Stillwell, 1960; Hall, 1978; Spradbery & Kirk, 1978). It has also been reported that trees killed by other pathogenic fungi such as *Armillaria* are often attacked (Spradbery & Kirk, 1978). Trees previously attacked by bark beetles (notably *Ips* species), defoliating insects or other wasps were also found to be of accentuated interest to siricid females (Spradbery & Kirk, 1978). Attack by some fungal species (such as *Trichoderma* and blue stain fungi) seem to inhibit oviposition (Spradbery & Kirk, 1978). This is possibly due to the fact that the wasps' fungal symbiont would not be able to compete under these circumstances. The age of a tree appears to be less important than its condition for making it attractive for attack by *Sirex* females (Neumann *et al.*, 1987). However, older moribund trees are often very prone to attack (Spradbery & Kirk, 1978).

Climatic conditions play an important role in severity of attack by the wasps. In the Southern Hemisphere, adult wasps tend to emerge over a shorter period of time during the warm, sunny seasons than in the Northern Hemisphere, were emergence is in the cooler autumn weather (Spradbery & Kirk, 1978). This brings about a higher number of wasps, and thus number of attacks, in a given time period in the Southern Hemisphere than is the case in the Northern Hemisphere. This coincides with a reduction in growth and an increase in resistance in the pine trees in Europe and the opposite scenario in Australasia (Spradbery, 1973; Spradbery & Kirk, 1978). This could in part explain the increased incidence of death of trees in the Southern Hemisphere due to *Sirex* attack, compared to the Northern Hemisphere.

The physiological condition of trees plays an important role in their resistance or attractiveness to siricids. Moisture and lipid content of trees are significant factors that are involved in the interaction. *Sirex noctilio* has, for example, been shown to be attracted to trees with lower moisture content and generally oviposits in parts of the tree with a low osmotic pressure in the phloem (Madden, 1974; Spradbery, 1977). Many volatiles such as monoterpenes, ketones and alcohols, that are components of the bark oils produced by the phloem-cambium tissues of pine material, also serve as attractants to siricid wasps

(Simpson & McQuilkin, 1976a & b; Madden, 1977). Damage to the tree leads to higher transpiration and phloem respiration, which results in lower osmotic pressure in the phloem, as well as larger amounts of bark-oil volatiles (Madden, 1977). These changes both attract and benefit the wasp and its fungal symbiont. Resin streaming from wounds or oviposition punctures is also regarded as an attractant for siricid females, but contrary to this, resinosis is also considered to be an important resistance mechanism (Madden, 1968b; Spradbery, 1973; Coutts & Dolezal (1966) cited in Talbot, 1977).

Resistance is related to the ability of the tree to maintain high moisture content in its phloem; produce less of certain lipids and exude enough resin in and around the oviposition hole as to inhibit fungal growth (Madden, 1968b & 1974; Vaartaja & King, 1964a; Spradbery, 1973; Spradbery & Kirk, 1978). In resistant trees a layer of polyphenols is laid down around the oviposition drill to inhibit fungal growth chemically (through α - and β -pinenes) (Spradbery, 1973). Resin then accumulates around this layer of polyphenols and further inhibits the fungus physically by engulfing the mycelium (Spradbery, 1973). Fong and Crowden (1973) also showed that a hypersensitive reaction in the foliage in response to the mucus could be correlated to resistance. The tree presumably rids itself of the mucal effects by discarding the affected needles.

Ethylene production is higher in resistant trees, and although it is not thought to be directly involved in resistance, it might be a useful parameter in breeding for disease resistance (Shain & Hillis, 1972). Despite signs of genetic resistance in certain pine trees to *S. noctilio*, attempts to breed for this trait have, however, not been successful (Simpson & Ades, 1990). This is mainly due to the long process involved in the breeding process (attack is uncommon in trees less than 9 years old) and the loss of initial material due to a forest fire (Simpson & Ades, 1990). Simpson and Ades (1990), however, call for renewed attempts to identify and breed for *P. radiata* trees resistant to attack by the *Sirex-Amylostereum* complex.

4.0 MANAGEMENT IN THE SOUTHERN HEMISPHERE

4.1 CHEMICAL CONTROL

Insecticides have been shown to be ineffective in *Sirex* control (Talbot, 1977; Spradbery & Kirk, 1978; Murphy, 1998a). According to these researchers this is due to the fact that *Sirex* adults are short-lived and do not feed. Furthermore, the larvae burrow deep in the wood of host trees. The only useful possibility is using insecticides on salvaged logs to prevent breeding in this attractive niche.

The dependence of the larva on A. areolatum also raises the possibility of using fungicides in the control programmes. Dispersal of these chemicals through the wood, however, proved to be insufficient (Talbot, 1977). Furthermore, volatiles produced by Amylostereum (possibly acetaldehyde), as well as by Saccharomyces sp. found in the oviposition holes, serve as attractants for some of the parasitoids of Sirex (Madden, 1968a & 1975a; Spradbery, 1970 & 1974). Killing these fungi would thus reduce the efficacy of these natural parasites. Programmes to breed for resistance in the trees have also not been successful. Biological control with natural enemies of Sirex thus presents the most viable method of managing this pest complex.

4.2 BIOLOGICAL CONTROL

4.2.1 Parasites of Sirex

Much research has been done on natural enemies of siricids in an attempt to control *Sirex* in areas where it has become established without them. Birds are important predators in some areas (Marshall, 1967), but their effect in large-scale control is doubtful (Chrystal, 1928; Hanson, 1939). Insect parasitoids (notably parasitic wasp species) hold much more promise. *Rhyssa persuasoria* Linnaeus was brought to New Zealand as early as 1928 and this was followed by the introduction of *Ibalia leucospoides* Hochenwarth (Hanson, 1939; Gourlay, 1951). These parasitoids did not pose a sufficient threat to *Sirex*, as was shown by the outbreak of 1946-1948. Other insect parasitoids were introduced over time and today seven are reared and released annually in Australasia (Taylor, 1967; Neumann *et al.*, 1987).

These include *Ibalia ensiger* Norton, *I. leucospoides*, *Megarhyssa nortoni nortoni* Cresson, *M. nortoni quebencesis* Provancher, *Rhyssa hoferi* Rohwer, *R. persuasoria* and *Schlettererius cinctipes* Cresson.

Most of the parasitic wasp species released as biocontrol agents have been shown to respond positively to the volatiles produced by the associated fungi, which would thus help them locate larvae of *Sirex* (Madden, 1968a & 1975a; Spradbery, 1970 & 1974). Species of *Megarhyssa*, *Rhyssa* and *Schlettererius* are lethal to late instar larva of *S. noctilio* (Hanson, 1939; Neumann *et al.*, 1987). After location, these insects bore down to the *Sirex* larvae, paralyse them, lay their eggs on them and subsequently develop first as endoparasitic and later as ectoparasitic larvae. In contrast, *Ibalia* species lay their eggs down the original oviposition hole of *Sirex* where its larvae then parasitise on the early instar larvae of *Sirex* before killing the more mature larvae.

The nematode, *Deladenus siricidicola* Bedding, found in 1962 by Zondag in New Zealand has proved to be the most successful biological control agent (Zondag, 1969). Of the seven species of *Deladenus* that parasitise siricids, *D. siricidicola* was found to be the only one that would feed on *A. areolatum* and not also parasitise *Rhyssa* spp. (Bedding, 1968 & 1995). The action of this nematode is through sterilisation of the female wasps, but without impairing their natural fitness and oviposition behaviour (Bedding, 1967 & 1972). This also counts in favour of its effectiveness as it facilitates the spread of the nematode to other trees possibly containing still uninfected wasps.

4.2.2 Biological control in Australasia

Use of different parasites, and especially *D. siricidicola*, in New Zealand, Tasmania and Australia, as biocontrol agents against *Sirex* has been the subject of extensive study. Much is to be learnt from the mistakes that were made in the control strategies implemented in these countries. Extensive releases of various biocontrol agents have characterised recent control programmes in Australia. Reviews of their use and effectivity in Australasia are given by Taylor (1967 & 1978), Neumann *et al.* (1987), Haugen (1990), Haugen and Underdown (1990a & b), the National Sirex Control Strategy – Operations worksheets of

Australia (Anonymous, 1991), Madden (1998b) and Murphy (1998b & c). Information is summarised in this section.

Among the insect parasitoids, *Ibalia* spp. have been the most successful in establishing and spreading after introductions, as well as recording high incidence of attack on *Sirex*. *Megarhyssa* spp. has also established well, but rates of parasitism were lower. The two *Rhyssa* spp. that have been used, did not establish well. Despite repeated introductions, parasitism has been disappointing. *Schlettererius cinctipes* and *Certonotus tasmaniensis* (an insect parasitoid native to Australasia) proved difficult to breed in captivity and accounts for a much smaller part in the biocontrol programmes. In combination the named parasitoids usually do not kill more than 40% of a *Sirex* population and are, therefore, not considered sufficient to control *Sirex* on their own.

By far the most effective biocontrol agent has been *D. siricidicola*. Since its discovery in the North and South Islands of New Zealand, much research has been conducted on its control (Zondag, 1969, 1971 & 1979). Since then methods have been improved to an extent where identified build-ups of the wasp can be brought under control in a few years (Neumann *et al.*, 1987; Bedding, 1995).

Various methods have been attempted in an effort to introduce *D. siricidicola* in the field. Zondag (1971) found introduction of already infected logs throughout the affected plantation to be the most effective. Emerging wasps would then spread the nematode to other trees. The use of trap trees, made attractive to *Sirex* wasps by physical damage, was the next step (Madden & Irvine, 1971). This was an improvement, but proved very labour intensive. Strategically placed groups of trap trees treated with Dicamba herbicide proved to be more effective (Neumann *et al.*, 1982; Neumann & Morey, 1984). It was further shown that maintaining the trap tree system over two seasons improved parasitism even further. Presently, a combination of random inoculation of trees, naturally infested with *Sirex*, and the trap tree system is used in Australia. As a medium for inoculating the nematodes into the chosen trees, gelatin solutions are the most successful (Bedding & Akhurst, 1974). This method results in good survival and establishment of the nematodes

as this overcome problems of starvation due to desiccation, the lack of aeration and migration from the medium.

By using the techniques described above, *Sirex* infections by *Delademus* were brought to rates of almost 100% in inoculated trees (Bedding & Akhurst, 1974). Due to the development of a non-infective strain and incomplete release strategies, these rates where drastically reduced in later years (Bedding, 1995). Mistakes made in planning the releases in the Green Triangle had disastrous effects. Continuous monitoring of *Sirex* spread and population build-up, as well as parasitoid and *D. siricidicola* establishment in areas of release, is essential in the control programme. Inoculations need to be done promptly at the advancing front of the *Sirex* infestations and then through adequately proportioned, carefully planned and well monitored programmes. In areas where these measures were followed strictly and good silvicultural practices implemented, *S. noctilio* numbers were successfully reduced to very low and insignificant economic levels.

4.2.3 Biological control in South America and South Africa

Biological control of *Sirex* in South America and South Africa is still in its infancy. The similarity to the Australasian situation and the depth of experience pertaining to this field has, however, contributed to establishment of biological control programmes rapidly after the detection of the pest complex in these regions.

From the reviews given by Filho, Iede & Do Rocio Chiarello Penteado (1998), Iede et al. (1998), Klasmer et al. (1998) and Maderni (1998) the following summary can be given for the state of biocontrol in South America up to 1996. The parasitoid *Ibalia leucospoides* was apparently introduced to South America with *Sirex* and subsequently spread with the pest complex through Uruguay, Argentina and Brazil. Natural parasitism rates of *Ibalia* on *Sirex* in Brazil are reported to be between 20% and 40% depending on the season, which correlates well with the parasitism rates obtained in Australasia. In an attempt to support the spread and parasitism by the *Ibalia* wasp they are also reared in captivity and released in areas where the parasitoid is absent or its population levels are low. This will, however, not be sufficient to control *Sirex* population build-up and eventually, serious occurences, as have been seen in Australasia will occur (Anonymous, 1991).

The parasitic nematode, *D. siricidicola*, was imported to South America from Australia in the late 1980's and although initial parasitism rates were low, high parasitism levels of up to 70% have since been recorded in Brazil. *Rhyssa persuaria* and *Megarhyssa nortoni* were also imported and released in 1996 and 1997, respectively, in Brazil. A further component of management of *Sirex* in South America is extensive surveys to monitor the spread of *Sirex* (especially through the use of herbicide treated trap trees) throughout this region and assessment of the damage caused by it. The fear of *Sirex* reaching the exclusive stands of exotic *P. radiata* in Chile, has also lead to extensive programmes for its exclusion (Aguilar, 1998; Poisson, 1998). Regular surveys are, for example, made in areas where introductions are likely to take place, such as at ports and boarder roads, as well as areas of arrival or movement of imported goods within wooden containers.

Deladenus siricidicola was imported into South Africa from Australia immediately after detection of the wasp, and the first releases were made as early as 1995 (Tribe, 1995a & b). Parasitism rates by the nematode were low during the first season after release, but steadily increased (23% - 1995/1996; 54% - 1996/1997; 94% - 1997/1998) (Tribe, 1996; Dr. G.D. Tribe, personal communication). These rates, however, only represent results from the initial plantation where the nematode was released, and results from other plantations where Sirex now occurs (even <5km away) show low or no parasitism (Dr. G.D. Tribe, personal communication). Control through natural spread of the nematode will thus not be sufficient to control Sirex throughout its distribution range and continual monitoring, evaluation and release of the parasite in new areas will thus be necessary. Ibalia leucospoides were imported from Uruguay in 1998 and is ear-marked to be released early in 1999 (Tribe, 1998). According to Dr. G. Tribe, the parasites Megarhyssa nortoni and Rhyssa persuasoria will also be imported (Tribe, 1998). Surveys to monitor the spread of Sirex are also undertaken regularly (Tribe, 1996, 1997 & 1998).

4.2.4 Biology and culture of Deladenus siricidicola

Deladenus siricidicola has been shown to possess a bicyclic life cycle (Bedding, 1967 & 1972) (Figure 1). Extensive reviews of the biology of *D. siricidicola* are given in Bedding 1984, 1993 and 1995 and are summarised here as follows:

A free-living cycle in the tree, where the nematode feeds on *Amylostereum* sp., is in the mycetophagous form. This is also the cycle where oviparous reproduction of the nematode occurs. Mating takes place between mycetophagous females and males that contain large amoeboid macrospermatozoa. The female lays 50-500 eggs in the tracheids, resin canals and *Sirex* galleries. The eggs may hatch within hours of being laid, depending on the moisture content of the wood (optimal being 50 % moisture content). Juvenile nematodes feed on the fungus and may develop in either of the two phases, depending on environmental stimuli. The free-living cycle can prevail indefinitely and ensures that millions of nematodes develop in the host trees. This is very important in the effectiveness of the nematode considering the large area of a tree to be efficiently invaded in order to locate a host insect. This cycle is also extensively used in mass rearing of the nematode for field liberations.

The parasitic cycle includes the phase of the life cycle of the nematode where larvae of S. noctilio are parasitised. This cycle may originate either from eggs laid by the mycetophagous female or from the progeny of infective females. Development of young nematodes arising from either of the two forms is governed by environmental conditions. It is thought that high CO_2 levels and a low pH induces the change from mycetophagous to infective forms. This change occurs early in the development of the juvenile and the resulting two forms differ sufficiently in morphology and ecology to be placed in separate families.

Infective nematode females are fertilised by male nematodes similar to those mating with mycetophagous nematode females, except that they possess microspermatozoa. The fertilised adult nematodes bore into the *Sirex* larvae, leaving small black dot-like entry scars. Here the nematodes passively feed through microvilli on its surface, growing tremendously in this time. Towards pupation of the *Sirex* larva, thousands of juvenile nematodes are formed and released viviparously into the haemocoel of the pupa, from where they migrate to the ovaries or testes. In female hosts, egg production is reduced and those that are produced are filled with 100-200 nematodes. Even though the testes of male insects become filled with nematodes, they are not sterilised. These nematodes are not transmitted during copulation and die together with the adult male wasp. Other than for

sterilisation, the insects are unaffected by the invasion of nematodes and oviposition commences as usual. Eggs of the wasp containing nematodes are thus placed in trees, where free-living nematode cycles may again follow and develop into infective forms which, once again attack the young larvae of uninfected wasps.

Culturing *D. siricidicola* is done using the methods provided by Bedding and Akhurst (1974). With these methods, the nematodes are reared on PDA agar plates containing a culture of *A. areolatum*. The nematodes are also stored on these plates at 5 – 6 °C. For mass rearing the PDA plate cultures are then used to inoculate flasks containing wheat. It is possible to maintain the nematode on *A. areolatum* cultures indefinitely and this was the method used earlier (Bedding & Akhurst, 1974). This method, however, necessitates continual sub-culturing which forces the nematode through repeated mycetophagous generations and eventually selects for strains that rarely form the infective stage (Bedding, 1995). This became a problem in Australia and reisolation of wild strains had to be done from the field sites were the original nematodes were released (Bedding, 1995). One alternative method of storing is in liquid nitrogen that would make indefinite preservation of the genetic integrity of the infective strains possible (Bedding, 1995).

4.3 THE INTEGRATED MANAGEMENT APPROACH

From past outbreaks of *Sirex*, and damage assessments, it is evident that good silvicultural practices and knowledge of the pest, are essential in control (Ray et al., 1981; Neumann et al., 1987; Madden, 1975b & 1988; Haugen, 1990). In previous sections of this review, it has been shown that *Sirex* has a definite preference for suppressed and unhealthy trees. Attack levels have been shown to be higher in overstocked and unhealthy plantations and mortality is higher in damaged, malformed or dominated trees with a smaller diameter at breast height, than surrounding trees (Neumann et al., 1987; Maderni, 1998). In healthy, well managed plantations the impact of *S. noctilio* is usually reduced to a secondary problem, and costly eradication campaigns and losses in production are prevented (Neumann et al., 1987; Chou, 1991). In these cases, *S. noctilio* aids in the natural propagation and spread of biocontrol agents, as well as in removing unwanted trees. A good example of the opposite situation can be found in the Green Triangle of Australia

established itself in many regions of the Southern Hemisphere. It is highly probable that it will spread to unaffected areas. Better understanding of the pest complex as a whole will also lead to more effective control of *Sirex*.

In the Southern Hemisphere less research has, however, been done to understand the *Amylostereum* symbiont of *S. noctilio* than was done for the insect itself. The studies contained in this thesis thus contribute important information to enhance our understanding of the pest complex as a whole, which is important to ensure the health of pine plantations for the future.

6.0 REFERENCES

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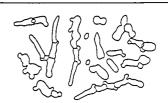
Table 1: Morphological characteristic of *Sirex noctilio* as described by Benson (1943) and Neumann *et al.* (1987).

	ADULTS			
	MALES	FEMALES		
General	Metallic dark-blue	Metallic dark-blue		
colouration				
Ovipositor	None	Saw-tipped, needle-like ovipositor		
		Straight, heavy and with average		
		length of 13.5 mm		
Sawsheath	None	Encasing ovipositor		
		Projects 2-3 mm behind female abdomen		
Antennae	20 flagellar black coloured segments			
Antennae	Average length of 6.8 mm	Average of 7.8 mm in length		
	Hair-like and slightly pubescent in colour Sensory patches on all segments			
Legs	Hind legs thick and powerful and	All legs relatively thin and amber		
6-	metallic dark-blue colour	coloured		
	Front and mid-legs thin and			
	chestnut brown			
Wings	Chestnut brown	Amber coloured		
	4 membranous wings, clipped together in flight			
Abdomen	Metallic dark-blue, except segment	All segments metallic dark-blue		
	III and IV that are chestnut brown			
	Terminates in prominent spine (vercus)			
General	Neumann et al. (1987), found the male and female to be on average about			
		les are often seen smaller		
	-	a higher ratio to females		
	EGGS			
General		White, soft, smooth and elongate		
Size	Mean length of 1-1.5 mm and width of 0.2-0.3 mm			
	Egg length increases with female size			
	LARVAE			
Colour	Creamy white			
General	Deeply segmented, distinctly S-shaped and near-uniform diameter			
Antennae	One-segmented Torminates in deals brown to block solorestic spins			
Abdomen		Terminates in dark brown to black sclerotic spine		
Legs		Thoracic and short		
Sexes	Males, on the first abdominal segment, contain 3 small brown sclerites the ventral surface, while females only have two			
PUPAE				
Canaval	Creamy white, later assuming colour of adult			
General	Creamy write, later a	assuming colour of adult		

Table 2: The morphological characteristics of *Amylostereum areolatum* as described by Talbot (1964) and summerised by Breitenbach & Kränzlin (1986).

SPORES IN MYCANGIUM OF SIREX NOCTILIO

- Fragmented mycelium in irregular shaped segments
- · Septa separating oidia are clamped
- · Clamps remain on end after break-up



AGAR CULTURE

- Generative hyphae
 Branched, thin walled and hyaline
 Abundant simple clamp connections
 Binucleate cells
 form arthrospores and skeletal hyphae
- Arthrospores
 Oblong to cylindrical
 Narrower and more regular in shape than from mycangia
 Lack clamp connections, except the last arthrospore in
 the chain that was attached to rest of mycelium
 1-3 per chain
- Skeletal hyphae
 Brownish with thicker walls
 Modified into cystidia towards apices
 Cystidia at first thin walled with wide lumen, becoming densely encrusted with hyaline mineral material later
- Basidia and basidiospores
 No basidiocarp or definite hymenium in agar cultures
 Groups of homobasidiate, irregular clavate basidia,
 with 4 straight or slightly curved sterigmata
- Basidiospores
 Hyaline, smooth and amyloid when mature
 Broadly ellipsoid and attenuated to a small apiculus or subcylindrical with flattened side
 Uninucleate

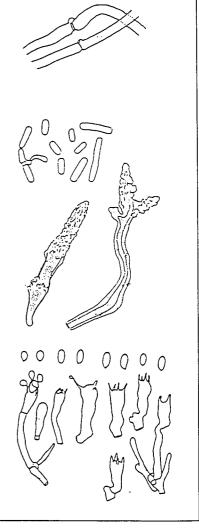


Table 2: continued from page 43

FRUCTIFICATION ON WOOD BLOCK CULTURE

· General

Resupinate

Smooth, undulating or tuberculate hymenium Varies in colour from light dale brown to deep umber

Margin lighter coloured and appressed

Underlying wood
 Clamped generative hyphae and skeletal hyphae
 Skeletal hyphae form cystidia in trama

· Trama

Gradually thickens and become stereoid in tissue distribution

Poorly defined cuticle and tomentum of skeletal and

generative hyphae

Medullary layer with horizontally arranged

skeletal

and generative hyphae

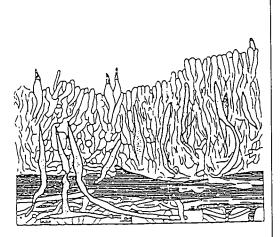
Subhymenial and hymenial layer with vertically arranged hyphae

· Cystidia

Formed in or near hymenium; short, erect and of tramal origin

Formed throughout growth and are found in every stage, including in or beyond level of basidia
Stain deep and quick with safranin

- Basidia and basidiospores
 Essentially as described from agar cultures
- Basidioles
 Same dimensions as basidia
 Terminate in apical constriction bearing small globose nipple
 Vacuoles or oil globules of appreciable size



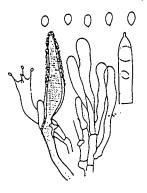


Table 3: A comparison of the morphological characteristics of *Amylostereum areolatum* and *A. chailletii* as described by Breitenbach & Kränzlin (1986) and Thomsen (1998).

	A. areolatum	A. chailletii
•Cultural	Mycelial mat is yellowish-, rust-	Cream coloured to pale-yellow or
characteristics	to leather-brown on MEA and	yellowish white on MEA and PDA
	PDA	
	Reverse side of medium darkens	Reverse side of medium darkens
	within 3 weeks	slowly and in patches
	Regularly forms arthrospores	Never forms arthrospores
•Macroscopic	Brown- to brown-violet coloured	Variable from cream, grey, to
features of fruiting	with	leather- or reddish-brown coloured
bodies	Undulating lighter margin that is	Margin ± demarked, darker brown
	wider than that of A. chailletii	to light but narrow
	Resupinte to effuso-reflexed,	Resupinate to effuso-reflexed
	1-2 mm thick	½ mm thick
	Dark line of demarcation between	Thin demarcation line between
	tomentum and trama	hymenium and cortex
•Microscopic	Basidiospores are elliptical and	Basidiospores are cylindrical to
features of fruiting	measures 4 - 6 μm x 2.4 - 3.2 μm.	slightly allantoid and measures 51/2-
bodies		8 μm x 2.4 - 4 μm
	Basidia are 18-25 x 3-4 µm in	Basidia are 33-45 x 4-5 μm in size
	size	
	Skeletocystidia are 40-60 x 6-9	Skeletocystidia are 40-50 x 3-6 μm
	μm in size and some extend	in size
	beyond the hymenium	

Figure 1: Mature and immature stages of the S. noctilio woodwasp. During the adult stage (a) male wasps (left) are characterised by the chestnut-brown coloured segments of the abdomen, while female wasps (right) are completely metallic darkblue. Pupae (b) are creamy white, characteristically S-shaped and the abdomen terminates in a dark brown to black sclerotypic spine.

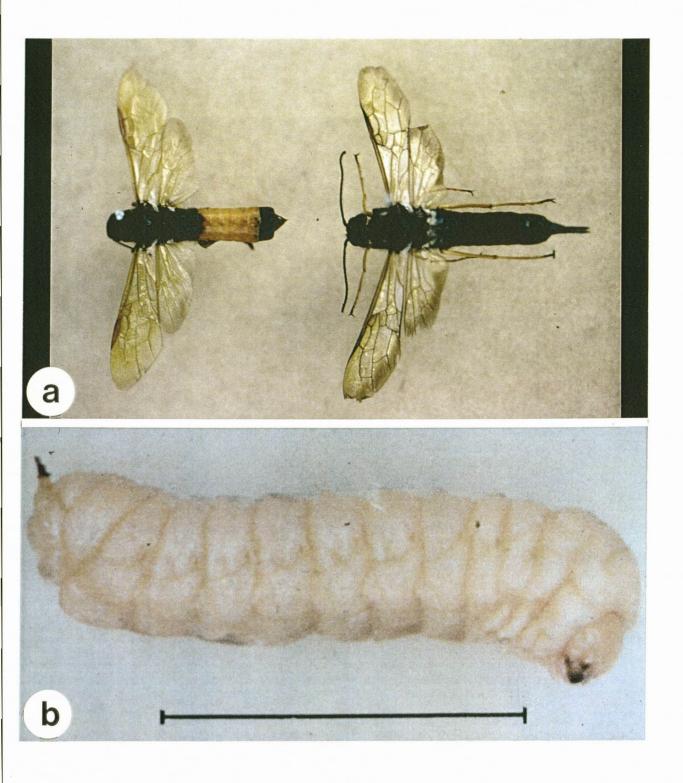


Figure 2: Micrographs of the morphological characteristics of A. areolatum in culture. (a) Hyaline encrusted cystidia and regular simple clamps at septa. A. areolatum also produce arthrospores in culture (b), unlike other Amylostereum spp. Arthrospores found in the mycangia of woodwasps (c) are regularly clamped and irregularly shaped, unlike the arthrospores found in culture. (Bars = $10 \mu m$)

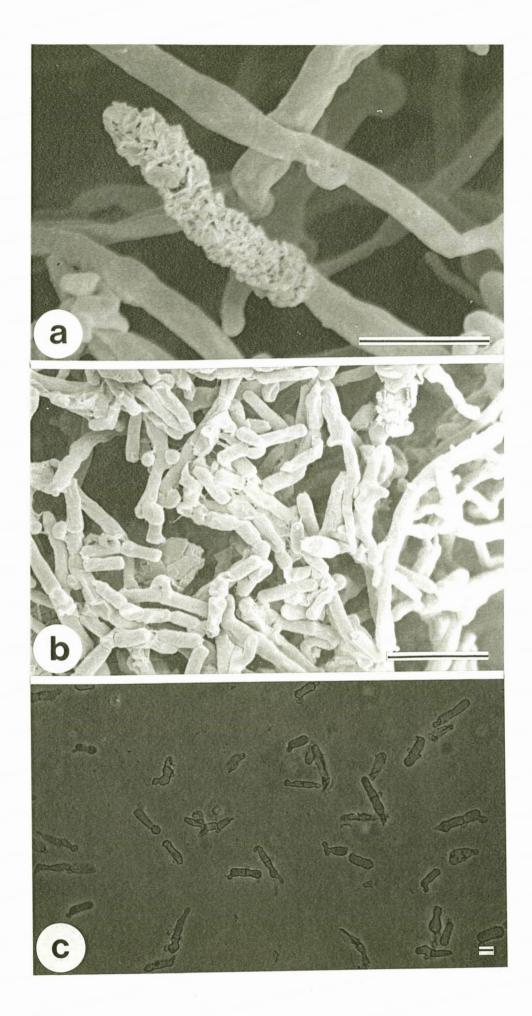
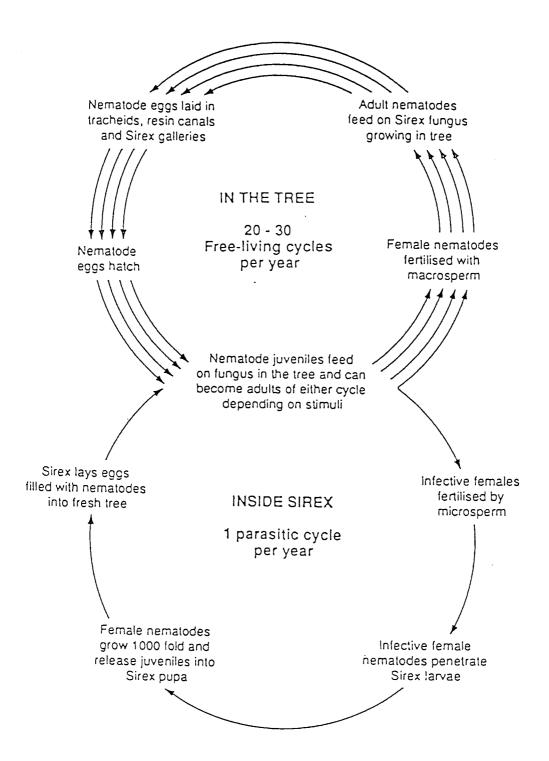


Figure 3: Symptoms of attack by S. noctilio on pine trees in the Southern Hemisphere include early symptoms, such as chlorosis and loss of needles (a), and are caused by the activity of the phytotoxic Sirex mucus. Attack is followed by the response of the tree in the form of resinosis and dribbles of resin can be seen running from oviposition holes (b). The tree is attacked all around the stem (c) and the overlapping dry zoned, as a result of the dry rot caused by the fungus, will cut of sapflow to the crown and kill the tree. Characteristic round exit holes (d) of the adult wasps, can be seen after one year in the Southern Hemisphere in the wood and bark of attacked trees.



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Figure 4: The bicyclic life cycle of *Deladenus siricidicola* that includes a mycetophagous and parasitic cycle (adapted from Bedding, 1995).



POPULATION STRUCTURE AND POSSIBLE ORIGIN OF AMYLOSTEREUM AREOLATUM IN SOUTH AFRICA

ABSTRACT

The woodwasp, Sirex noctilio, and its symbiotic fungus, Amylostereum areolatum, have been responsible for extensive damage to softwood plantations in the Southern Hemisphere. In 1994 S. noctilio was reported for the first time from standing pine trees in South Africa. The aim of this study was to assess the population diversity in this recently introduced population of A. areolatum, as well as to determine the possible origin of the pest complex. Vegetative incompatibility was tested by pairing the heterokaryotic isolates in order to determine vegetative compatibility groups (VCG), that serve as a character to delineate different genetic entities. Using this method, the South African population of A. areolatum was shown to constitute a single genetic entity. A collection of isolates from South America also represented only one VCG. Furthermore, this South American VCG was shown to represent the same genet as that occurring in SA. Isolates from Tasmania and New Zealand represented one VCG. This VCG produced a weaker incompatibility reaction when paired against isolates from the VCG found in SA and South America, than did any other isolate. Isolates associated with the biocontrol nematode, Deladenus siricidicola, from Australia, however, constituted a distinct genetic entity, different from field isolates in SA, South America, New Zealand and Tasmania. No compatibility was found between the isolates from the Southern Hemisphere and a collection of isolates from the Northern Hemisphere. We have, therefore, shown a close relationship between field isolates from the Southern Hemisphere, with the SA and South America sharing the same origin. The fact that isolates associated with the biocontrol nematode were distinct from those from SA and Brazil implies that this genetic entity has been accidentally introduced into these countries as part of a biological control initiative. It might also imply that biological control, using a nematode that was reared on a different genetic entity of A. areolatum, might be less effective.

INTRODUCTION

Sirex noctilio Fabricius and its symbiotic fungal associate, Amylostereum areolatum (Fr.) Boidin, are indigenous in the temperate regions of the Northern Hemisphere and are thought to be of Eurasian origin (Benson, 1943; Morgan, 1968; Spradbery & Kirk, 1978). In these regions this insect-fungus complex is considered a secondary problem of little economic importance (Chrystal, 1928; Hanson, 1939; Hall, 1978; Spradbery & Kirk, 1978). During this century S. noctilio and A. areolatum have, however, been introduced to Australasia, South America and South Africa (Madden, 1988; Baxter, Rong & Schutte, 1995; Reardon, Eav & Wetterberg, 1995; Tribe, 1995). In these Southern Hemisphere regions, Sirex has been responsible for great economic losses in softwood industries. The large monocultured stands of pine, favourable bioclimatic conditions and general absence of natural enemies of Sirex, have all contributed to elevating this pest complex to a primary status (Spradbery & Kirk, 1978; Madden, 1988; Haugen, 1990; Neumann & Marks, 1990; Chou, 1991).

Gaut (1969) showed conclusively that the fungus associated with *Sirex noctilio* in Australasia is *Amylostereum areolatum*. This was accomplished using the biological species tests and protein gel electrophoresis. Moreover, homologous protein and enzyme patterns of isolates of *Amylostereum* from the same geographical origin were also found (Gaut, 1970). The greatest similarity was found between electrophoretic protein patterns of isolates from Australia and those originating from Belgium and Switzerland. Talbot (1977) viewed electrophoretic protein patterns as a useful tool in tracing origins of introduced fungi, and in the case of *Amylostereum*, also of the symbiotic woodwasp.

An simple method of recognising genotypes in fungi is through the use of the natural phenomenon of non-self rejection or vegetative incompatibility (Rayner, 1991; Worrall, 1997). This technique has been widely used in population studies of Basidiomycetes (Barrett & Uscuplic, 1971; Rayner & Todd, 1977 & 1978; Adams, Todd & Rayner, 1981; Adaskaveg & Gilbertson, 1987; Chamuris & Falk, 1987; Kay & Vilgalys, 1992). These studies are, however, often on a smaller spatial scale as dispersive clones (Anderson &

Kohn, 1995) are rare in these fungi. Clones of Basidiomycetes fungi are usually territorial and arise through vegetative growth (Thompson & Rayner, 1982; Stenlid, 1985; Rizzo, Blanchette & May, 1995; Worrall, 1994). This is because the normal spread of Basidiomycetes via basidiospores will result in mating of primary mycelia and the formation of heterokaryotic secondary mycelia that are genetically unique, except in non-outcrossing populations (Coates, Rayner & Todd, 1981; Ainsworth & Rayner, 1990; Ainsworth *et al.*, 1990).

Vasiliauskas, Stenlid & Thomsen (1998), Thomsen & Koch (1999) and Vasiliauskas & Stenlid, 1999 reported the existence of extensive clonal lineages or vegetative compatibility groups (VCG's) in A. areolatum. Amylostereum areolatum is a heterothallic fungus with a tetrapolar nuclear state (Boidin & Lanquetin, 1984). Thus, heterokaryotic isolates arising through pairing of primary mycelium from different basidiospores would represent separate genetic entities. These fungi are, however, spread through asexually produced arthrospores that are carried in a very specific association with siricid woodwasps (Talbot, 1977). This seems to be the predominant means of reproduction of the fungus in most cases. The sporocarps are rare in the Northern Hemisphere and have never been reported from the Southern Hemisphere (Thomsen, 1998). Through this process, clonal lines are spread over large areas and are preserved for long periods of time (Vasiliauskas et al., 1998; Thomsen & Koch, 1999; Vasiliauskas & Stenlid, 1999). The origins of introduced isolates of A. areolatum could thus be determined by tracing these clonal lines.

Much research has been directed towards controlling *S. noctilio* in the Southern Hemisphere. In contrast, the symbiotic fungus has received little attention, despite the important role that it plays in the mutualism. No thorough population studies of *A. areolatum* in the Southern Hemisphere have, for example, been conducted. Thus, the possibility of using such knowledge to trace the spread of *Sirex* has not been exploited. Such information could also be important for biological control programmes, as the biological control agents are as intimately involved in the complex as are the fungus and woodwasp. In the present study we used vegetative or mycelial compatibility as character for investigating the population structure of the *Amylostereum* symbiont of *S. noctilio* in South Africa and South America. These populations are also compared to all other

available isolates of A. areolatum to determine the possible spread of S. noctilio in the Southern Hemisphere and the origin of the initial introductions.

MATERIALS AND METHODS

Collection and isolation of fungal isolates

Isolates of the fungal symbiont of *S. noctilio* in South African and South America were made from mycangia of female wasps or from wood around tunnels of the larvae of the wasp (Figure 1). *Sirex noctilio* wasps from South Africa were supplied by Dr. G. Tribe (Plant Protection Research Institute, Agricultural Research Council, Rosebank). These wasps were collected during each of the flight seasons from 1994/1995 to 1997/1998 from plantations in and around Cape Town or were raised in insectaries from stumps collected in the same area (Table 1). Wasps (*S. noctilio*) from various regions in Brazil were supplied by Mr. E. Schaitza (Table 1). One wasp from Uruguay was collected by Judy Moore (Plant Protection Research Institute, Agricultural Research Council, Rosebank).

To isolate the fungus from the mycangia of the wasps, the abdomens of a female wasps were cut from the rest of the body approximately two to three segments preceding the point of attachment of the ovipositor. A section was made either along the sides or the bottom of the abdomens and the abdomens spread open by pinning them onto a solid paraffin wax base. The mycangia were then exposed at the base of the ovipositor and the arthrospores contained in these structures were removed with a syringe needle or tweezers (Figure 1). The arthrospores were then plated onto a selective medium for Basidiomycetes (1 % Malt Extract, 1,5 % Agar, 2 ppm benomyl powder and 100 ppm streptomycin) (Hsiau, 1996), MYA (2% Malt Extract, 0,2% Yeast Extract and 1,5 % Agar) or pine extract MYA (PMYA) (150 - 200 g pine wood per liter of water was double autoclaved and poured through cheese cloth before adding the ingredients of MYA in same concentrations as described for normal MYA).

Isolates of A. areolatum were obtained from cultures of the nematode Delademus siricidicola that are exported from Australia to various Southern Hemisphere countries as a

biological control agent. This nematode feeds and is maintained on isolates of A. areolatum. Isolations were made directly from nematode cultures imported to South Africa during 1995 (Table 1).

Dr. I.M. Thomsen and Dr. R Vasiliauskas supplied isolates of *A. areolatum* from Europe (Table 1). Further isolates from different parts of the world were obtained from CBS (Centraal Bureau voor Schimmelcultures) and DAOM (Centre for Land and Biological Resources Research, Canada) culture collections (Table 1). All isolates were maintained on 9 cm diameter Petri dishes containing MYA or PMYA at 25 °C. The cultures were stored on MYA slants at 4 °C.

Heterokaryon compatibility

Pairings of heterokaryons were done by placing two ± 0.5 cm mycelial plugs, cut from the edges of actively growing cultures, one centimeter apart at the side of a Petri dish. Isolates were sometimes also paired by placing plugs from more than two isolates on a plate. This method was, however, not preferred, as full confrontation between all isolates did not always occur. Pairings were done on MYA and PMYA. No differences were observed between reactions of a given set of isolates paired on MYA or PMYA. As the growth rates on MYA was slower than those on PMYA, the latter medium was preferred as it shortened the time needed for reactions to develop. Reactions were scored after two to three weeks, but cultures were also incubated for longer periods in order to confirm that the reaction did not change over time. Pairings were always repeated to confirm initial results.

Rayner (1991) stresses the need for controlled self pairings to distinguish between true incompatibility and "mutual staling or nutrient depletion". Reactions between paired isolates were, therefore, always scored alongside control reactions where isolates were paired against themselves (positive controls) and against isolates known to be incompatible from initial trial experiments (negative controls). Reactions were normally scored as compatible or incompatible, but an intermediate reaction was also observed. In such intermediate reactions, opposing cultures formed a zone of sparse mycelium growth in the

interaction zone, but did not show the brown discoloration characteristic of the interactions of incompatible reactions.

Pairings to determine VCG's occurred in different phases:

South African population South African (SA) isolates collected during each season (six isolates - 1994/1995; 56 isolates - 1995/1996; 45 isolates 1996/1997) were paired in all possible combinations, for each season. As isolates from each season formed one VCG, a smaller number of isolates collected during each of the different seasons (three from 1994/1995, more than 10 from 1995/1996 and 1996/1997, respectively, and one from 1997/1998) were then paired against each other.

South American population The 25 Brazilian isolates were first paired in all possible combinations with each other. Later five of these were paired against the single Uruguayan isolate.

South African vs South American population The South American isolates (ten from Brazil and one from Uruguay) were then paired against SA isolates representing each of the different seasons. In all the above experiments, Australian isolates were paired against the SA and South American isolates. As these pairings were known from initial trial experiments to be incompatible, they served as negative controls.

South Africa & South America vs rest SA isolates (at least two for each collection season from 1994/1995 – 1996/1997 and one for 1997/1998) and South American isolates (four from Brazil) were also paired with isolates from other culture collections. These included isolates from Central Europe (CBS305.82 and CBS334.66), Northern Europe (L204, L236, DK782, DK37, S225 and S227), New Zealand (DAOM 21785) and Tasmania (WaiteInst.6195). The isolates from Central Europe, Northern Europe, New Zealand and Tasmania and Australia were also paired with each other in all possible combinations.

RESULTS

All isolates (108) collected within South Africa during the course of four seasons (1994/1995 - 1997/1998) were somatically compatible (Figure 2). Colony morphologies

and interactions sometimes appeared to be less uniform when compared to controls, but the mycelium always intermingled freely. Similarly all South American isolates (25 from Brazil and one from Uruguay) were compatible with each other and grew as a single entity when paired in various combinations. All South African and South American isolates were also vegetatively compatible with each other (Figure 3). Colony morphologies of the South African and South American cultures showed minor variations, but incompatible reactions between isolates were never observed.

The isolates from New Zealand (DAOM 21785) and Tasmania (Waite Inst. 6195), were fully compatible with each other (Figure 3). These isolates showed an intermediate reaction when paired against isolates from South Africa and South America (Figure 3 & 4). These intermediate interactions were much less intense than reactions between these isolates (from New Zealand, Tasmania, South Africa and South America) and any of the other isolates used in the study (Figure 4). The discoloration of the demarcation line at the interaction zone between isolates was very slight to almost undetectable, but the cultures did not grow as an entity as was seen in the positive controls. Colony morphologies of isolates DAOM 21785 and Waite Inst. 6195 were similar to those of isolates from South America and South Africa.

All pairings between South African and South American isolates and Australian isolates were strongly incompatible (Figure 3 & 4). Pairings between representative isolates from the single South African/South American VCG and isolates from the CBS culture collection (from Central Europe) and from the culture collections of Dr. Thomson and Dr. Vasiliauskas (Northern Europe) were strongly incompatible (Figure 4). None of the isolates from the CBS and DAOM culture collections were compatible, except isolates DAOM 21785 and Waite Inst. 6195 (as described above). The VCG's of isolates from Denmark, Lithuania and Sweden used in this study were the same as was determined for these isolates by Thomsen & Koch, 1999. These isolates were, however, not compatible with any of the other isolates used in this study.

DISCUSSION

In this study we have shown that A. areolatum isolates collected over four seasons in South Africa, and soon after its introduction together with S. noctilio into the country, represent a single vegetatively compatible genetic entity. This suggests that the introduction of S. noctilio was through a limited number of wasps and probably from a single area. Thomsen & Koch (1999) showed that the wasps from the same tree usually carry isolates of Amylostereum representing the same VCG. Neumann, Morey & McKimm (1987) suggested that up to a few hundred wasps can emerge from a single tree. The introduction of Sirex into SA, therefore, did not have to be by a single female to account for the single VCG representing the population of A. areolatum. Furthermore, this finding indicates that the introduction of S. noctilio and A. areolatum could either have been a single event or could have taken place more than once, but then from the same source.

The single genetic entity of A. areolatum in South Africa has been preserved and spread over the last four seasons (1994/1995 – 1997/1998). This indicates that vegetative reproduction through arthrospores and spread through symbiosis with S. noctilio, is the predominant or only form of propagation of this fungus in South Africa. This might explain why no basidiocarps of A. areolatum have yet been found in South Africa.

Similar to the South African situation, a reasonably large collection of isolates of A. areolatum from South America also represented a single VCG. Here a small introduction, or alternatively spread of S. noctilio from surrounding countries, could account for the compatible genetic pool of the isolates collected. Sirex noctilio has been known from this region for more than 10 years, which means that the genetic entity has been preserved over an even longer period in South America, than is the case in South Africa.

The fact that the genet from South Africa and South America is the same was of considerable interest. This indicates that *S. noctilio* in these two countries either share a common origin, or that this foreign pest was introduced into South Africa from South America where it has been known for a longer time period. New introductions of *S. noctilio* into the Southern Hemisphere have, thus, not necessarily been separate

introductions from the Northern Hemisphere, but have more likely been between countries in the Southern Hemisphere.

Although incompatible reactions were never observed between isolates from South Africa and South America, interactions were sometimes not as uniform as seen in the positive controls. Thomsen & Koch (1999) and Vasiliauskas *et al.* (1998) also noted the variability in the degree of the interactions and incorporate the results of molecular screening to support their results obtained from vegetative compatibility tests. This phenomenon has also been reported by various other researchers when pairing either monokaryotic, synthesised heterokaryons or heterokaryotic field isolates from a population (Adams & Roth, 1967; Coates *et al.*, 1981; Boddy & Rayner, 1982; Rayner & Turton, 1982; Stenlid, 1985). General conclusions were that the rejection reaction was weaker between more closely related isolates than between unrelated isolates or isolates separated by larger geographical distances. These conclusions were incorporated in the interpretation of the results of the current study.

Isolates of *A. areolatum* from New Zealand and Tasmania (DAOM 21785 and Waite Inst. 6195) were vegetatively compatible with each other and similar to the South African – South American VCG. As *Sirex* was first reported in New Zealand, these results suggest that the introduction of *Sirex* into Tasmania was probably from New Zealand or that they share a common origin. Isolates from South Africa and Brazil were not fully compatible with the isolates from New Zealand and Tasmania, but were evidently more closely related to them than to any of the other isolates used in the study. These two isolates from New Zealand and Tasmania have been in culture for many years (1962 in the case of isolate Waite Inst. 6195) and might be expected to have lost vigour. Genetic change during subculturing could also explain the slight differentiation seen here. The possibility, therefore, exists that the introductions of *Sirex* to South America and South Africa originated in New Zealand or Tasmania.

The D. siricidicola nematode used in biocontrol programmes, are reared on cultures of A. areolatum in Australia, from where it is imported by other countries throughout the Southern Hemisphere. Considering the close relationship between other isolates from the

Southern Hemisphere (from New Zealand, Tasmania, South Africa and South America), the strong antagonism of all the isolates from the Southern Hemisphere towards the strain of A. areolatum from Australia on which the nematode is reared, was surprising. These isolates from Australia were not necessarily collected from the field in Australasia, but possibly originated from earlier isolations of the nematode in Europe, and might even have originated from S. juvencus (R. A. Bedding, CSIRO, Australia; personal communication).

The strong antagonism between the isolates from the nematode cultures and isolates from other countries in the Southern Hemisphere, that import this isolate with cultures of the biological control nematode, has two possible consequences. Firstly, it might influence the feeding and reproduction of the biocontrol nematode, when introduced to new countries or areas. This would be consistent with suggestions that certain isolates of A. areolatum from the field in Australia are better than others for rearing the nematode (R.A. Bedding, personal communication). Secondly, it implies that a different genetic entity of A. areolatum has been introduced into South Africa and South America with the nematode and it will be interesting to see how this influences the population structure of A. areolatum in these countries in the future.

Although it was possible to show that A. areolatum, and, therefore, also S. noctilio, in South Africa and South America probably had the same origin, it was not possible to show where this might have been. All pairings between isolates from South Africa, South America, Tasmania and New Zealand suggest that these cultures are genetically related, but their pairings with isolates from all other sources available were always strongly incompatible. Isolates from Switzerland and Belgium could not be obtained, which would have made it possible to test Gaut's (Gaut, 1970) findings that isolates from Australia are most similar to isolates from these two countries.

In this study, we have shown that vegetative compatibility tests can be useful in determining the original source of introduction of *Sirex* to the Southern Hemisphere, should isolates from a wide enough range be obtained. This technique has also been used by Vasiliauskas *et al.* (1998), Thomsen & Koch (1999) and Vasiliauskas & Stenlid (1999) to exploit the formation of dispersive clones (where clonal genets are spatially separated) in

A. areolatum and A. chailletii. One advantage of this technique is that it allows for relatively easy and inexpensive screening of a large number of isolates for genetic similarities and dissimilarities (Stenlid, 1985). Some disadvantages, however, include the fact that while mycelial incompatibility clearly constitutes genetic difference, mycelial compatibility does not necessarily constitute clonality or somatic compatibility (Worrall, 1997). Worrall (1997), therefore, urges the use of molecular techniques to detect nuclear identity in addition to vegetative pairings. Although indications from work of Vasiliauskas et al. (1998) and Thomsen & Koch (1999) are that the genetic entities represented by a VCG in A. areolatum are clonal, the true clonality of the VCG found in South Africa and South America cannot be implied from the present results.

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Table 1 Isolates of Amylostereum areolatum used in this study in heterokaryon pairings.

Culture nr.	I.D.	Host or source of isolation	Origin	Date isolated	Isolator
CBS cultures 305.82	Amylostereum areolatum	Unknown	France	1964	J. Boiden
334.66	A. areolatum	From Picea abies	Germany	1967	Dimitri
CLBRR cultures Waite Inst. 6195	Amylostereum sp.	Mycangium of S. noctilio	Tasmania	1962	Unknown
DAOM 21785	Amylostereum sp.	Wood of <i>P. radiata</i> around oviposition bores of <i>S. noctilio</i>	New Zealand	Unknown	G.B. Rawlings
Other European isola					
L204	A. areolatum (± Clone S)*	Wood of wounded <i>P. abies</i>	Lithuania	1994	R. Vasiliauskas
L236	A. areolatum (Clone A)*	Wood of wounded P. abies	Lithuania	1995	R. Vasiliauskas
DK37	A. areolatum (Clone A)*	Fruiting body on P. abies	Denmark	1993	I.M. Thomson
DK782	A. areolatum (Clone B)*	Fruiting body on P. abies	Denmark	1987	J. Koch
S225	A. areolatum (Clone S)*	Wood of wounded P. abies	Sweden	1994	R. Vasiliauskas
S227	A. areolatum (Clone S)*	Wood of wounded P. abies	Sweden	1994	R. Vasiliauskas
Australian isolates					
A3, A4, A6, A7, A8,	Amylostereum sp.	Isolates from nematode cultures from CSIRO	Australia	1995	B. Slippers
A9, A10. A11					
South American isola 25 Isolates numbered	tes Amylostereum sp.	Mycangia of S. noctilio wasps	Brazil	1997	B. Slippers
Br1 –Br94					
Ul	Amylostereum sp.	Mycangia of S. noctilio wasps	Uruguay	1998	B. Slipper

^{*} Clones as reported by Thomson (1996).

Table 1 (continued)

Culture nr.	I.D.	Host or source of isolation	Origin	Date isolated	Isolator
South African isolate 1994/1995	S				
M1W, M5W, M6W,	Amylostereum sp.	P. radiata wood after attack by S. noctilio	South Africa	1994	M.J. Wingfield
M7W					
B3S, B5S	Amylostereum sp.	Mycangia of S. noctilio wasps	South Africa	1995	B. Slippers
1995/1996					
56 Isolates numbered	Amylostereum sp.	Mycangia of S. noctilio wasps	South Africa	1996	B. Slippers
SN1 – SN 49 (A/B)					
1996/1997					
45 Isolates numbered	Amylostereum sp.	Mycangia of S. noctilio wasps	South Africa	1997	B. Slippers
B1, B2 and					
K1.1 - K77					
1997/1998					
C1	Amylostereum sp.	Mycangium of S. noctilio wasp	South Africa	1998	B. Slippers

Figure 1: Isolations of A. areolatum were made from female S. noctilio woodwasps (a). In female woodwasp the abdomen was removed to expose the mycangium (b), that contain the arthrospores of A. areolatum, at the base of the ovipositor. Isolations of A. areolatum were also made from wood of attacked pine trees around tunnels (c) of S. noctilio larva.

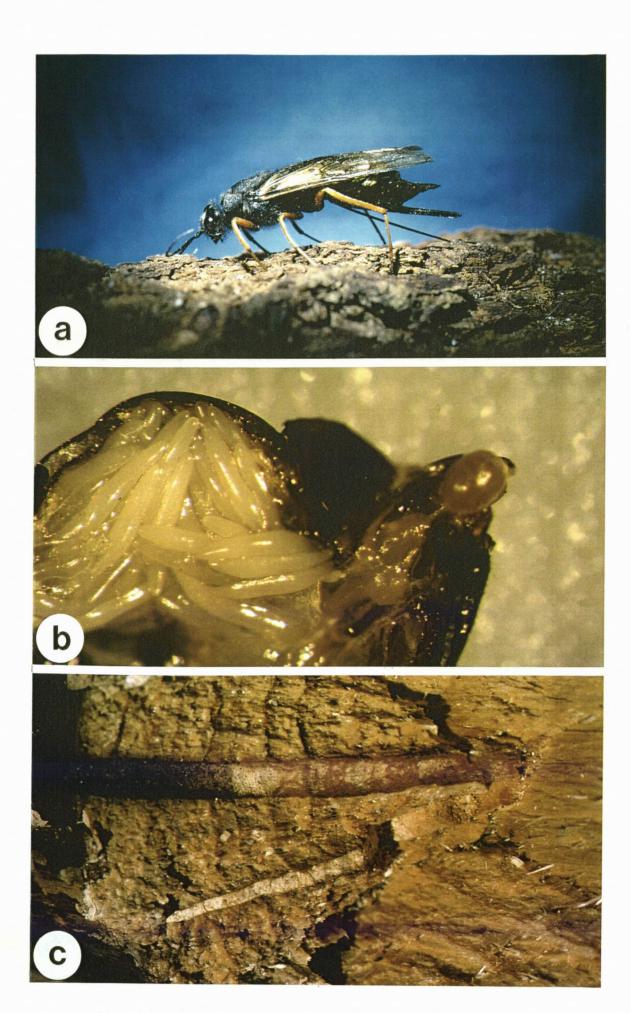


Figure 2: Top (a) and bottom (b) view of South African isolates (A1, A2, B1 and B2 – isolates M7W, B5S, SN31, K34.2, and C1) of *A. areolatum* paired in various combinations, as well as a positive (B3 - isolate K34.2) and negative control (A3 - isolates L279 and K7.2).

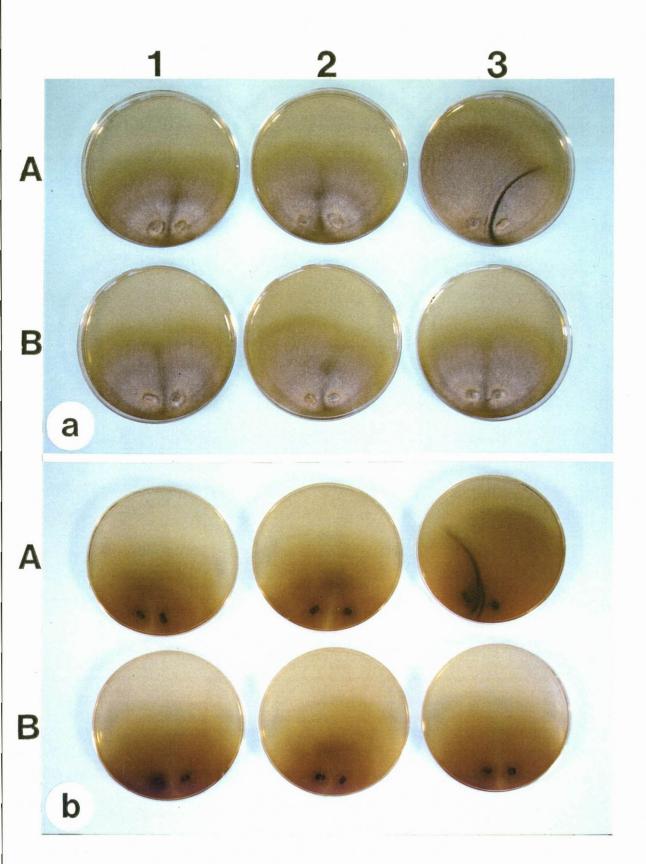


Figure 3: Reactions between heterokaryotic isolates from the Southern Hemisphere, as viewed from the top (a) and the bottom (b), when paired on Petri dishes containing PMYA. Lines and columns one and two represent field isolates from Tasmania (WaiteInst.6195) and New Zealand (DAOM21785) respectively, while numbers four and five represent field isolates from South Africa (B5S) and Brazil (Br.7), respectively. Line 3 and column 3 represents isolates of A. areolatum collected from cultures of the biocontrol nematode, D. siricidicola, that were imported into South Africa from Australia.

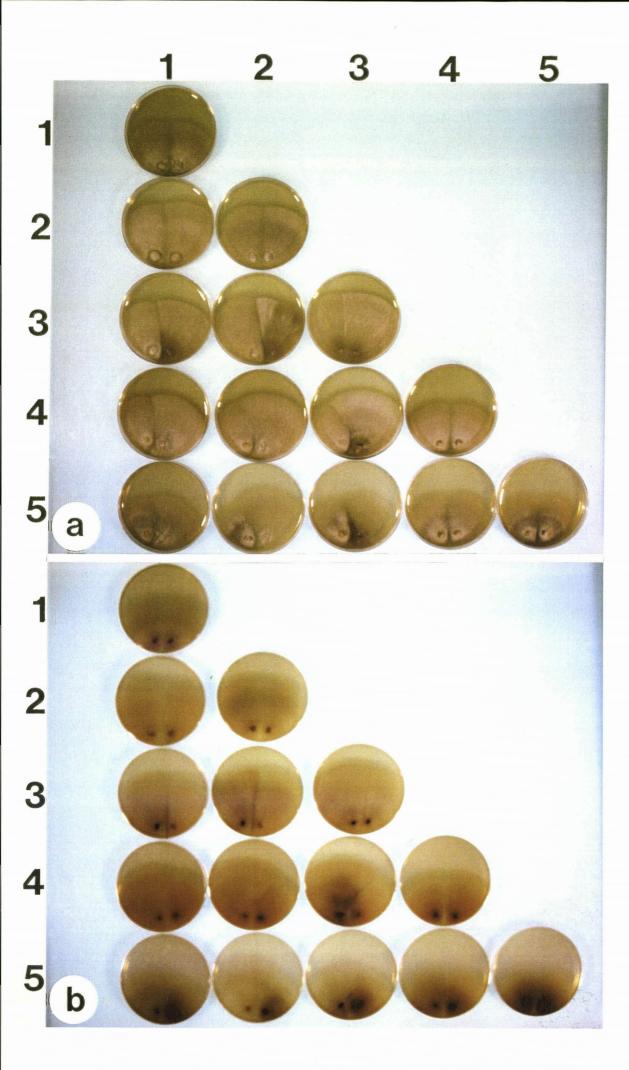
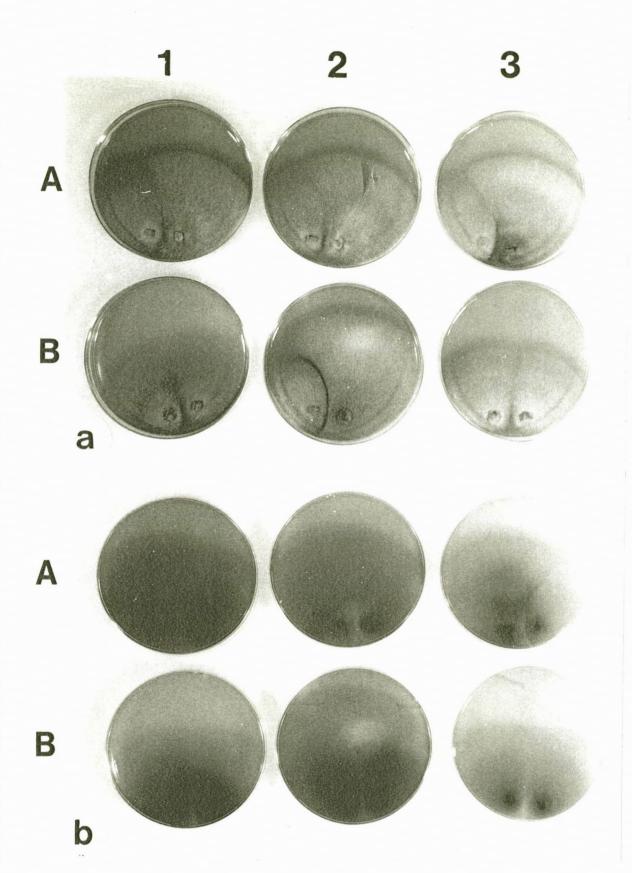
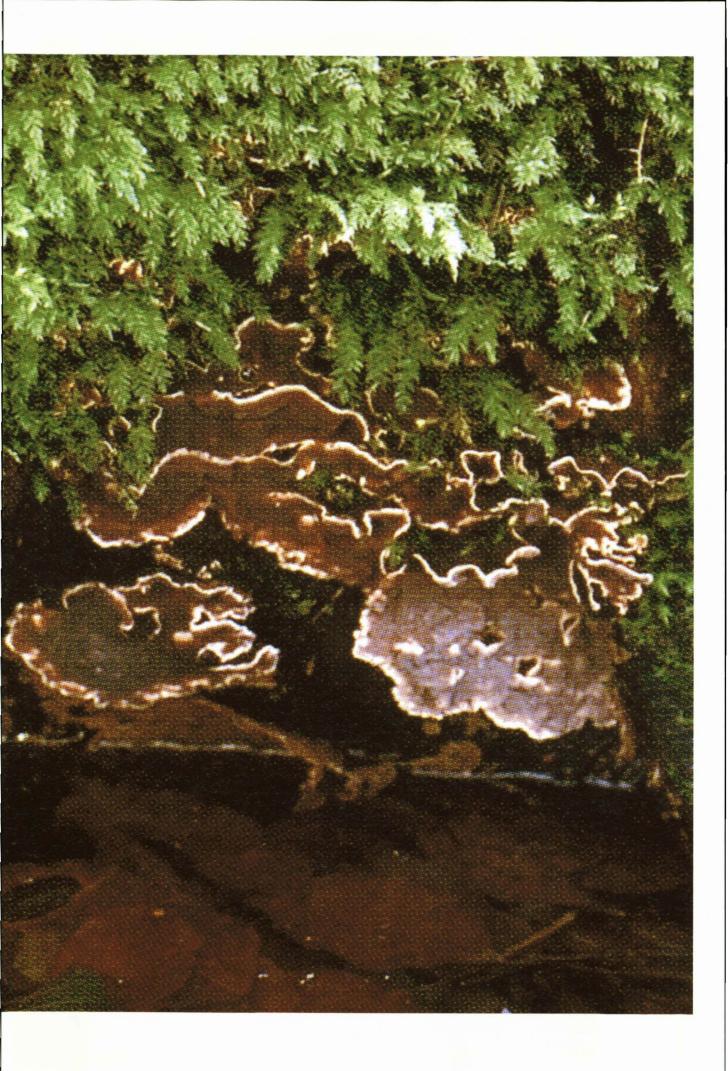


Figure 4: Vegetative incompatibility reactions between isolates of A. areolatum representing the South African VCG (B5S and K7.2) and isolates from Tasmania (A1 – isolate Waite Inst.6195), New Zealand (A2 – isolate DAOM 21785), Australia (A3 – isolate A9), Brazil (B1 – isolate Br.7) and Europe (B2 – isolate CBS305.82), as viewed from above (a) and below (b). Pairing B3 represents a positive control self pairing (K7.2).





PHYLOGENY AND TAXONOMY OF THE GENUS AMYLOSTEREUM INFERRED FROM MITOCHONDRIAL RIBOSOMAL DNA SEQUENCE

ABSTRACT

The genus Amylostereum currently includes four species, namely A. areolatum, A. chailletii, A. laevigatum and A. ferreum. Two of these species, A. areolatum and A. chailletii, are well known for their association with siricid woodwasps. Despite much interest in these fungus-woodwasp symbioses, the taxonomy and phylogeny of this genus received little attention in the past. The aim of this study was to investigate the phylogenetic relationship between the four species of Amylostereum. The placement of Amylostereum spp. among the Basidiomycetes was also investigated based on mt-SSUrDNA sequence analyses. These data also clarify the taxonomic status of previously unidentified isolates. In this study, we have shown that A. areolatum is more distantly related to the three other species of Amylostereum, than they are to each other. Of the remaining three species, A. ferreum and A. laevigatum are more closely related to each other. One isolate that was collected from Sirex areolatus, and, therefore, expected to be A. chailletii, was more closely related to A. laevigatum and A. ferreum. As neither of the latter species have been implicated in associations with woodwasps, this finding warrants further investigation. Our data show that Amylostereum spp. groups with neither Stereum nor Peniophora, as has been previously hypothesised, but rather with Echinodontium tinctorium. From this and other studies there was also an obvious relationship between Amylostereum/Echinodontium and Russula.

INTRODUCTION

Members of the genus Amylostereum are best known for their mutualistic association with Siricidae, a family of woodwasps with a woodboring larval state (Talbot, 1977). These woodwasps and their associated fungi have the potential to cause serious damage and mortality to various species of conifers such as Pinus, Abies, Picea, Pseudotsuga (Spradbery & Kirk, 1978 & 1981). In the Northern Hemisphere where woodwasps originate, a natural balance exists between them, their natural parasites and their host trees, such that they are generally considered as secondary invaders (Hall, 1978; Spradbery & Kirk, 1978).

The Sirex noctilio-Amylostereum areolatum complex has been introduced into a number of countries in the Southern Hemisphere where it causes severe damage to exotic pine plantations (Neumann & Marks, 1990; Chou, 1991; Bedding, 1995). In these regions this pest complex is considered a primary problem. A combination of the environmental stresses on pine trees, the genetic uniformity of these plantations and the absence of natural enemies of Sirex have all contributed to the increase in pathogenicity of this wasp-fungus association in the Southern Hemisphere (Spradbery, 1973; Spradbery & Kirk, 1978).

Boidin (1958) first described the genus Amylostereum as distinct from species of Stereum and Peniophora. General morphological characters include smooth amyloid basidiospores, brown encrusted cystidia and regular simple clamps. Amylostereum chailletii (Pers.:Fr.) Boid., the type species, and A. areolatum (Fr.) Boid. are the only two species of Amylostereum implicated in associations with woodwasps (Gaut, 1970; Boidin & Lanquetin, 1984). Both species were initially included in the genus Stereum as S. chailletii (Pers.:Fr. as Thelophora) Fr. and S. areolatum (Fr.:Fr. as Thelophora) Fr. respectively (Boidin, 1958). Amylostereum chailletii and A. areolatum are morphologically very similar, but can be distinguished in culture based on the fact that only A. areolatum forms arthrospores in culture (Thomson, 1998).

The third species described by Boidin (1958) in the genus Amylostereum, A. laevigatum (Fr.) Boid., was known as Peniophora laevigata (Fr. as Thelephora) Karst. and later as S.

juniperi (Karst.) Boid. Amylostereum laevigatum is also found in softwood trees, predominantly species of Juniperus. This species differs from A. chailletii and A. areolatum in the absence of horizontal hyphae in the fruiting structures, as well as in the fact that it has a monomytic hyphal system (Breitenbach & Kränzlin, 1986).

Boidin and Lanquetin (1984) described A. ferreum (Berk. & Curt.) Boid. & Lanq. (= Stereum ferreum) as a fourth species in the genus Amylostereum. A major difference between A. ferreum and the three other species of Amylostereum is its occurrence exclusively in Podocarpus species. Unlike the other three species that are known from the Northern Hemisphere, A. ferreum, has been found only in South America (Boidin & Lanquetin, 1984).

Boidin and Lanquetin (1984) evaluated the genus Amylostereum based on mating studies and the Buller phenomenon (Buller 1931). They concluded that A. chailletii, A. laevigatum and A. ferreum are more closely related to each other than they are to A. areolatum. No positive mating reactions were observed between A. areolatum and the other three species. No compatible mating was observed between A. chailletii and A. laevigatum, but A. ferreum gave partially compatible crosses with both these species. Boidin and Lanquetin (1984) also hypothesised that, based on morphological evidence, the genus Amylostereum could be more closely related to Peniophora than to Stereum.

Morphological studies of the Basidiomycetes are complicated by the limited number of available characters, as well as the influence of convergent and parallel evolution (Hibbett et al., 1997). For example, in a study of 89 Basidiomycete species, using sequence data from the nuclear and mitochondrial small subunit rRNA operon, Hibbett et al. (1997) showed that a major character such as gills might have evolved six times. Similarly various researchers have used the combined features of conserved and less conserved regions in the rRNA genes to resolve problematic phylogenetic and taxonomic questions in the Basidiomycetes, often in conjunction with morphological data (Hibbett & Vilgalys, 1991 & 1993; Hibbett, 1992; Swann & Taylor, 1993 & 1995; Zambino & Szabo, 1993, Hibbett & Donoghue, 1995; Hsiau, 1996).

The aim of this study was to test the hypotheses of Boidin and Lanquetin (1984) as well as other researchers regarding the phylogenetic relationships between the different species of *Amylostereum*, based on part of the mitochondrial ribosomal gene complex. In addition, relationships between species of *Amylostereum* and other Basidiomycetes are also considered. The taxonomic status of isolates of unknown or uncertain identity is also investigated using these data.

MATERIALS & METHODS

Isolates used in the study

Isolates used in this study were obtained from a variety of sources (Table 1). These include those made from *S. noctilio* collected in South Africa and Brazil, those from cultures of the parasitic nematode *Deladenus siricidicola*; isolates from Europe supplied by Dr. I.M. Thomson (Danish Forest and Landscape Research Institute, Hoersholm, Denmark), Dr. R. Vasiliauskas (Swedish University of Agricultural Sciences, Uppsala, Sweden), those from culture collections CBS (Centraal Bureau voor Schimmelcultures, Baarn, Netherlands) and DAOM (Centre for Land and Biological Resources Research, Canada). Isolates were maintained on MYA (2 % Malt Extract, 0.2 % Yeast Extract and 1.5 % Agar) at 25 °C and stored in McCartney bottles containing MYA at 4 °C.

DNA isolation

Mycelium from actively growing cultures on MYA was used to inoculate liquid MY (2% Malt Extract and 0.2% Yeast Extract) medium (100 ml in 250 ml Erlen meyer flasks). These were incubated at 25 °C on a shaker for approximately two weeks. A modification of the method of Raeder and Broda (1985) was used for isolating DNA from mycelium. Unlike the Raeder and Broda (1985) method, each sample was divided into two equal amounts for the whole extraction procedure, after cell debris had been removed. Furthermore, the phenol chloroform extraction (1:1 phenol to chloroform) step was repeated several times until the interphase between the aqueous and upper phases was clean from contaminating proteins and cell debris. Precipitation of the nucleic acids was done

using 3M NaAc (0,1 v/v) and isopropanol (0,6 v/v) and was incubated overnight at -20 °C. After centrifugation, to harvest the nucleic acids, and washing with 70 % EtOH, the pellet was resuspended in 200 µl sterile SABAX water. The two samples of each isolate were then combined. One µl RNaseA (10mg/ml) was added to the resuspended sample and left at 37 °C overnight to degrade all RNA in the sample. DNA concentrations were subsequently determined using an UV spectrophotometer (Beckman Du Series 7500) (Maniatis *et al.*, 1982).

PCR amplification and purification

A portion of the mitochondrial small sub-unit ribosomal RNA gene (mt-SSU-rDNA) was amplified with the primers MS1 and MS2 (White *et al.*, 1990) using the Polymerase Chain Reaction (PCR). PCR was performed using the ExpandTM High Fidelity Polymerase System. Total volumes of the reaction mixtures varied from 50 μl, 75 μl and 100 μl. The reaction mixture consisted of a final concentration of 2,65 mM MgCl, 200 μM of each of the four dNTP's, Expand High Fidelity buffer with MgCl, 0,375 μM of each of the two primers and 2,6 U ExpandTM High Fidelity Taq polymerase mixture (Boehringer Mannheim, South Africa). Extracted genomic DNA (50 ng to 80 ng) was used as template for the amplification reactions.

PCR reactions were performed on a Hybaid TouchDown PCR machine (Hybaid limited, U.K.). Reaction conditions included an initial denaturation step of 3 minutes at 94 °C followed by 10 cycles of denaturation at 94 °C for 15 seconds, primer annealing at 55 °C for 45 seconds and elongation at 72 °C for 1 minute. This was followed by 20 cycles using the same reaction conditions, but with an increase of 20 seconds elongation time per cycle. A final elongation step at 72 °C for 7 minutes ensured complete elongation of the amplification product. PCR products were subjected to electrophoresis on an 1 % (wt/v) ethidium bromide stained agarose (Molecular biology grade, Techcomp Ltd., Hong Kong) gel and visualised under UV illumination. Size estimates of the PCR fragments were done using a 100 bp ladder (Promega, Madison, Wisconsin, U.S.A.) as a molecular weight marker.

DNA sequencing and sequence data analysis

DNA sequencing of the amplified mt-SSU-rDNA was performed on an ABI PRISMTM 377 automated DNA sequencer. PCR products were purified prior to sequencing, using a NucleonTMQC PCR/OLIGO clean up kit (Amersham Life Science Inc.). Thermo SequenaseTM dye terminator cycle sequencing pre-mix kit (Amersham Life Science Inc.) with Thermo SequenaseTM DNA polymerase was used for all sequencing reactions. The primers MS1 and MS2 were used to sequence both DNA strands.

To determine the phylogenetic relationships amongst *Amylostereum* species, mt-SSU-rDNA sequences of all isolates (Table 1) were manually aligned by inserting gaps. All characters were given equal weight and gaps were coded as newstate (fifth character). Analysis of the data was done using PAUP (Phylogenetic Analysis Using Parsimony) version 3.1.1 (Swofford, 1993). Heuristic searches using TBR (Tree Bisection Reconstruction) branch swapping and MULPAR on, were done to determine the most parsimonious relationships between the taxa. Strict and semi-strict consensus trees were obtained in PAUP for all equally parsimonious trees saved. Trees were not rooted to an outgroup taxon, but rather by midpoint rooting. Branch supports and confidence intervals were determined using BOOTSTRAP analysis (1000 replicates) (Felsenstein, 1993).

In order to consider the relationship of Amylostereum spp. with other Basidiomycetes, sequence data of the mt-ssu-rDNA for 89 species of Basidiomycetes (Hibbett and Donoghue, 1995; Hibbett et al., 1997) were obtained from Genbank and TREEBASE. Sequence data of A. chailletii was initially compared to all 89 species using PAUP to resolve a clade of maximum relationship. Sequence data from the most closely related taxa determined using this analysis, were then compared to DNA sequence data of all four described species of Amylostereum. Sequence analysis was done using PAUP, as described above, except that all resulting trees were rooted to an outgroup taxon. Here, Laxitextum bicolor (Fr.) Lentz. was chosen as an outgroup because of its basal relationship to the taxa selected as closely related to Amylostereum in the analysis of Hibbett et al. (1997).

RESULTS

PCR amplification

The region of the mt-SSU-rRNA gene targeted with the MS1 and MS2 primers was highly conserved in all the species of Amylostereum, based on the size of the amplified PCR fragments. Fragments of approximately 570 bp were observed for all but three isolates used in this study (Figure 1). The three exceptions, isolates Stillwell 309(3), CBS 624.84 (A. laevigatum) and CBS 633.84 (A. ferreum), produced PCR amplification fragments of approximately 590 bp in length (Figure 1).

Sequence data

Manual alignment of sequences representing the amplified region of the mt-SSU-rDNA of the different species of *Amylostereum* resulted in the total alignment of 538 characters (Figure 2). Absolute lengths of the sequences ranged from 518 bp to 537 bp. Sequences of the above-mentioned region were highly conserved for all the species of *Amylostereum*. One variable region was observed between 190 and 226 bp (aligned length) of the fragment.

Heuristic searches using PAUP of these sequences resulted in 18 equally parsimonious trees (CI = 0.968; HI = 0.032; RI = 0.986) of 31 steps each (Figure 3). The topology of these trees was similar and differences were due to variations in branch length and the arrangement among isolates CBS624.84 (A. laevigatum), CBS633.84 (A. ferreum) and Stillwell 309(3) (isolated from S. areolatus).

The main feature of the trees obtained from heuristic searches of sequence data of the different Amylostereum spp., was the appearance of two major clades supported by a 100 % confidence interval at the branching point. The one clade contained representative isolates of A. areolatum. Within the A. areolatum clade only one branch was retained in consensus trees that was weakly supported by bootstrap analysis (65 %). The second main clade was comprised of representative isolates of A. chailletii, A. laevigatum, A. ferreum

and isolate Stillwell 309(3). A. chailletii grouped on a separate branch (93 % confidence interval) within this second clade from A. laevigatum, A. ferreum and isolate Stillwell 309(3). A. ferreum, Stillwell 309(3) and A. laevigatum were grouped together and basal to A. chailletii in strict and semi-strict consensus trees, as well as by bootstrap analysis. Therefore, a revised form of the evolutionary tree of decent reported by Boidin and Lanquetin (1984) (Figure 4(a)), is proposed (Figure 4(b)).

Manual alignment of sequence data of 16 selected species from the data set of Hibbett *et al.* (1997) and the four species of *Amylostereum* (Figure 5) resulted in a total aligned data set of 771 characters. Absolute values varied from 513 bp for *Russula compacta* Frost to 674 bp for *Peniophora nuda* (Fr.) Bres. Sequences could be divided into four relatively conserved regions, interspersed with three hypervariable regions, as was reported by other researchers (Hibbett and Donoghue, 1995; Hsiau, 1996; Hibbett *et al.*, 1997). The three hypervariable regions were located between bases 55 and 128, bases 266 and 400 and bases 623 and 671 (based on aligned values).

Alignment in these hypervariable regions was difficult and often impossible. This resulted in a large amount of ambiguity in their alignment. Analysis of the data was thus performed with and without these hypervariable regions. In the latter case, this resulted in the exclusion of 258 bp (aligned values). The general topology of the trees showed some variation compared to the trees resulting from analysis of the full sequence, but most of the species groupings were not affected.

Heuristic searches of the full sequence data set resulted in three equally parsimonious trees of 1495 steps (CI = 0.601; HI = 0.399; RI = 0.522) (Figure 6). The topology of the trees were the same except for variations in branch lengths and whether A. laevigatum and A. ferreum were put on separate branches or not. Seven most parsimonious trees of 639 steps (CI = 0.604; HI = 0.396; RI = 0.595) was obtained when analysis were conducted on the DNA sequences with the variable regions excluded (Figure 7). Differences in the seven trees could again be ascribed to variation in branch lengths.

The four species of Amylostereum formed a monophyletic clade basal to Echinodontium tinctorium Ell. & Ev. The branch separating the Amylostereum spp. from Echinodontium was supported by a 98 % bootstrap value irrespective of the inclusion or exclusion of the hypervariable regions. The bootstrap branch support for the Echinodontium -Amylostereum grouping was 70 % when the hypervariable regions were included and 94 % when they were excluded. Heterobasidion annosum (Fr.) Bref. and R. compacta grouped together and neighbouring the group that contained Echinodontium and Amylostereum spp. Lentinellus omphalodes (Fr.) Kar. and L. ursinus (Fr.) Küh., Auriscalpium vulgare S. F. Gray, Clavicorona pyxidata (Fr.) Doty and Hericium ramosum (Bull. ex Mér) Let. were also grouped close to Ecinodontium, Amylostereum, Heterobasidion and Russula in analysis of the data set without exclusion of the hypervariable regions. In analyses ignoring the sequence of the hypervariable regions, Hericium and Clavicorona were removed from this group. Heterobasidion and Russula also grouped closer to Lentinellus and Auriscalpium spp. than to the Echinodontium - Amylostereum group in this analysis. Neither Stereum nor Peniophora spp. grouped in the above-mentioned groups, in any of the analyses. Instead, Stereum spp. were grouped with Gloeocystidiellum leucoxantha (Bres.) Boid. and P. nuda with Scitinostroma alutum Lang. in all trees.

DISCUSSION

In this study the phylogenetic relationships of the four species of Amylostereum could be resolved using sequence data of the mt-ssu-rDNA. Isolates representing A. areolatum clustered on a well supported branch, separate from all the other species in the genus. This confirms the hypothesis of Boidin and Lanquetin (1984) that A. areolatum is the most clearly defined species in the genus. In their study, no mating compatibility was observed between isolates of A. areolatum and any of the other Amylostereum species in this group, whereas partial compatibility was observed between some of the other species of Amylostereum.

Boidin and Lanquetin (1984) could not clearly define the relationship between A. chailletii, A. laevigatum and A. ferreum. In their study European isolates of A. chailletii and A. laevigatum showed no mating compatibility, but both these species showed partial mating

compatibility with A. ferreum. Our analysis showed that A. chailletii, A. laevigatum and A. ferreum formed a cluster together and separate from A. areolatum, which is in agreement with their mating studies. Isolates of A. chailletii formed a separate group within the latter clade, while A. laevigatum and A. ferreum could not be separated in strict analyses of the data. These results suggest a closer relationship between A. ferreum and A. laevigatum than between either of these species and A. chailletii.

In this study, it was possible to confirm the identity of isolates of *Amylostereum* that could previously not be assigned species names. The two CLBBR cultures identified only as *Amylostereum* sp. (Waite Inst 6195 and DAOM 21785) from Tasmania and New Zealand, clearly resided in the clade containing identified isolates of *A. areolatum* (CBS 305.82, CBS 334.66 and isolates from Europe that were identified by Drs. Thomsen and Vasiliauskas). Also represented in this group are isolates from South Africa, Brazil and isolates obtained from nematode (*Delademus siricidicola*) cultures imported to South Africa from Australia. Furthermore, the two Canadian isolates of *A. chailletii* (DAOM 21327 and 54-95) clearly clustered with other identified isolates of *A. chailletii* (L234, Sc62.8 and CBS 483.83). Boidin and Lanquiten (1984) found partial mating compatibility between two Canadian *Amylostereum* isolates and authentic isolates of *A. chailletii*, *A. laevigatum* and *A. ferreum*. According to our data this mating behaviour, therefore, only supports the close relationship between the three last named species.

Isolate Stillwell 309(3) is reported to have been isolated by Dr. Stillwell from the mycangium of *S. areolatus*. We would, therefore, expect it to be *A. chailletii* as was suggested by Gaut (1970). This isolate was deposited in DAOM as an *Amylostereum* sp. Results of this study show that the isolate is most closely related to *A. laevigatum* and *A. ferreum*. Neither of these species have previously been implicated in associations with woodwasps. If this isolate is, therefore, an actual sub-culture of the isolate collected from *S. areolatus*, it might represent a link between the species associated with woodwasps (*A. areolatum* and *A. chailletii*) and the other two species (*A. laevigatum* and *A. ferreum*). It might also represent an undescribed species of *Amylostereum*. Further study of this isolate is clearly warranted.

Various hypotheses have been proposed for the placement of Amylostereum amongst the Basidiomycetes (Boidin & Lanquetin, 1984; Parmasto, 1995; Hsiau, 1996), but in general Amylostereum is considered most closely related to Stereum and Peniophora (in which Amylostereum spp. were originally described). Boidin and Languetin (1984) speculated that Amylostereum might be more closely related to Peniophora based on the presence of gloeocystidia positive in sulfuric-aldehyde, normal nuclear behaviour and the tetrapolarity in all four species. Parmasto (1995) in a cladistic study using 86 morphological characters to test the phylogeny amongst the genera of the Corticoid fungi reduced the Stereaceae to synonymy with the Peniophoraceae. In his analysis, A. chailletii groups sister to Stereum and Xylobolus (P. Karst.) and the former three genera form a group basal to the group that contains the genus Peniophora. In a study by Hsiau (1996) using mt-ssu-rDNA, A. chailletii grouped sister to Stereum and further away from Peniophora. In the present study the four Amylostereum spp. formed a monophyletic group that was sister to neither Stereum nor Peniophora, but rather to E. tinctorium. This observation was supported by strong bootstrap values for this grouping in all analyses (70 % when the hypervariable regions were included in the analysis and 94 % when they were excluded). It is interesting to note that E. tinctorium is also characterised by amyloid basidiospores and encrusted cystidia, such as is formed by Amylostereum spp.

Echinodontium tinctorium has been described as closely related to Stereum (Gross, 1964; Stalpers, 1978). Hibbett et al. (1997), however, found that E. tinctorium is more closely related to Peniophora nuda than to any of the Stereum spp. included in their analysis. In the present study, the Amylostereum-Echinodontium group was, however, more closely related to Russula, Heterobasidion, Lentinellus and Aurisclapium in all analyses, than to either Stereum or Peniophora.

Topologies of the trees derived in this study differed from those reported by Hibbett *et al.* (1997), from which some of the sequences were obtained. The major differences in tree topologies are in the arrangements of the species groupings, while the species contained in each group were less affected. Some of these differences are in accordance with findings in other studies. For example, the *Heterobasidion-Russula* grouping indicated by this study, that was closely linked to the group containing *Amylostereum*, is consistent with the data of

Hsiau (1996), while Hibbett et al. (1997) group Echinodontium and Russula together. Despite these differences, it is obvious from this study that there is a closer relationship between Amylostereum and Echinodontium than was previously recognised. There is also an obvious relationship between Amylostereum/Echinodontium and Russula

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Table 1: Isolates of different species of Amylostereum used in this study.

Culture Number	Identity.	Host or source of isolation	Origin	Date isolated	Isolator
CBS cultures 305.82	Anudontamin			Date isolateu	Isolator
334.66	Amylostereum areolatum	Unknown	France	1964	J. Boiden
-	A. areolatum	From Picea abies	Germany	1967	Dimitri
483.83	A. chailletii	Mycangium of woodwasp Urocerus gigas	Scotland, UK	1981	D.B. Redfern
624.84	A. laevigatum	Juniperus nana	France	1978	P. Lanquetin
633.84	A. ferreum	Podocarpus lambertii	Brazil	1978	R.T. Guerrero
CLBRR cultures DAOM 21327	A. chailletii	Sansahara a 41: 1 1			
54-95	A. chailletii	Sporophore on Abies balsamea	Ontario, Canada	1948	R.F. Cain
		Sporophore on fallen log in stand of hemlock conifers	Ontario, Canada	1954	A. Hill & S. Gibson
Stillwell 309(3)	Amylostereum sp.	Mycangium of Sirex areolatus	California, U.S.A.	Unknown	Stillwell
Waite Inst. 6195	Amylostereum sp.	Mycangium of S. noctilio	Tasmania	1962	Unknown
DAOM 21785	Amylostereum sp.	Wood of P. radiata around oviposition bores of S. noctilio	New Zealand	Unknown	G.B. Rawlings
Other European is	olates				5
Sc 62.8	A. chailletii	Fruiting body on Picea sitchensis	Scotland, U.K.	1981	D.B. Redfern
L234	A. chailletii	Wood of wounded P. abies	Lithuania	1995	R. Vasiliauskas
L204	A. areolatum	Wood of wounded P. abies	Lithuania	1994	R. Vasiliauskas
DK37	A. areolatum	Fruiting body on P. abies	Denmark	1993	I.M. Thomson
S225	A. areolatum	Wood of wounded P. abies	Sweden	1994	R. Vasiliauskas
Australian isolates					T. Vasinauskus
A3	Amylostereum sp.	Isolates from nematode cultures from CSIRO	Australia	1995	B. Slippers
South American iso	lates	·		1993	D. Suppers
Br 38	Amylostereum sp.	Mycangia of S. noctilio	Brazil	1997	B. Slippers
South African isolates					
M5W	Amylostereum sp.	Wood around S. noctilio in P. radiata	South Africa	1994	M.I. Winefield
SN19A	Amylostereum sp.	Mycangia of S. noctilio	South Africa	1994	M.J. Wingfield B. Slippers

Figure 1: PCR fragments of the mt-SSU-rDNA of the different species of *Amylostereum*, visualised on a 1.5 % agarose gel stained with ethidium bromide. A 100 bp molecular size marker was run in the outer lanes of the gel.

A. chailletii

A. areolatum

Figure 2: Aligned DNA sequence data of part of the mt-SSU-rDNA of Amylostereum spp., obtained using the primers MS1 and MS2. Gaps that were inserted due to alignment are indicated by a dash (-). Isolates SN19A, M5W, Br 38, A3, Waite Inst. 6195, DAOM 21785, CBS 305.82, CBS 334.66, L204, DK37 and S225 represent isolates of A. areolatum or expected to be A. areolatum (Table 1). Isolates CBS483.83, 54-95, DAOM 21327, L234 and Sc62.4 represent A. chailletii, isolate CBS 624.84 A. laevigatum and isolate CBS 633.84 A. ferreum (Table 1). Isolate Stillwell 309(3) represent an Amylostereum sp. (Table 1).

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DAOM21785	CTATTAGTGT CGTCCAAAT	C TGGTGCCAGA AGACTCGGTA	A AGGCCAGAGA CGCAAACG	TT AATCGTCTTA AACAGGCGTA
CBS305.82	CTATTAGTGT CGTCCAAAT	C TGGTGCCAGA AGACTCGGTA	A AGGCCAGAGA CGCAAACG	TT AATCGTCTTA AACAGGCGTA
SN19A	CTATTAGTGT CGTCCAAAT	C TGGTGCCAGA AGACTCGGTA	A AGGCCAGAGA CGCAAACG	TT AATCGTCTTA AACAGGCGTA
M5W	CTATTAGTGT CGTCCAAAT	C TGGTGCCAGA AGACTCGGTA	AGGCCAGAGA CGCAAACG	TT AATCGTCTTA AACAGGCGTA
A3	CTATTAGTGT CGTCCAAAT	C TGGTGCCAGA AGACTCGGTA	AGGCCAGAGA CGCAAACG	TT AATCGTCTTA AACAGGCGTA
CBS334.66	CTATTAGTGT CGTCCAAAT	C TGGTGCCAGA AGACTCGGTA	A AGGCCAGAGA CGCAAACG	TT AATCGTCTTA AACAGGCGTA
Br38	CTATTAGTGT CGTCCAAAT	C TGGTGCCAGA AGACTCGGTA	AGGCCAGAGA CGCAAACG	TT AATCGTCTTA AACAGGCGTA
L204	CTATTAGTGT CGTCCAAAT	C TGGTGCCAGA AGACTCGGTA	AGGCCAGAGA CGCAAACG	IT AATCGTCTTA AACAGGCGTA
DK37	CTATTAGTGT CGTCCAAAT	C TGGTGCCAGA AGACTCGGTA	AGGCCAGAGA CGCAAACG	IT AATCGTCTTA AACAGGCGTA
S225	CTATTAGTGT CGTCCAAAT	C TGGTGCCAGA AGACTCGGTA	AGGCCAGAGA CGCAAACG	TT AATCGTCTTA AACAGGCGTA
WaiteInst.6195	CTATTAGTGT CGTCCAAAT	C TGGTGCCAGA AGACTCGGTA	AGGCCAGAGA CGCAAACG	TT AATCGTCTTA AACAGGCGTA
CBS483.83	CTATTAGTGT CGTCCAAAT	C TGGTGCCAGA AGACTCGGTA	AGGCCAGAGA CGCAAACG	IT AATCGTCTTA AACAGGCGTA
54_95	CTATTAGTGT CGTCCAAAT	C TGGTGCCAGA AGACTCGGTA	AGGCCAGAGA CGCAAACG	TT AATCGTCTTA AACAGGCGTA
DAOM21327	CTATTAGTGT CGTCCAAAT	C TGGTGCCAGA AGACTCGGTA	AGGCCAGAGA CGCAAACG	TT AATCGTCTTA AACAGGCGTA
L234	CTATTAGTGT CGTCCAAAT	C TGGTGCCAGA AGACTCGGTA	AGGCCAGAGA CGCAAACG	TT AATCGTCTTA AACAGGCGTA
Sc62.8	CTATTAGTGT CGTCCAAAT	C TGGTGCCAGA AGACTCGGTA	AGGCCAGAGA CGCAAACG	TT AATCGTCTTA AACAGGCGTA
CBS624.84	CTATTAGTGT CGTCCAAAT	C TGGTGCCAGA AGACTCGGTA	AGGCCAGAGA CGCAAACG	TT AATCGTCTTA AACAGGCGTA
Stillwell309_3	CTATTAGTGT CGTCCAAAT	C TGGTGCCAGA AGACTCGGTA	AGGCCAGAGA CGCAAACG	TT AATCGTCTTA AACAGGCGTA
CBS633.84	CTATTAGTGT CGTCCAAAT	C TGGTGCCAGA AGACTCGGTA	AGGCCAGAGA CGCAAACG	TT AATCGTCTTA AACAGGCGTA

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DAOM21785	AAGGGTTTGT	AGGCTGCTTT	AAATTTTATT	T		-GTGAAGATA	GCCCAAC-AG	ATAATTAATT
CBS305.82	AAGGGTTTGT	AGGCTGCTTT	AAATTTTATT	T		-GTGAAGATA	GCCCAAC-AG	ATAATTAATT
SN19A	AAGGGTTTGT	AGGCTGCTTT	AAATTTTATT	T		-GTGAAGATA	GCCCAAC-AG	ATAATTAATT
M5W	AAGGGTTTGT	AGGCTGCTTT	AAATTTTATT	T		-GTGAAGATA	GCCCAAC-AG	ATAATTAATT
A3	AAGGGTTTGT	AGGCTGCTTT	AAAATTTATT	T		-GTGAAGATA	GCCCAAC-AG	ATAATTAATT
CBS334.66	AAGGGTTTGT	AGGCTGCTTT	AAAATTTATT	T		-GTGAAGATA	GCCCAAC-AG	ATAATTAATT
Br38	AAGGGTTTGT	AGGCTGCTTT	AAATTTTATT	T		-GTGAAGATA	GCCCAAC-AG	ATAATTAATT
L204	AAGGGTTTGT	AGGCTGCTTT	AAAATTTATT	T		-GTGAAGATA	GCCCAAC-AG	ATAATTAATT
DK37	AAGGGTTTGT	AGGCTGCTTT	AAAATTTATT	T		-GTGAAGATA	GCCCAAC-AG	ATAATTAATT
S225	AAGGGTTTGT	AGGCTGCTTT	AAAATTTATT	T		-GTGAAGATA	GCCCAAC-AG	ATAATTAATT
WaiteInst.6195	AAGGGTTTGT	AGGCTGCTTT	AAATTTTATT	T	-	-GTGAAGATA	GCCCAAC-AG	TTAATTAATT
CBS483.83	AAGGGTTTGT	AGGCAGCTTT	GAATTTTCTC	TT	TT-CC	AAG-T-	AATTAG	ATAATTAATC
54 95	AAGGGTTTGT	AGGCAGCTTT	GAATTTTCTC	TT	TT-CC	AAG-T-	AATTAG	ATAATTAATC
DAOM21327	AAGGGTTTGT	AGGCAGCTTT	GAATTTTCTC	TT	TT-CC	AAG-T-	AATTAG	ATAATTAATC
L234	AAGGGTTTGT	AGGCAGCTTT	GAATTTTCTC	TT	TT-CC	AAG-T-	AATTAG	ATAATTAATC
Sc62.8	AAGGGTTTGT	AGGCAGCTTT	GAATTTTCTC	TT	TT-CC	AAG-T-	AATTAG	ATAATTAATC
CBS624.84	AAGGGTTTGT	AGGCTGCTTT	GAATATTATC	TTTTAAT	TTACC-TTAT	GGTAAA-ATA	GCGC-ATTAG	ATAATTAATC
Stillwell309 3	AAGGGTTTGT	AGGCTGCTTT	TAATTTTATC	TATAACAAA-	TTACCCCTCC	GGTAAACATA	GCACAAT-AG	ATACTTAATA
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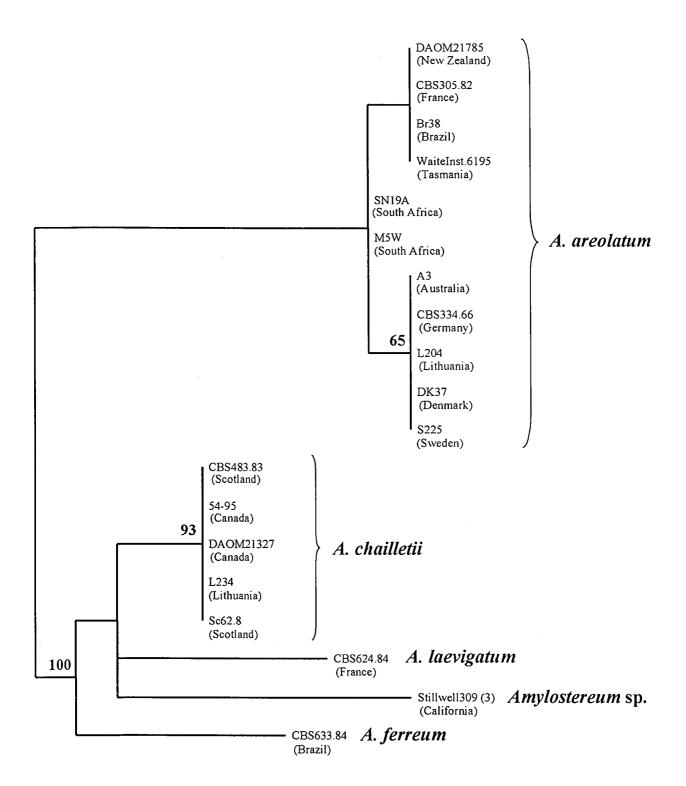
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CBS305.82	AAAGCTAGAA	TCAAATAGAG	GTTATATTAT	ATAATGCTTA	AAGTAGGTCT	AATATCCTAA	CATATTAAGT	GGAATATTAA	
SN19A	AAAGCTAGAA	TCAAATAGAG	GTTATATTAT	ATAATGCTTA	AAGTAGGTCT	AATATCCTAA	CATATTAAGT	GGAATATTAA	
M5W		TCAAATAGAG							
A3		TCAAATAGAG							
CBS334.66		TCAAATAGAG							
Br38		TCAAATAGAG							
L204		TCAAATAGAG							
DK37		TCAAATAGAG							
S225		TCAAATAGAG							
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54 95	AAAGCTAGAA	TCAAATAGAG	GTTATATTAT	ATAATGCTTA	AAGTAGGTCT	AATATCCTAA	CAGATTAAGT	GGAATATTAA	
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L234	AAAGCTAGAA	TCAAATAGAG	GTTATATTAT	ATAATGCTTA	AAGTAGGTCT	AATATCCTAA	CAGATTAAGT	GGAATATTAA	
Sc62.8	AAAGCTAGAA	TCAAATAGAG	GTTATATTAT	ATAATGCTTA	AAGTAGGTCT	AATATCCTAA	CAGATTAAGT	GGAATATTAA	
CBS624.84	AAAGCTAGAA	TCAAATAGAG	GTTATATTAT	ATAATGCTTA	AAGTAGGTCT	AATATCCTAA	CAGATTAAGT	GGAATATTAA	
Stillwell309 3	AAAGCTAGAA	TCAAATAGAG	GTTATATTAT	ATAATGCTTA	AAGTAGGTCT	AATATCCTAA	CAGATTAAGT	GGAATATTAA	
CBS633.84	AAAGCTAGAA	TCAAATAGAG	GTTATATTAT	ATAATGCTTA	AAGTAGGTCT	AATATCCTAA	CAGATTAAGT	GGAATATTAA	

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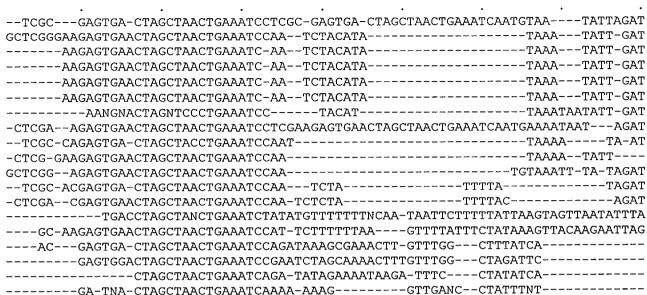
	4:	10 42	20 43	30 4	40 4	50 4	60 4	70 480)
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DAOM21785	ACCCCTCTCT	GTCAACGATG	AATGGTGGTT	GCTAATTATA	CAATTAGTAG	CTATGTTAAC	ACGATAACCA	TTCCGCCTTG	
CBS305.82	ACCCCTCTCT	GTCAACGATG	AATGGTGGTT	GCTAATTATA	CAATTAGTAG	CTATGTTAAC	ACGATAACCA	TTCCGCCTTG	
SN19A	ACCCCTCTCT	GTCAACGATG	AATGGTGGTT	GCTAATTATA	GAATTAGTAG	CTATGTTAAC	ACGATAACCA	TTCCGCCTTG	
M5W	ACCCCTCTCT	GTCAACGATG	AATGGTGGTT	GCTAATTATA	GAATTAGTAG	CTATGTTAAC	ACGATAACCA	TTCCGCCTTG	
A3	ACCCCTCTCT	GTCAACGATG	AATGGTGGTT	GCTAATTATA	GAATTAGTAG	CTATGTTAAC	ACGATAACCA	TTCCGCCTTG	
CBS334.66	ACCCCTCTCT	GTCAACGATG	AATGGTGGTT	GCTAATTATA	GAATTAGTAG	CTATGTTAAC	ACGATAACCA	TTCCGCCTTG	
Br38	ACCCCTCTCT	GTCAACGATG	AATGGTGGTT	GCTAATTATA	CAATTAGTAG	CTATGTTAAC	ACGATAACCA	TTCCGCCTTG	
L204	ACCCCTCTCT	GTCAACGATG	AATGGTGGTT	GCTAATTATA	GAATTAGTAG	CTATGTTAAC	ACGATAACCA	TTCCGCCTTG	
DK37	ACCCCTCTCT	GTCAACGATG	AATGGTGGTT	GCTAATTATA	GAATTAGTAG	CTATGTTAAC	ACGATAACCA	TTCCGCCTTG	
S225	ACCCCTCTCT	GTCAACGATG	AATGGTGGTT	GCTAATTATA	GAATTAGTAG	CTATGTTAAC	ACGATAACCA	TTCCGCCTTG	
WaiteInst.6195	ACCCCTCTCT	GTCAACGATG	AATGGTGGTT	GCTAATTATA	CAATTAGTAG	CTATGTTAAC	ACGATAACCA	TTCCGCCTTG	
CBS483.83	ACCCCTCTCT	GTCAACGATG	AATGGTGGTT	GCTAATTATA	AAATTAGTAG	CTATGTTAAC	ACGATAACCA	TTCCGCCTTG	
54 95	ACCCCTCTCT	GTCAACGATG	AATGGTGGTT	GCTAATTATA	AAATTAGTAG	CTATGTTAAC	ACGATAACCA	TTCCGCCTTG	
DAOM21327	ACCCCTCTCT	GTCAACGATG	AATGGTGGTT	GCTAATTATA	AAATTAGTAG	CTATGTTAAC	ACGATAACCA	TTCCGCCTTG	
L234	ACCCCTCTCT	GTCAACGATG	AATGGTGGTT	GCTAATTATA	AAATTAGTAG	CTATGTTAAC	ACGATAACCA	TTCCGCCTTG	
Sc62.8	ACCCCTCTCT	GTCAACGATG	AATGGTGGTT	GCTAATTATA	AAATTAGTAG	CTATGTTAAC	ACGATAACCA	TTCCGCCTTG	
CBS624.84	ACCCCTCTCT	GTCAACGATG	AATGGTGGTT	GCTAATTATA	AAATTAGTAG	CTATGTTAAC	ACGATAACCA	TTCCGCCTTG	
Stillwell309 3	ACCCCTCTCT	GTCAACGATG	AATGGTGGTT	GCTAATTATA	AAATTAGTAG	CTATGTTAAC	ACGATAACCA	TTCCGCCTTG	
CBS633.84	ACCCCTCTCT	GTCAACGATG	AATGGTGGTT	GCTAATTATA	AAATTAGTAG	CTATGTTAAC	ACGATAACCA	TTCCGCCTTG	

Figure 3: One of the most parsimonious trees obtained by heuristic searches of the sequence data of the mt-SSU-rDNA for isolates representing the different species of *Amylostereum* (Table 1). The length of the tree = 31 steps, CI = 0.968, HI = 0.032 and RI = 0.986. Bootstrap values (1000 replicates) are given at the branching points.



- **Figure 4:** (a) The tree of descent of *Amylostereum* spp. reported by Boidin and Lanquetin (1984). This tree is based on mating behaviour between the four *Amylostereum* spp. The results of their mating studies between the *Amylostereum* spp. are indicated here as sexually incompatible (-) or partially compatible (±).
- **(b)** The tree of descent indicated by the results from the present study based on mt-SSU-rDNA sequence data analysis.

Figure 5: Aligned DNA sequence data of part of the mt-SSU-rDNA of the four Amylostereum spp., as well as 15 other Basidiomycetes. All sequences, except those of the Amylostereum spp. were obtained from TREEBASE and originate from Hibbett et al. (1997). Gaps that were inserted due to alignment are indicated by a dash (-). Amylostereum areolatum is represented by isolate SN19A, A. chailletii by isolate CBS483.83, A. laevigatum by isolate CBS 624.84 and A. ferreum by isolate CBS 633.84.



90	100	110	120	130	140	150	160
•	•	•	•	•	•	•	•
T				G	SATAACATAAGGG	AGAA-TAAT(GATGT
T				G	SATAACGTAAGGG	AAAA-TAAT(GATAT
T					SATAACGTAAGGG	AAAA-TAAT(GATAT
T					SATAACGTAAGGG	AAAA-TTAT(GATAT
T					GATAACGTAAGGG	AAAA-TTAT(GATAT
Т					SATAACGTAAGGG	AAAA-TTAT	GATAT
T					SATAACGTAAGGG	AAAAATAAT(GATAT
Ψ					SATAACGTAAGGG	AAAA-TAAT	GATAT
Т					SATAACATAAGGG	AAAA-TAAT	GATAT
				_	SATAACGTAAGGG		
Ψ				_	SATAACGTAAGGG		
Τ				_	SATAACGTAGGGG		
±				_	ATAACGTAGGG ATAACGTAGGGG		
-							
TTAAGAAAAA							
TTTACTAGTTTAAGTGA	'I''I''I'AA'I'AAAAA	TAAACAAAAT.	AAAATAAAA				
					SATAT-GTAAGGC		
				_	SATAT-GTAAGGC		
				~	SATAT-GTNAGGO		
					ATAACGTAAGGG	;AAAA-TAAT(GATAT

180

170

220

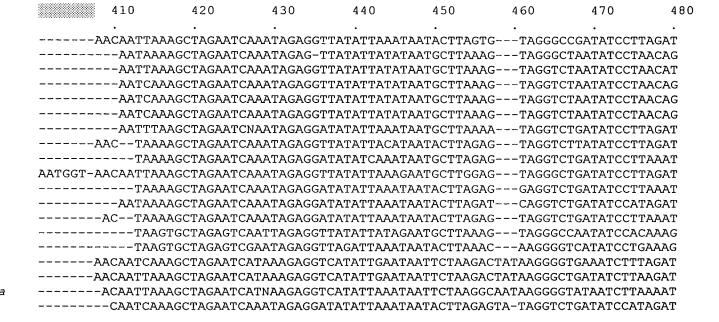
Bondarzewia berkleyi Echinodontium tinctorium Amylostereum areolatum Amylostereum chailletii Amylostereum laevigatum Amylostereum ferreum Clavicorona pyxidata Heterobasidion annosum Russula compacta Hericium ramosum Auriscalpium vulgare Lentinellus omphalodes Lentinellus ursinus Scytinostroma alutum Peniophora nuda Stereum annosum Stereum hirsutum Gloeocystidiellum_leucoxantha Laxitextum bicolor

TACCTTATTAATAGTGTCGCCCAAAGCTGGTGCCAGAAGACTCGGT-AAGGCCAGAGACGCAAACGTTAGTCGTCCTAAT TACCTTACTATTAGTGTCGCCCAAATCTGGTGCCAGAAGACTCGGTCAAGGCCAGAGACGCAAACGTTAATCGCCATAAT TACCTTACTATTAGTGTCGTCCAAATCTGGTGCCAGAAGACTCGGT-AAGGCCAGAGACGCAAACGTTAATCGTCTTAAA TACCTTACTATTAGTGTCGTCCAAATCTGGTGCCAGAAGACTCGGT-AAGGCCAGAGACGCAAACGTTAATCGTCTTAAA TACCTTACTATTAGTGTCGTCCAAATCTGGTGCCAGAAGACTCGGT-AAGGCCAGAGACGCAAACGTTAATCATCTTAAA TACCTTACTATTAGTGTCGTCCAAATCTGGTGCCAGAAGACTCGGT-AAGGCCAGAGACGCAAACGTTAATCGTCTTAAA TACCTTACTAATAGTGTTGTCCAAAGCTGGTGCCAGAAGACTCGGT-AAGGCCAGAAACGCAAACGTTAGTCGTCTTAAT TACCTTACTATTAGTGTCGCCCAAAACTGGTGCCAGAAGACTCGGT-AAGGCCAGAGACGCAAACGTTAATCGTCTTAAT TACCTTATTATTAGTGTCGCCCAAAACTGGTGCCAGAAGACTCGGT-AAGGCCAGAGACACAAACGTTAATCGTCTTAAT TACCTTACTATAAGTGTCGCCCAAATCTGGTGCCAGAAGACTCGGT-AAGGCCAGATACGCGAACGTTAATCGCCTTAAT TACCTTACTAATAGTGTTGTCCAAAACTGGTGCCAGAAGACTCGGT-AAGGCCAGAAACGCAAACGTTAGTCGTCTTAAT TACCTTACTATTAGTGTCGCCCAAAACTGGTGCCAGAAGACTCGGT-AAGGCCAGAGACGCAAACGTTAGTCGTCTTAAT TACCTTACTATTAGTGTCGCCCAAAACTGGTGCCAGAAGACTCGGT-AAGGCCAGAGACGCAAACGTTAGTCGTCCTAAT TACCTTACTA-TAGTGTTGTCAAAATTTGGTGCCAGAAGACTCGGT-AAGGCCAAAAACGCAAACGTTAGNCATCTTTAT TACTTTACTA-TAGTGTTGTCAAAAATTGGTGCCAGAAGACTCGGT-AAGACCAAAAACGCAAACGTTAGTCATCTTTAT AACCTTACTATTAGTGTCGCCCAAAACTAGTGCCAGAAGACTCGGT-AAGGCCAGAGACGCAAACGTTAGTCGTCATTAT AACCTTACTATTAGTGTCGCCCAAATCTAGTGCCAGAAGACTCGGT-AAGGCCAGAGACGCGAACGTTAGTCGTCATTAT ATCCTTACTATGAGTGTCGTCAAAAACTAGTGCCAGAAGACTCGGT-AAGGGCAGAGACGCAGACGTTAGTCGTCATTAT TACCTTACTAATAGNGTCGCCCAAAACTGGTGCCAGAAGACTCGGT-AAGGCCAGAGACGCAAACGTTAATCGTCTTAAT

200

CAGGCGTAAAGGGTTTGTAGGCAGCTT-GAAATTT---CTTTCTTAT-ATAGCACTAACTTAAAATACAAACTATTATAG CAGGCGTAAAGGGTTTGTAGGCTGCTTTAAA-TTTTATTT------GTGAAGATAGCCCAACA CAGGCGTAAAGGGTTTGTAGGCAGCTTTGAA-TTTTC-CT----TTT-CCAA---GT-AA----CAGGCGTAAAGGGTTTGTAGGCTGCTTTGAA-TATTATCTTTTA-A-TTTACCTTATGGTAAAAT-AGCGCA-CAGGCGTAAAGGGTTTGTAGGCTGCTTTGAA-TTTTATTTAATAGACTTTACCCCAAGGTAAAAT-AGCACA---CAGGCGTAAAGGGTGTGTAGGCGGCTTAAAAATTTT-CCTTTTCT-ATATTGCTCTAATTNGAAATAAGTAAAGTATAAA CAGGCGTAAAGGGTTTGTAGGCTGCTTTAA----CTTAGAATATAA-----CAGGCGTAAAGGGTTTGTAGGCGGTTTTAAA-TTTA-CTTACAAAAAAATTAATAAGTTAAGAA-----CAGGCGTAAAGGGTGTGTAGGCAGCTT-GACACTAT-CAATTTTCAAT-TAGCACAATATAAAATTAATAAAGCTTTTAA CAGGCGTAAAGGGTTTGTAGGCTGCTT-CAAATTCT-CCTTATT--ATATAGCTTCCGCTAATATGAATAATAAAGGAGG CAGGCGTAAAGGGTTTGTAGGCAGCTT-CAAATTT-ACCTTTTTT-ATATAGCTCCTTACTTTAAGAGTATTAAAGAGAA CAGGCGTAAAGGGTTTGTAGGCTGCTT-CAAATTT-ACCTTTTTT-ATATAGCTCCATAGAATAAGAGTATTAAAGAGAAA CAGGCGTAAAGGGTTTGTAGGCGGCCTTAATAG----CTTTTAAATTTTATTATTATTAAACAAAAGAAAATTTACTTAAA CAGGCGTAAAGGGTTTGTAGGCGGCCT-AATT----ACCTGTCACAGTAGATTTTCTACTAACAA-----TTACT-ACA CAGGCGTAAAGGGTTCGTAGGCGGCTT-GAAATCT---CTTTCTTT--AAAAATAGCACTCTTCTATTTTAA---CAGGCGTAAAGGGTTCGTAGGCGGCTT-AAGATTT---CTTTTTTT-AAAAAATAGCACTCTTCTCATTTAAATTTGGTT CAGGNGTAAAGGGTTCGTAGGCGGCTTTGAGAT----CTTTTTCTTTAAAAATAGCACTCTTCTTAGAGTTAAGGAAAG CAGGCGTAAAGGGTGTGTAGGCGGCTTTGAAATTTTA-CTTTTTTTAATAGCA----CTTTTTAATTTTTCATTAAATT

330	340 35	50 360	370	380	390	40
TTATTTAAAGGAGTTA-	· · ·					
TAAGGTAGGC-TTAA TTA- TTA-	GATAATT GATAATT GATAATT					
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CATTTTTTTTAAAATA AAACGATTGAACTTA-A AAACTTAATTATCCATC AAACAATTCT ATTAAGTAAACTAA-	ATTAAATTTT-AAG CATTAAAAAGT	GTAACATCTTATAG.	ATAT		·	
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ACTA-AGGGGAATATT-AAGG-GCGAAAGCTTTTTT-CC-----ACTAATG-ATT-----GACTCTGAGAAACGA-GG ATTA-AGTGGAATATT-AAAA-GCGAAGGCTTATTTTCC-----ATAAATG-ATT-----GACGCTGAGAAACGAAGG ATTA-AGTGGAATATT-AAAA-GCGAAGGCTTATTTTCC-----ATAAATG-ATT-----GACGCTGAGAAACGAAGG ATTA-AGTGGAATATT-AAAA-GCGAAGGCTTATTTACC-----ATAAATG-ATT-----GACGCTGAGAAACGAAGG ATTA-AGTGGAATATT-AAAA-GCGAAGGCTTATTTACC-----ATAAATG-ATT-----GACGCTGAGAAACGAAGG ATTA-AGTGGAATATT-AAAA-GCGAAGGCTTATTTACC----ATAAATG-ATT-----GACGCTGAGAAACGAAGG ATTA-AGTAGAATATT-AAAG-GCGAAGGCTTTTTTTCC----NNAAATG-ATT-----GACGCTGAGAAACGAAGG ACTA-AGGGGAATATT-AAGG-GCGAAAGCTTTTTTACC-----ATTAATG-ATT-----GACGCTGAGAAACGAAGG ACTA-AGTAGAATATT-AAAG-GCGAAAGCTTTTTT-CC-----ATTAATG-ATT-----GACGCTCAGAAACGAAGG ACCA-GGTAGAATATT-AAGA-GCGAAGGCTTTTTT-CC----ATTGATG-ATT-----GACGCTGAGACACGAAGG ACTA-AGTGGAATATT-AACG-GCGAAGGCTTTTTTTCC-----ATTAATG-ATT-----GACGCTGAGAAACGAAGG ACTA-AGTGGAATATT-AACA-GCGAAAGCTTTTTTTCC-----AATAATG-ATT-----GACGCTGAGAAACGAAGG ACTA-AGTGGAATATT-AACA-GCGAAAGCTTTTTTTCC-----AATAATG-ATT-----GAC-CTGAGAAACGA-GG ATTA-AGCAGAATATT-AAGG-GCGAAGGCTTTTTCTCCACTACGGAAAATATAAT--AACTGACGCTGAGAAACGAAGG ATTA-AGTAGAATACT-AAGA-GCGA-GGCTTTTTTTCC---ACTACCGAAC-AATAAAACTGACGCTGAGAAACTAAGG ACTT-GGAGGAATATTAAAGG-GCGAAGGCTTTTTTTCC-----ATAAATG-ATT-----GACGCTGAGGAACGAAGG ACTT-GGAGGAATATTAAAGG-GCGAAGGCTTTTTTTCC-----ATAAATG-ATT-----GAC-CTGAGGACCGAAGG TTCTTAGAGGAATATTAAAGG-GCGAAGGCTTTTTTTCC-----ATAAATG-ATT-----GACGCTGAGGAACGAAGG ACTA-AGGGGAATATT-AATA-GTGAAAGCTTTTTTTCT---AC--TAA-TG-ATT-----GACGCTGAGAAACGAAGG

TGAGGATAGGAATAGGATTAGATACCCAAATTACCCCTCTCTGTCAACGATGAATGGTGGCT--ACTAGTGAATCA---TGAGGATAGGAAATAGGATTAGATACCCAAAATACCCCTCTCTGTAAACGATGAATGGTGGTT--GCTAATTAGTAAA--TGAGGATAGGAATAGGATTAGATACCCAAAATACCCCTCTCTGTCAACGATGAATGGTGGTT--GCTAATTATAGAA--TGAGGATAGGAAATAGGATTAGATACCCCAAAATACCCCTCTCTGTCAACGATGAATGGTGGTT--GCTAATTATAAAA--TGAGGATAGGAAATAGGATTAGATACCCAAAATACCCCTCTCTGTCAACGATGAATGGTGGTT--GCTAATTATAAAA--TGAGGATAGGAATAGGATTAGATACCCCAAATACCCCTCTCTGTCAACGATGAATGGTGGTT--GCTAATTATAAAA--TGAGGATAGGAATAGGATTAGATACCCCAAAATACCCCTCTCTGTCAACGATGAATGGTAGTT--ACTAGTAAATGAA--TGAGGAAAGGAAATAGGATTAGATACCCCAAAATACCCCTCTCTGTCAACGATGAATGGTAACTA--TTAGTAATAAAA--TGAGGATAGGAATAGGATTAGATACCCCAAAATACCCCTCTCTGTCAACGATGAATGGTAGTTA--TTAGTAATAAAT--GGAGGAAAGGAAATAGGATTAGATACCC-AAATACCCCTCCCTGTCAACGATGAATGGTGGTT--ACTAGTTATAATAA-TGAGGAAAGGAAATAGGATTAGATACCCCAAAATACCCCTCTCTGTCAACGATGAATGGTGGTT--GCTAGT-ATAAA---TGAGGATAGGAATAGGATTAGATACCCCAAAATACCCCTCTCTGTCAACGATGAATGGTGGTT--ACTAGTAAAAAACC-GGAGGATAGGAAAAAGGATTAGATACCC-AATTACCCCTCTCTGTCAACGATGAATGGTAATTT--CTAGTGATTTGTAA GGAGGAGCGGAATTAGGATTAGATACCC-AACTACCCCTCTCTGTCAACGATGAATGGTAGTTAACCTGTAGACAAAA--GGAGGAGAGGAATTAGATTAGATACCC-AACTACCCCTCCCTGTCAACGATGAATGGTAGTTAACCTGTAGACAAAAA-GGAGGATAGGAATAAGGATTAGATANCC-AACTACCCCTCTCTGTCAACGATGAATGGTAGTTAACCTGT-AATAA----TGAGGATAGGAATAGGATTAGATACCCAAAATACCCCTCTCTGTCAACGATGAATGGTGGTCA--CTAGTCAAA-----

640

Bondarzewia_berkleyi Echinodontium_tinctorium Amylostereum_areolatum Amylostereum_chailletii Amylostereum_laevigatum Amylostereum_ferreum Clavicorona_pyxidata Heterobasidion_annosum Russula_compacta Hericium_ramosum Auriscalpium_vulgare Lentinellus_omphalodes Lentinellus_ursinus Scytinostroma_alutum Peniophora_nuda Stereum_annosum
Stereum_annosum Stereum_hirsutum Gloeocystidiellum_leucoxantha
Laxitextum_bicolor

650	660 670	680	690	700	710	720
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		TTG-0	TGGCGATGTTA	ACACGATAA	CCATTCCGCCT	TGTG
		TTG-G	TAGCTATGTTA	ACACGATAA	CCATTCCGCCT	TTGTG
		TTA-G	TAGCTATGTTA	ACACGATAA	CCATTCCGCCT	TGTG
		TTA-C	TAGCTATGTTA	ACACGATAA	CCATTCCGCCT	TGTG
		TTA-C	TAGCTATGTTA	ACACGATAA	CCATTCCGCCT	TGTG
		TTA-0	TAGCTATGTTA	ACACGATAA	CCATTCCGCCI	TGTG
	T	TATTG-0	TGGCGATGTTA	ACACGATAA	CCATTCCGCCI	TTGTG
		TTA-0	TAGTAATGTTA	ACACAATAA	CCATTCCGCCT	TTGTT
	T	TATTAA-	TGGCAATGTTA	ACACGATAA	CCATTCCGCCI	TGTG
		TTA-C	TGGCGATGTTA	ACACGATAA	CCATTCCGCCT	TGTG
	T	TATTA-G	TGGCGATGTTA	ACACGATAA	CCATTCCGCCT	TGTG
	T	TATTA-G	TGGCGATGTTA	ACACGATAAC	CCATTCCGCCT	TGTG
		TATTA-G	TGGCGATGTTA	ACACGATAAC	CCATTCCGCCT	TGTG
AAAATAACCAATA		TTA-G	TTTTAATGTTA	ACACGTTAAC	CCATTCCGCCT	TGTG
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		TAGG	TGGCAAAGCTA	ACGCGATAAC	CCATTCCGCCA	TGCG
		CAGG	AGGCAAAGCTA	ACGCGATAAC	CCATTCCGCCA	TGCG
		TAGG	TAGCAATGCTA	ACGCTATAAC	CATTCCGCCA	TGCG
		TTA-G	TGGCGATGTTA	ACACGATAAC	CATTCCGCCT	TGTG

AGTACGACTGC-AAAGTTGAAAA-CCAAAAAATTAGTCGGTCTCGAA--CAAA-CGAAGC-AGTACGACTGC-AAAGTTGAAA--CCAAAAAATTAGTCGGTTTCGGAG-CAC--CGAA-TG AGTACGACTGC-AAAGTTGAAAA-CAAAAAAATTAGTCGGTTTCGGAG-CAAA-CGAAGTG AGTACGACTGC-AAAGTTGAAAAACAAAAAA-TTAGTCGGTTTCGGAG-CAAA-CGAAGTG AGTACGACTGC-AAAGTTGAAAA-CAAAAAAATTAGTCGGTTTCGGAG-CAAA-CGAAGTG AGTACGACTGC-CAAGTTGAAAA-CAAAAAAATTAGTCGGTTTCGGAG-CAAA-CGAAATG AGTACGACTNC-AAAGTTGAAAACCCAAAAAATTATTCGGTCTCGAAN-CNTAACGGANTG ACTACGACTGC-AAAGTTAAAAACCCAAAAAATTAGTCGGTCTCGAAG-CAC---GAAAAC AGTACAACTGC-AAAGTTGAAAACCCAAAAAATTAGTCGGTTTCGGAG-CACT-CGAAGTG AGTACGACTGC-AAAGTTAAAAA-CCAAAAAATTAGTCGGTTTCGAAG-CAAA-CGAAGTC AGTACGACTGC-AAAGTTGAAAA-CCAAAAAATTAGTCG-TCTCGAAG-CAAA-CGAA-TC AGTACGACTGC-AAAGTTGAAAACCCAAAAAATTAGTCGGTTTCGAAG-CACA-CGAAGTG AGTACGACTGC-AAAGTTGAAAA-CCAAAAAATTAGTCGGTCTCGAAG-C----CGAAGTG AGTACGATTGN-NAAATTGAAAA-NNAAAAATTAGTCGGTTTCGG-AGC-GANCGAA---AGTACGATTGCCAAA-TTGAAAA-CCAAAAAATTAGTCGGTTTCGGAG-CG-ATCGAAGTG AGTACGACTGC-AAAGTTGAAA--CCAAAAAATTAGTCGGTTTCGAAG-CA-TACGAAGTG AGTACGACTGC-AAAGTTGAAA--CCAAAAAATTAGTCGGTTTCGAAG-CACTACGAAGTG AGTACGACTGC-AAAGTTGAAAG-NCAAAAAATTAGTCGGTTTCGAAGC--AAACGAA-TG AGTACGACTGC-AAAGTTGAAAA-NNAAAAATTAGTCGGNNTCGA-AGCA-NNCGGATCG **Figure 6:** One of the most parsimonious trees obtained by heuristic searches of the full sequence data set (including the hypervariable regions) of the mt-SSU-rDNA for 19 different Basidiomycetes spp, including the four *Amylostereum* spp. The tree length = steps, CI = 0.601, HI = 0.399 and RI = 0.522. Bootstrap values (1000 replicates) are given at the branching points.

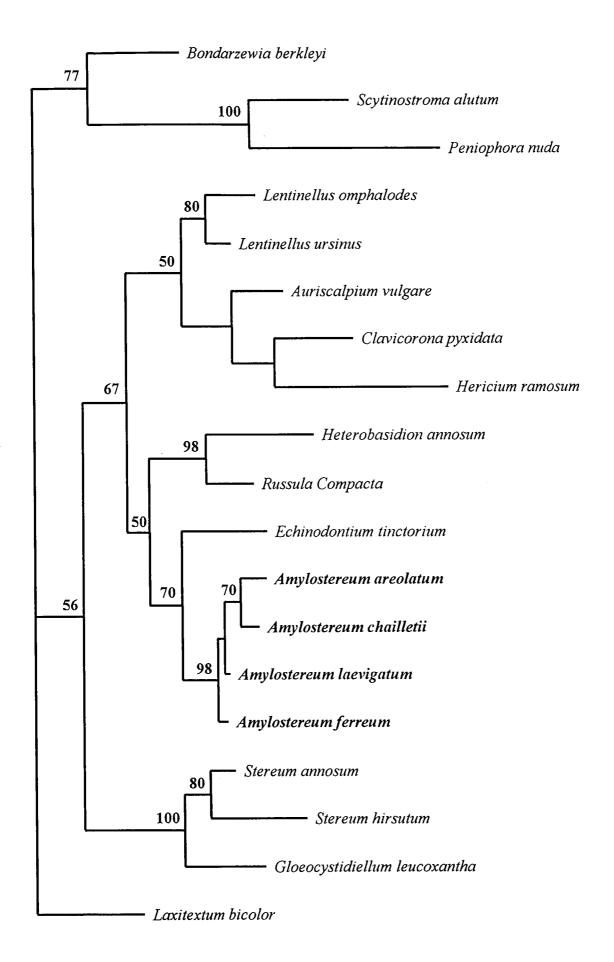
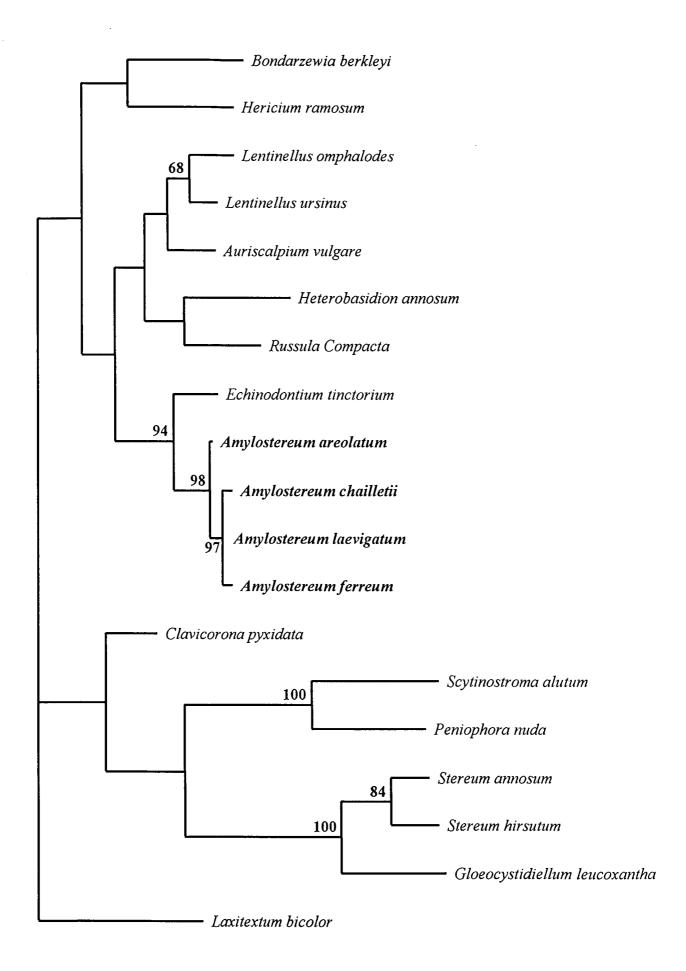
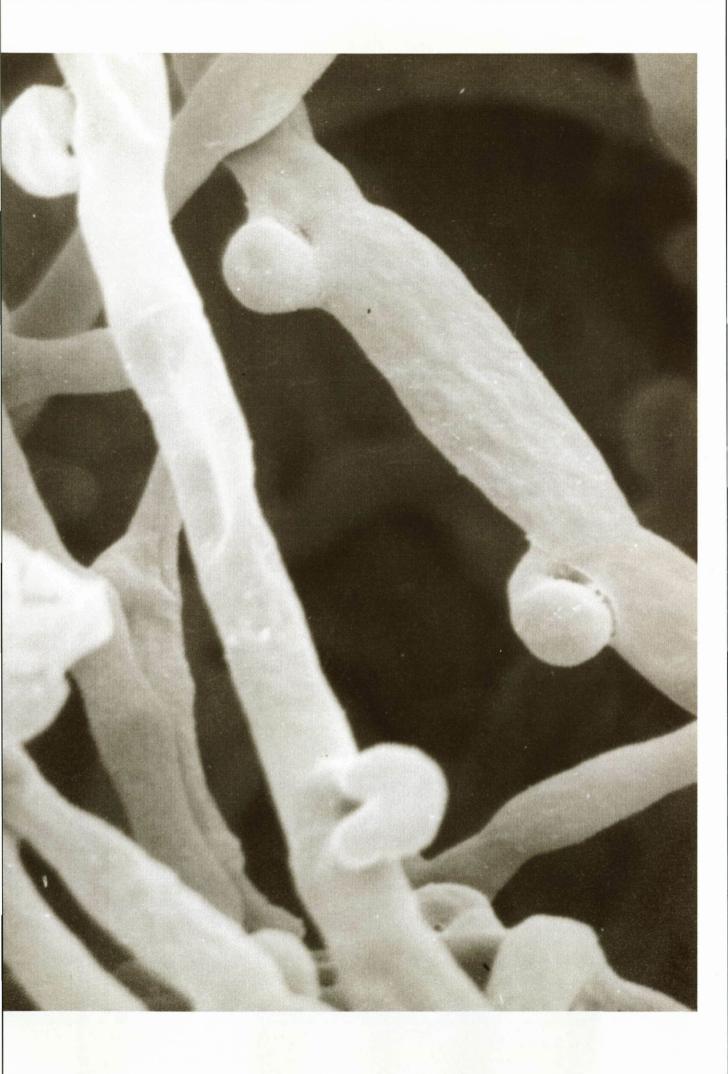


Figure 7: One of the most parsimonious trees obtained by heuristic searches of the mt-SSU-rDNA for 19 different Basidiomycetes spp, including the four *Amylostereum* spp., where the hypervariable regions were excluded. Bootstrap values (1000 replicates) are given at the branching points. Tree length = 639 steps, CI = 0.604, HI = 0.396 and RI = 0.595.





TAXONOMY OF AMYLOSTEREUM, WITH SPECIAL REFERENCE TO A. AREOLATUM ASSOCIATED WITH THE WOOD WASPS SIREX NOCTILIO AND S. JUVENCUS

ABSTRACT

Members of the genus Amylostereum (Basidiomycetes) are best known for their symbiotic relationship with siricid wood wasps. In this study, the phylogenetic relationship between Amylostereum areolatum, A. chailletii, A. laevigatum and A. ferreum was investigated using sequence and RFLP analyses of the variable nuc-IGS-rDNA region. Special attention was given to isolates of A. areolatum associated with S. noctilio and S. juvencus, as the specificity of the associations separates populations of the fungus. RFLP analysis of this DNA region is also evaluated as a potential diagnostic tool to delineate Amylostereum spp. The DNA sequence analysis showed that A. ferreum and A. laevigatum are most closely related to each other. Of the two other species in the genus, A. chailletii was more closely related to these two species than to A. areolatum, which was the most clearly defined species in the genus. One isolate that was obtained from S. areolatus and was expected to be A. chailletii, grouped more closely to A. laevigatum. This isolate might represent a new species or a distinct group in of one of the species. Isolates of A. areolatum associated with both S. noctilio and S. juvencus contained four heterogenic sequences in the DNA region analysed. These heterogenic sequences were contained in each isolate of the fungus in one of five combinations. Neither the heterogenic sequences contained in the fungal isolates, nor the different combinations of these sequences, were consistent in their association with S. noctilio or S. juvencus. The isolates of A. areolatum associated with these two species of wood wasps could thus not be defined in two separate groups using these methods. Despite the heterogenic nature of this DNA region in some isolates, RFLP analysis could effectively be used to distinguish between the different species of Amylostereum.

INTRODUCTION

Members of the wood wasp family Siricidae have larval states that either live in the stems of plants or are woodborers. For example the genera *Sirex* and *Urocerus*, infest softwoods and especially conifers (Benson, 1943; Chamberlin, 1960; Morgan, 1968). A further common characteristic of these two genera is the highly evolved association with specific wood-infecting basidiomycetes (Cartwright, 1929; Francke-Grosmann, 1939; Morgan, 1968). Conidia (oidia) or bundles of fungal mycelium are carried in a pair of specialised intersegmental mycangia near the base of the ovipositor of the adult female wasps and in external hypopleural organs of the female larvae (Buchner, 1928; Francke-Grosmann, 1939; Parkin, 1941). The fungus is then inoculated into the wood together with the eggs during oviposition, and it has been hypothesised that this infection is necessary for the subsequent development of the larvae (Madden & Coutts, 1979; Madden, 1981).

Using polymorphisms in protein banding patterns and mating studies, Gaut (1970) showed that the relationship between Siricidae and fungi is species specific. One fungal species can, however, be carried by more than one species of Siricidae. Gaut (1970) also found that Amylostereum areolatum (Fr.) Boid. is the symbiont of S. noctilio Fabr., S. juvencus Linn. and S. nitobei Mats., while Amylostereum chailletii (Pers.:Fr.) Boid. is carried by S. cyaneus Fabr., S. imperiales Kirby, S. areolatus Cress., S. californicus Nort., Urocerus gigas Linn., U. augur augur Klug. and U. augur sah Mocs. The morphological differences between the different woodwasp species are often subtle and their identities have frequently been confused, as have the identities of their fungal associates (Benson, 1943; Thomsen, 1996). The specificity of the symbiosis can thus serve as a useful taxonomic character when attempting to identify a woodwasp or its fungal symbiont.

During the last century, S. noctilio and its fungal symbiont have become established and is a serious pest in pine plantations of Australasia (Neumann, Morey & McKimm, 1987; Madden, 1988; Chou, 1991). The fungal symbiont associated with this wood wasp proved difficult to identify and it was not until 1969 that it was correctly identified as A. areolatum (Gaut, 1969). Recently the Sirex-Amylostereum complex has been reported from South America (1980) and South Africa (1994) and now pose a threat to the

softwood industries of these countries (Baxter, Rong & Schutte, 1995, Reardon, Eav & Wetterberg, 1995, Tribe, 1995).

The rarity and absence of sporocarps in nature has resulted in significant problems in the taxonomy of the fungal associates of Siricidae. The result is that these fungi often had to be studied entirely in culture or based on structures in the mycangia of the insect vectors (Talbot, 1964; King, 1966). Fruiting structures can be obtained artificially by using the wood-block culture method described by Tamblyn & Da Costa (1958), but Talbot (1964) reported that differences exist between the different stages of maturity using this method. He, therefore, suggested caution when using this method. A further complicating factor is that A. areolatum and A. chailletii are very similar in culture and fruiting body morphology. The clearest difference between these two species is that A. areolatum produces arthrospores in culture and these structures are absent in A. chailletii.

The phylogenetic relationship between isolates of one fungal species associated with different siricid species has not been addressed previously. In this study the evolutionary distance between A. areolatum isolates associated with S. noctilio and S. juvencus was considered using PCR based RFLP fingerprinting, as well as analysis of nuclear IGS sequence. Sequence data and RFLP data of this region was also used to evaluate the phylogenetic relationships between the four different species of Amylostereum.

The taxonomy of the Siricidae as well as that of their fungal symbionts is complicated. It would, therefore, be useful to find an easy and reliable technique to distinguish both these parties. Harrington & Wingfield (1995) showed the value of restriction fragment length polymorphism's (RFLP's) of PCR fragments, in the delineation of Basidiomycetes in culture. A second aim of this chapter was, therefore, to use PCR based RFLP analysis of the intergenic spacer (IGS) region of the nuclear ribosomal DNA (nuc rDNA) operon to distinguish between A. areolatum, A. chailletii, A. laevigatum (Fr.) Boid. and A. ferreum (Berk. & Curt.) Boid. & Lanq.

MATERIALS AND METHODS

Isolates studied

Isolates (Table 1) were maintained on Petri dishes (9 cm diameter) containing MYA (2% malt extract, 0,2% yeast extract and 1,5% agar) or pine extract MYA (pine extract prepared by autoclaving pieces of pine wood in the water to be added to the medium) at 25 °C. The cultures were stored in McCartney bottles on MYA at 4 °C. South African isolates of the fungal symbiont of S. noctilio were all made from mycangia of female S. noctilio wasps. A detailed description of the technique used in these isolations is given in Chapter 2. Isolates from Brazil were also obtained from the mycangia of female S. noctilio wasps (supplied by Mr. E. Schaitza, Embrapa, Colombo, Brazil). Isolates from Australia were purified from cultures of the nematode Deladenus siricidicola, imported into South Africa from Australia as part of a biological control programme for S. noctilio. These nematodes are maintained on cultures of A. areolatum and nematode inoculum de facto carries the fungus. Isolates of A. areolatum and A. chailletii from Europe were supplied by Dr. I. M. Thomsen (Danish Forest and Landscape Research Institute, Hoersholm, Denmark) and Dr. R. Vasiliauskas (Swedish University of Agricultural Sciences, Uppsala, Sweden). Other authenticated isolates of the four Amylostereum spp. from different parts of the world were obtained from CBS (Centraal Bureau voor Schimmelcultures, Baarn, Netherlands) and DAOM (Centre for Land and Biological Resources Research, Canada).

DNA isolation, PCR amplification

DNA was extracted from cultures using a modified version of the method described by Raeder & Broda (1985). The extracted genomic DNA (50 - 80 ng) was used directly as template for PCR. The intergenic spacer region (IGS) between the nuclear large subunit (LSU) and the 5S gene of the ribosomal RNA (rRNA) operon) was amplified using PCR. New primers specific for basidiomycetes, P-1 (5' TTG CAG ACG ACT TGA ATG G 3') (Hsiau, 1996) and 5S-2B (5' CAC CGC ATC CCG TCT GAT CTG CG 3') (Coetzee, 1997) were tested. IGS PCR fragments were generated using the Expand™ High Fidelity PCR System on a Hybaid TouchDown (Hybaid limited, U.K.) PCR unit. PCR reaction mixes and reaction conditions were the same as those described previously (Chapter 3).

PCR amplification for some isolates of A. areolatum resulted in two fragments of different size. To separate these bands for analysis, DNA represented by the bands on agarose gels were used as template DNA for secondary PCR, for isolates A8 and DK 37. A sterile disposable tip of a Gilson Pipetman was pushed into the band on the gel and stirred in the reaction mixture. The reaction mixture and reaction cycle used for were the same as those used for the initial PCR.

DNA sequencing and sequence data analysis

DNA sequence of the IGS region of was determined for isolates CBS 483.83 (A. chailletii), CBS 624.84 (A. laevigatum) and CBS 633.84 (A. ferreum), Stillwell 309(3) (Amylostereum sp. isolated from S. areolatus) and all isolates of A. areolatum (Table 1). DNA sequencing of PCR products was performed using an ABI PRISMTM 377 automated DNA sequencer. PCR products were purified using a NucleonTMQC PCR/OLIGO clean up kit (Amersham Life Science Inc.) prior to sequencing. Thermo SequenaseTM dye terminator cycle sequencing pre-mix kit (Amersham Life Science Inc.) with Thermo SequenaseTM DNA polymerase was used in all sequencing reaction mixtures. Sequencing of both strands of amplified PCR products was acheived using the primers P-1 and 5S-2B.

To interpret the double product amplified for some isolates of *A. areolatum* and to obtain sequence for the whole amplified fragment, secondary PCR products of isolate DK 37 were cloned for sequencing. PCR fragments were purified with the NucleonTMQC PCR/OLIGO clean up kit (Amersham Life Science Inc.) and cloned using the pGEM®-T Easy Vector System as described in the pGEM®-T and pGEM®-T Easy Vector Systems technical manual (Promega corporation, U.S.A.). Screening for positive colonies containing the insert were done by PCR using the M13U and M13R primers. Cloned products were precipitated and purified as described above and sequenced using primers M13R and M13U. Sequence obtained from the cloned products was compared to sequence of *Armillaria* species from South Africa (Coetzee, 1997), to identify the flanking regions of the large subunit (28S) and 5S genes to which the P-1 and 5S-2B primers bind respectively.

DNA sequences were manually aligned by inserting gaps, which were treated as a fifth character (newstate). PAUP version 3.1.1 (Phylogenetic Analysis Using Parsimony) (Swofford, 1993) was used to analyse the sequence data by executing heuristic searches with TBR (Tree Bisection Reconstruction) branch swapping and MULPAR activated. Bootstrapping (1000 replicates) (Felsenstein, 1993) was used to determine confidence intervals of branching points on the shortest tree. Sequence data were used to determine exact sizes of PCR products, as well as the restriction sites of the restriction endonucleases AluI and CfoI.

Restriction analysis

Restriction analysis of the amplified IGS fragment was done using the restriction endonucleases AluI and CfoI (Boehringer Mannheim, Germany). Both enzymes (10 Units) were added to 20 µl of the unpurified PCR reaction mix containing the amplified products and digested overnight at 37 °C. Amplification products containing two PCR products of different size were digested in the same way, without separating the two products. Resulting restriction fragments were separated by electrophoresis on ethidium bromide stained 2 % (wt/v) agarose gels and visualised under UV illumination. Size estimates of RFLP fingerprints were made using a 100 bp ladder run as a molecular size marker. RFLP fingerprint fragments smaller than 100 bp were not included in the analysis, due to their weak visibility and the absence of comparative bands smaller than 100 bp in molecular marker. Exact restriction fragment sizes were, however, deduced from sequence data.

RESULTS

PCR amplification

Strong amplification products of the IGS region were obtained using the primers P-1 and 5S-2B (Figure 1). PCR fragment sizes were calculated to be 552 bp from sequence data for isolates of A. chailletii (CBS 483.83; DAOM 21327; 54-95), 583 bp for A. laevigatum (CBS 624.84), 558 bp for A. ferreum (CBS 633.84) and 569 bp for the isolate Stillwell 309(3).

PCR fragment sizes for isolates of *A. areolatum* or isolates thought to represent *A. areolatum* could be divided into three forms that were consistently present and reproducible in each isolate (Figure 2). In the first form, a single fragment of approximately 630 bp for isolates Waite Inst. 6195, DAOM 21785, Br17, Br60, M5W, SN19A, DK 782 and CBS 305.82, was observed on the agarose gels. Sequencing results, however, showed that this apparent single band was heterologous and represented two fragments of 622 and 638 bp. An exception was isolate CBS 305.82 for which a single fragment of 618 bp was amplified. In the second form, a single PCR fragment of 570 bp was amplified (CBS 334.66). In the third form, two PCR fragments with sizes of 638 and 570 bp or 622 and 570 bp were observed for each of isolates L204, L236, S225, S227, DK37, A3, A4 and A11. These double bands were successfully reamplified using each DNA band from the gel as template in a PCR reaction for isolates A4 and DK 37. Two single bands were thus obtained with fragment sizes (638 and 570 bp) identical to each of the original DNA fragments obtained with the initial PCR.

DNA sequencing and sequence data analysis

Full sequence of the PCR product including the primer binding sites was obtained for the each of the separately cloned double products of isolate DK 37. There was a greater than 90% homology between the first 100 bp from the 5' end and last 94 bp on the 3' end sequences of this isolate, and the corresponding flanking sequence obtained from the IGS region of different isolates of *Armillaria* from South Africa. Sequences obtained using the primers P-1 and 5S-2B for other isolates of *Amylostereum* extended into these highly conserved 28S (5' end) and 5S (3' end) genic regions. They were, however, between 16 and 54 bp short of the full sequence of the PCR fragment, that would include the primer binding sites. Isolate DAOM 21785 (*A. areolatum*), however, lacked 95 bases on the 3' end of the fragment. Due to the highly conserved nature of these regions, it was assumed that these absent sequences were identical to the sequences obtained for these regions from isolate DK37. Sequence from isolate DK 37 was, therefore, used to complete the flanking sequences of other isolates, in order to calculate total sizes for the restriction map. These full sequences amounted to a total of 694 characters after alignment (Figure 3).

Four different sequences (hereafter referred to as sequence A, B, C and D) for the nuc-IGS-rDNA region were observed for isolates of A. areolatum (Figure 3). Sequences B, C and D were the same, other than in two sites where major indels were observed. Most isolates of A. areolatum contained two of these four sequences in any of five combinations (Table 2). Isolates Waite Inst. 6195; DAOM 21785; Br17; Br60; M5W; SN19A; DK782 contained sequences A and B. Isolates L204, S225 and S227 contained sequences A and D, while isolates L236, DK37, A3, A4 and A11 contained sequences B and D. Sequence for the IGS region was homologous in isolates CBS 305.82 (sequence C) and CBS 334.66 (sequence D). The heterogenic sequences contained in some isolates of A. areolatum were all included in the analyses. The heterogeneity in sequences of the IGS region observed in isolates of A. areolatum was, however, not observed in any of the other species of Amylostereum. However, fewer isolates were used for the other species, than for A. areolatum.

Heuristic search analysis of the sequence data from all isolates used in this study resulted in one tree of 537 steps (CI = 0.912; HI = 0.088; RI = 0.900) (Figure 4). The separation of sequences A, B, C and D from isolates of A. areolatum was supported by high confidence intervals of 99 % at the branching points. The different sequences within A. areolatum were separated from the other species of Amylostereum with a 100 % confidence interval at the branching point. A. laevigatum and A. ferreum together formed a sister group to A. chailletii. Isolate Stillwell 309(3) grouped closest to A. laevigatum, with a high confidence interval at the branching point of 79 %.

Restriction analysis

Restriction maps for both the restriction endonucleases AluI and CfoI were determined from sequence data (Figure 5a & b). PCR products of all Amylostereum spp. gave different restriction patterns when digested with the restriction endonuclease AluI (Figure 6a). Isolates representing or thought to represent A. areolatum showed different restriction patterns using this endonuclease (Figure 6a & 7a). The restriction fragment pattern that was produced for isolate CBS 305.82, had three fragments of 98, 159 and 361 bp in size, while that for isolate CBS 334.66 had two bands of 159 and 381 bp. Another pattern, comprised of 98, 159 / 163, 361 and 381 bp bands, was derived for isolates Waite Inst.

6195, DAOM 21785, Br17, Br60, M5W, SN19A and DK 782. For isolates S225, S227 and L204 a restriction pattern of 159 / 163, 361 and 381 bp bands was produced, while a pattern of 98, 159 and 381 bp bands was produced for isolates L236, DK37, A3, A4 and A11. These RFLP fingerprints obtained using *Alu*I thus support the heterogenic nature of the IGS region as indicated by the sequence data.

Restriction fragment sizes obtained with AluI were 187 and 329 bp for isolates of A. chailletii (CBS 483.83; DAOM 21327; 54-95), 188 and 350 bp for A. laevigatum (CBS 624.84) and 176 and 381 bp for A. ferreum (CBS 633.84) (Figure 6a). The restriction fingerprints for isolate Stillwell 309(3) (218 and 351 bp) differed from RFLP fingerprints obtained for all isolates used in this study representing the different species of Amylostereum (Figure 6a).

The restriction fingerprints obtained using the restriction endonuclease *CfoI* for isolates of *A. areolatum* varied between different isolates (Figure 6b & 7b). Isolates with PCR fragments of 622 and 638 bp (Waite Inst. 6195; DAOM 21785; Br17; Br60; M5W; SN19A; DK 782), gave restriction fragments of 315 / 310 (indistinguishable on agarose gels), 187, 120 and 99 bp. The restriction fingerprint obtained for isolate CBS 305.82 (PCR fragment size of 618 bp) had fragments of 310, 187 and 100 bp in size. For isolate CBS 334.66, that had a PCR product of 570 bp, fragments of 242, 187 and 120 bp were produced. For isolates L204, S225 and S227 (PCR fragments of 622 and 570 bp) restriction fragments of 315, 242, 187 and 120 bp were obtained, while fragments of 310, 242, 187 and 120 bp were obtained for isolates L236, DK37, A3, A4 and A11 (PCR fragments of 638 and 570 bp). RFLP fingerprints obtained using the endonuclease *CfoI* thus also support the heterogenic nature of the IGS region as indicated by the sequence data. Together with the *AluI* fingerprints all five combinations of sequences, as seen during sequence analysis, could be distinguished.

All isolates of A. areolatum could be distinguished from isolates of A. chailletii, A. laevigatum and A. ferreum by RFLP fingerprints obtained using the restriction endonuclease CfoI (Figure 6b). Restriction fingerprints using the restriction endonuclease CfoI (Figure 6b) also differentiated isolates of A. chailletii from isolates of A. laevigatum (CBS 624.84) and A. ferreum (CBS 633.84). The isolates of A. laevigatum (CBS 624.84)

and A. ferreum (CBS 633.84), however, produced identical fingerprints when the PCR products were digested with CfoI. The PCR product of isolate Stillwell 309(3) produced restriction fragments of similar size to A. laevigatum and A. ferreum when cleaved with CfoI. Restriction fragment size patterns were 139 and 351 bp for A. laevigatum, 139 and 353 for A. ferreum and 139 and 337 for isolate Stillwell 309(3). PCR products from isolates of A. chailletii resulted in restriction fragments with sizes of 261 and 139 bp.

DISCUSSION

In this study we have shown that isolates of A. areolatum used, contained one or two of four different sequences (groups A, B, C and D) in any of five combinations (A/B, A/D, B/D, C and D). Two different sized PCR products indicated the existence of heterogenic sequence in the IGS of the nuclear rDNA locus in isolates of A. areolatum. This was confirmed by RFLP analysis, cloning and sequencing of these fragments. Such heterogenic sequences are known to occur in some Basidiomycetes and could be contained in different ways in the genome of the fungus. Hibbett & Vilgalys (1991) reported on heterogeneity between rDNA copies in the genome of Lentinus. Gieser & Rizzo (1998) also noted the possibility of amplification of multiple haplotypes that could be contained as heterozygous loci in nuclei contained in dikaryons or as divergent paralogs. The existence of such paralogs in some isolates of A. areolatum is not unexpected considering the heterokaryotic nuclear state that dominates its life cycle. The predominantly vegetative form of reproduction of the fungus, in association with the wood wasp vector, would help to sustain such heterogeneity. This association is highly specific, with a clonal line of the fungus carried by a specific wasp and its descendants (Vasiliauskas, Stenlid, & Thomsen, 1998; Thomsen, 1999; Chapter 2). This would certainly prevent the mixing of the different sequence groups described in this study. Sexual reproduction could allow for the recombination of such polymorphisms, but the specificity of the wasp-fungus association and somatic incompatibility (Vasiliauskas, Stenlid, & Thomsen, 1998; Thomsen, 1999; Chapter 2) would still prevent these sexually derived fungal descendants from recombining with isolates of the fungus carried by wood wasps.

Isolates, presumably from S. noctilio, always contained the group A sequence, but group A sequence was also found in isolates presumed to be from S. juvencus. The same

situation applied to sequence group B that was present in isolates of the fungus from S. noctilio and S. juvencus. Sequence group D was always associated with isolates believed to be from S. juvencus, but sequence D was always associated with either sequence A or B. Both groups A and B were found associated with both S. noctilio and S. juvencus. Neither the heterogenic sequences contained in some isolates of A. areolatum, nor the different combinations of these sequences, were thus always consistent in their association with S. noctilio or S. juvencus. This observation can be explained in two ways. Firstly, the formation of the polymorphic loci and differentiation in the sequences could have occurred before the association of the fungus with the wasp. Alternatively the association of the wood wasp and the fungus could have been less specific in the initial stages of its development than is the case today. This would allow the different species of wasp to come in contact with the different DNA sequence groups of A. areolatum.

Gaut (1969) reported differences in protein banding patterns between the isolate of A. areolatum from France that he uses as reference culture, and his isolate from S. noctilio-infested wood in Tasmania. He ascribes these differences, that are quite substantial (6 bands out of 20 were variable), as normal variation within the species. Isolate CBS 305.82 is a sub-culture of the isolate that Gaut (1969) used as reference culture, and which from our data is homogenic for sequence C. In contrast, the isolate from Tasmania used in our study contains sequence groups A and B. The differences in protein banding patterns in A. areolatum isolates reported by Gaut (1969) could be explained by the different groupings within A. areolatum that are highlighted by this study.

Isolates of A. areolatum from South Africa, Brazil, New Zealand and Tasmania contain the same heterogenic combination of sequences for the IGS region, namely sequence groups A and B. This is consistent with the results from a previous study (Chapter 2) where isolates of the fungus from these regions showed a high degree of similarity. Isolates A3, A4 and A11 (isolated from cultures of the biocontrol nematode, Deladenus siricidicola) contained sequences B and D, while isolates from South Africa and Brazil contained sequences A and B. These results confirm those of somatic compatibility studies (Chapter 2) that showed that these are distinct genetic entities. It is also in accordance with the conclusion that a different genetic entity of A. areolatum has been inadvertently

introduced into to the countries of the Southern Hemisphere that have imported D. siricidicola as biocontrol agent from Australia.

DNA sequence analysis of the region from all four species of Amylostereum showed that A. ferreum and A. laevigatum are the most closely related species within the genus. These two species are also the only two species of Amylostereum not associated with wood wasps. Together, A. ferreum and A. laevigatum were more closely related to A. chailletii than to A. areolatum. A. areolatum was the most clearly defined species within the genus. These results confirm the findings and conclusions of a previous study (Chapter 3) that were based on analysis of the more conserved mt-SSU-rDNA region.

Despite the heterogenic sequences contained in the IGS region of some isolates of A. areolatum, RFLP analysis of the PCR fragment of this region, successfully distinguished the different species of Amylostereum. The two species most often confused in the past, A. areolatum and A. chailletii, were easily and clearly distinguished from each other, as well as from the other species of Amylostereum, using both AluI and CfoI restriction endonucleases. A. laevigatum and A. ferreum gave similar restriction patterns using the endonuclease CfoI, but could be delineated using the endonuclease AluI. The sum of RFLP fragment sizes resulting in a total size that is smaller than the size of the original PCR product were attributable to the existence of unresolved fragments smaller than 100 bp. Hibbett & Vilgalys (1991) also attributed such smaller sums to small unresolved fragments or fragments of similar size, migrating together. Including these smaller fragments, that were inferred from sequence data, in the analysis, defied the objective of developing an easy method for identifying species specific RFLP fingerprints for identifying the different species of Amylostereum. Such fragments were thus excluded for the purposes of this study. These results now provide a means to easily distinguish between species, such as has been achieved with other fungi (Harrington & Wingfield, 1995).

Isolate Stillwell 309(3) collected from the mycangium of *S. areolatus* (thus expected to be *A. chailletii* according to Gaut, 1970), gave a unique RFLP banding pattern (with the endonuclease *Alu*I) when compared to all other isolates included in the study. With the endonuclease *CfoI* the restriction fragment pattern of isolate Stillwell 309(3) was very

similar (except for a small size difference in one fragment) to that of A. laevigatum and A. ferreum. Sequence analysis of the region also showed that isolate Stillwell 309(3) is different to all the known species of Amylostereum, although it is most closely related to A. laevigatum. This finding supports the view (Chapter 3) that isolate Stillwell 309(3) is closely related to, but different from A. laevigatum and A. ferreum. This isolate might represent a species of doubtful authenticity, a distinct species or a sub-group of A. laevigatum and A. ferreum. As neither A. laevigatum nor A. ferreum has been implicated in associations with wood wasps, this finding warrants further investigation.

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Table 1: Isolates of Amylostereum used in this study.

Culture nr.	Identity			Host or source of isolate	Origin	Date isolated	Collector	
CBS cultures 305.82	Amylostereum areolatum		ım areolatum	Unknown	France	1964	J. Boiden	
334.66	A. areolatum		n	Picea abies	Germany	1967	Dimitri	
483.83	A. ch	ailletii		Mycangium of Urocerus gigas	Scotland, UK	1981	D.B. Redfern	
624.84	A. lae	vigatu	m	Juniperus nana	France	1978	P. Lanquetin	
633.84	A. ferreum			Podocarpus lambertii	Brazil	1978	R.T. Guerrero	
CLBRR cultures DAOM 21327	A. chailletii			Sporophore on Abies balsamea	Ontario, Canada	1948	R.F. Cain	
54-95	A. chailletii		•	Sporophore on fallen log in stand of hemlock	Ontario, Canada	1954	A. Hill & S. Gibson	
Stillwell 309(3)	Amylostereum sp.		ım sp.	Mycangium of S. areolatus	California, U.S.A.	Unknown	Stillwell	
Waite Inst. 6195	A. areolatum¹		n^1	Mycangium of S. noctilio	Tasmania	1962	Unknown	
DAOM 21785	n 1		1	Oviposition sites of S. noctilio in P. radiata wood	New Zealand	Unknown	G.B. Rawlings	
Other European is	olates		•				•	
L204	A. areolatum (± Clone S) ²		m (± Clone S) ²	Wood of wounded P. abies	Lithuania	1994	R. Vasiliauskas	
L236	"	"	(Clone A) ²	Wood of wounded P. abies	Lithuania	1995	R. Vasiliauskas	
DK37	"	••	(Clone A) ²	Fruiting body on P. abies	Denmark	1993	I.M. Thomson	
DK782	"	"	(Clone B) ²	Fruiting body on P. abies	Denmark	1987	J. Koch	
S225	"	"	(Clone S)2	Wood of wounded P. abies	Sweden	1994	R. Vasiliauskas	
S227	"	"	(Clone S) ²	Wood of wounded P. abies	Sweden	1994	R. Vasiliauskas	
Australian isolate	5							
*A3, A4, A11	A. ar	eolatui	n^1	Isolates from nematode cultures from CSIRO	Australia	1995	B. Slippers	
South American is	solates							
*Br17, Br60	Br17, Br60 A. areolatum¹		n^1	Mycangia of S. noctilio wasps	Brazil	1997	B. Slippers	
South African isol	ates							
*M5W	A. ar	eolatui	m^1	Wood around S. noctilio in P. radiata	South Africa	1994	M.J. Wingfield	
*SN19A	· · · · · · · · · · · · · · · · · · ·		1	Mycangia of S. noctilio wasps	South Africa	1996	B. Slippers	

 ^{1/} Identity as determined in a previous study (Chapter 3).
 2/ Vegetative compatibility group as determined by Thomsen (1996).

Table 2: Combinations of heterogenic sequences of the nuc-IGS-rDNA region of isolates of A. areolatum.

Sequence 1	Isolate nr.	Origin	Associated wasp species	VCG ²
A/B	DAOM 21785	New Zealand	Sirex noctilio	SH (±)
	WaiteInst. 6195	Tasmania	S. noctilio	SH (±)
	Br17	Brazil	S. noctilio	SH (±)
	Br60	Brazil	S. noctilio	SH
	M5W	South Africa	S. noctilio	SH
	SN19A	South Africa	S. noctilio	SH
	DK782	Denmark	S. juvencus	В
A/D	L204	Lithuania	S. juvencus	S (±)
	S225	Sweden	S. juvencus	S
	S227	Sweden	S. juvencus	S
B/D	L236	Lithuania	S. juvencus	A
	DK37	Denmark	S. juvencus	Ä
	A3	Australia	Unknown	?
	A4	Australia	Unknown	?
	All	Australia	Unknown	?
C	CBS 305.82	France	Unknown	?
D	CBS 334.66	Germany	Unknown	?

^{1/} These sequences were observed during sequencing and their presence confirmed using RFLP analysis of the PCR fragments. Their simultaneous presence in sequencing reactions, however, made it impossible to obtain their full sequence without cloning, as was done for isolate DK 37.

²/ VCG's as determined in a previous study (Chapter 2) and by Thomsen (1996).

Figure 1: A 1.5 % agarose gel stained with ethidium bromide, showing the IGS PCR fragments of the different species of *Amylostereum*. A 100 bp size marker was run on either side of the set of PCR fragments. Isolates S19A, Br60, Waite Inst. 6195, DAOM 21785, CBS305.82 and CBS334.66 represent *A. areolatum*. Isolate Stillwell 309(3) represent an *Amylostereum* sp. Isolates CBS483.83, 54-95 and DAOM 21327 represent *A. chailletii*, isolate CBS624.84 *A. laevigatum* and isolate CBS633.84 *A. ferreum*.

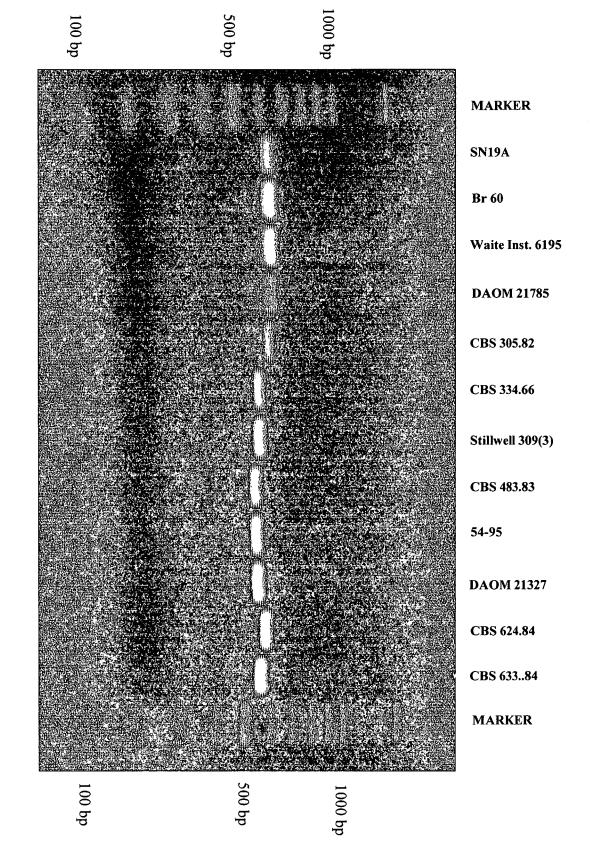


Figure 2: IGS PCR fragments of isolates of A. areolatum visualised on a 1.5 % agarose gel stained with ethidium bromide. 100 bp size marker were included as size standards in marker lanes. Isolates are those identified in Table 1.

Figure 3: Aligned DNA sequence data for the IGS of the rDNA operon for isolates representing the species of Amylostereum. Unknown sequence on the flanking regions of the fragment are indicated by lettering in italics. These sequences were inferred from the matching sequence of the highly conserved 5S (3') and 28S (5') rDNA genes between isolate DK37 (full sequence were determined after cloning) and various Armillaria species (Coetzee, 1997). Restriction sites for the restriction endonuclease AluI are shaded (3) and underlined (1) for CfoI. Gaps inserted due to alignment are indicated by a dash (-).

A. ferreum is represented by isolate CBS 633.84, A. laevigatum by isolate CBS 624.84, A. chailletii by isolate CBS 483.83 and the Amylostereum sp. by isolate Stilwell 309(3). Sequence for A. areolatum (A) was obtained from isolate DAOM 21785, A. areolatum (B) from cloned PCR products of isolate DK 37, A. areolatum (C) from isolate CBS 305.82 and A. areolatum (D) also from cloned PCR products of isolate DK 37. These sequences were also observed for other isolates of A. areolatum (Table 2).

	10	20	30) 40	0 50	0 6	70	80
A. ferreum	TTGCAGACGA CT	TGAATGGA	ACGGGGTACT	<i>G</i> TAAGCGGTA	GAGTAGCCTT	GTTGCTACGA	TCCGCTGAGG	TTAAGCCCTT
A. laevigatum	TTGCAGACGA CT							
Amylostereum.sp.	TTGCAGACGA CT							
A. chailletii	TTGCAGACGA CT							
A. areolatum (A)	TTGCAGACGA CT	TGAATGGA	ACGGGGTACT	GTAAGCGGTA	GAGTAGCCTT	GTTGCTACGA	TCCGCTGAGG	TTAAGCCCTT
A. areolatum (B)	TTGCAGACGA CT							
A. areolatum (C)	TTGCAGACGA CT							
A. areolatum (D)	TTGCAGACGA CT	TGAATGGA	ACGGGGTACT	GTAAGCGGTA	GAGTAGCCTT	GTTGCTACGA	TCCGCTGAGG	TTAAGCCCTT
	90	10	0 11	10 12	20 13	30 14	10 15	50 160
A. ferreum	GTTCGACAGA TT							
A. laevigatum	GTTCGACAGA TT						GGGGGCTTAA	
Amylostereum.sp.	GTTCGACAGA TT						GGGGGCTTAA	
A. chailletii	GTTCGACAGA TT						GGGGGCTTAA	
A. areolatum (A)	GTTCGACAGA TT							
A. areolatum (B)	GTTCGACAGA TT							
A. areolatum (C)	GTTCGACAGA TT							
A. areolatum (D)	GTTCGACAGA TT	'TGTTCAAC	CTCGGTTGGA	CTTCTCTCTC	TTCTCTTTTT	-CTTCCGCAC	GACGGCTTTA	GGGCAGGGC-
	170	18	0 19	0 20	00 21	10 22	20 23	30 240
A. ferreum	TTTCAGAC TT	GTGCTGTT	CCACGCGCGT	GTG-AGGAAA	-GGGAAGGGG	GTTT	CGCAATTT	TGAAGGGTT-
A. laevigatum	TTTCAGAC TT	GTGCTGTT	CCACGCGCGT	CTG-AGGAAA	-GGGAAGGGG	ATT	-GCGCAATTT	TGAAGGGTT-
Amylostereum.sp.	TTTCAGAC TT	GTGCGGTT	CCACGTGCGT	GTG-AGGAAA	-GGGA-GGGG	GGTT	-GCGCAATTT	TGAAGGGCT-
A. chailletii	TGTCAGAC TT							
A. areolatum (A)	TGTTCCAGAC TT							
A. areolatum (B)	TGTTCCAGAC TT							
A. areolatum (C)	TGTTCCAGAC TT							
A. areolatum (D)	TGTTCCAGAC TT							

	250	260	270	280	290	300	310 320
A. ferreum A. laevigatum Amylostereum.sp. A. chailletii A. areolatum (A) A. areolatum (B) A. areolatum (C) A. areolatum (D)	GCATACAAAA ACGAAGG	CTGCTGCTG AGGTTCTC AGGTTCTC	STA CAGAGCGA STA CAGAATGA STGC CGA CAGAATGG CGA CGGAATGA CGGAATGA	AG GGGG-AGT' AG GGGGGACT' AG GGGGT' TT GAGGTACT' AG GCGGACCT' AG GCGGACCT'	TG -A-AGGG-GA TG -A-AGGG TG -A-AGGGTGA TG TCCGAGGTAA TG TACAGGGTGA TG TACAGGGTGA	AA A GTGGAACT A AGTGCGACA A AGTGCGACA	T GT <u>GCGC</u> AAAA T TT <u>GCGC</u> AAAA
	330	340	350	360	370 3	380	390 400
A. ferreum A. laevigatum Amylostereum.sp. A. chailletii A. areolatum (A) A. areolatum (B) A. areolatum (C) A. areolatum (D)	TTGGA	A-A AAAATG A-C AAAATG A AAAATG A-C AAAATGTA A-G AAAATG A-G AAAATG	GG AGGTACCT	A A GA GAAGGATAA A	AAGGGAGCA- AAGGGTGCA- AAGGGG <u>GC</u> AG GATGGAACAA AG -AGGGAACAA AG -AGGGAACAA	CTTGAAAG CTTGAAAA - GCTTGAAGG A AGATGTGGG A GGA-GGGGG A GGA-GGGGG	A AATTGAA A AATTGAA G GCGGTTTGAA A G TCAA A G-GGTTTGAA A G-GGTTTGAA A G-GGTTTGAA
	410	420	430	4.40	450 4	160	470 480
A. ferreum A. laevigatum Amylostereum.sp. A. chailletii A. areolatum (A) A. areolatum (B) A. areolatum (C) A. areolatum (D)	GGGGCGGTTT GAACGAA GGGACGGTTT GAACAAA CGAAATG CAAGGTATAA TCGA CGAAGTGTAG TGGA CGAAGTGTAG TGGA CGAAGTGTAG TGGA	ACG AAGGTGCG ACA AAGGTGCG AAGGTGCG TC TCA AAAGGGAA TCA AAAGGGAA	AC ATTTTTGC AC ATTTGTAC AC GTTTGTAC CA AACAAAAG CA AACAAAAG	GA AACGTACTO GT AACGTAGTO GA AACGTAGTO TTCA TG TTCAAACTT TG TTCAAACTT	CG TCAAAC CG TCAAAC CA TCAAGC CG CTTGAA-CAA CG CTTGAA-CAA	CAAAATGAA CAAAATGAA CAGGAATGAA TGCCATATG AGCCATATG AGCCATATG	C AAAGTGTTTG C AAAGTGTTTG C AAAGTGTTTG CG CG CG

	490	500	510	520	530	540	550	560
A. ferreum A. laevigatum Amylostereum.sp. A. chailletii A. areolatum (A) A. areolatum (B) A. areolatum (C) A. areolatum (D)	AA-CTGG A-TCG AMMEGACTG AAGCA ACGCCGAGTG AAGCAG AAGCA ACGGAT-CTG AAGGCA AGGGAT-CTG AAGGAA AGGGAT-CTG AAGGAA	######################################	AAAG TGAAG AAAG TGAAG AAAA TGAAG GATC TGAAG AATG TGAAG AATG TGAAG	GGAGATATC GGATA -TTC GGAGAT-TC -GGGA -TTA-C GGGGA -TTA-C	AGGT GTGGA(AGG- GTG AGGT TTGGA(TGGGC TGGGC TGGGC	TTCA -GGGTO TTCA -GGGTO TTCA CGGGCO TTCA -GGGCO TTCA -GGGCO	GGGCC TAAAA- GGGCC TAAAA- ATTGC TCCATG AG-GC TCAAA- AG-GC TCAAA-	A-TC AG-C AGTC AGTC AGTC AGTC
•	570	580	590	600	610	620	630	640
A. ferreum A. laevigatum Amylostereum.sp. A. chailletii A. areolatum (A) A. areolatum (B) A. areolatum (C) A. areolatum (D)	GGGTTT -G-AC-CAAAAATTT CG-ATTCAAAAAAATTT CG-ATTCAAAAAAAAGT CG-ATTCAAAAAAAAGT CG-ATTCAAAAAAAAGT CG-ATTCAAAAAAAAGT CG-ATTCAAAAAAAAGT CG-ATTCAAAAAAAAGT CG-ATTCAAAAAAAAAGT CG-ATTCAAAAAAAAAAGT CG-ATTCAAAAAAAAAAGT CG-ATTCAAAAAAAAAAGT CG-ATTCAAAAAAAAAAAAAGT CG-ATTCAAAAAAAAAAAGT CG-ATTCAAAAAAAAAAAAAAGT CG-ATTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	TAT TTTTAA TATTT TATTAA TATTT TATTAA TATTT TATTAA TATTT TATTAA TATTT TATTAA	TTAA AAT-G/ TTAA AAT-G/ TTAA AAT-G/ TTAA ATTCG/ TTAA AAT-G/ TTAA AAT-G/	AATTA AAACCA(AATTA AAACCA(AATTA AAACCA(AAT-A AAACCA(AAT-A AAACCA(AAT-A AAACCA(CAGC ACCCAG CAGC ACCCAG CAGC ACCCAG CAGC ACCCAG CAGC ACCCAG	GATT CCCGCC GATT CCCGCC GATT CCCGCC GATT CCCGCC GATT CCCGCC GATT CCCGCC	STGGT CCCCA STGGT CCCCA STGGT CCCCA STGGT CCCCA STGGT CCCCA STGGT CCCCA	CCGT CCGT CCGT CCGT CCGT CCGT
	650	660	670	680	690			
A. ferreum A. laevigatum Amylostereum.sp. A. chailletii A. areolatum (A) A. areolatum (C) A. areolatum (C) A. areolatum (D)	GGTACTAAGT GGGCGGCA GGTACTAAGT GGGCGGCA GGTACTAAGT GGGCGGCA GGTACTAACT GGGCGGCA GGTACTAACT GGGCGGCA GGTACTAACT GGGCGGCA GGTACTAACT GGGCGGCA GGTACTAACT GGGCGGCA	ACT GTGGTTA ACT CTGGTTA ACT GTGGTTA ACT GTGGTTA ACT GTGGTTA ACT GTGGTTA	ACT GCGCAGA ACT GCGCAGA ACT GCGCAGA ACT GCGCAGA ACT GCGCAGA ACT GCGCAGA	ATCA GACGGA! ATCA GACGGGA! ATCA GACGGGA! ATCA GACGGGA! ATCA GACGGGA! ATCA GACGGGA!	TGG GGTG TGG GGTG TGG GGTG TGG GGTG TGG GGTG			

Figure 4: The most parsimonious phylogenetic tree of 537 steps (CI = 0.912; HI = 0.088; RI = 0.900) generated after a heuristic search with TBR (Tree Bisection Reconstruction) of the manually aligned IGS sequence data of the different species of *Amylostereum*. The midpoint is used to root the tree. Bootstrap values (1000 replicates) are given at the branching points. Different combinations of heterogenic sequences (A / B / C / D) contained in isolates of *A. areolatum* and the origin of the isolates containing each combination, are indicated (see Table 2).

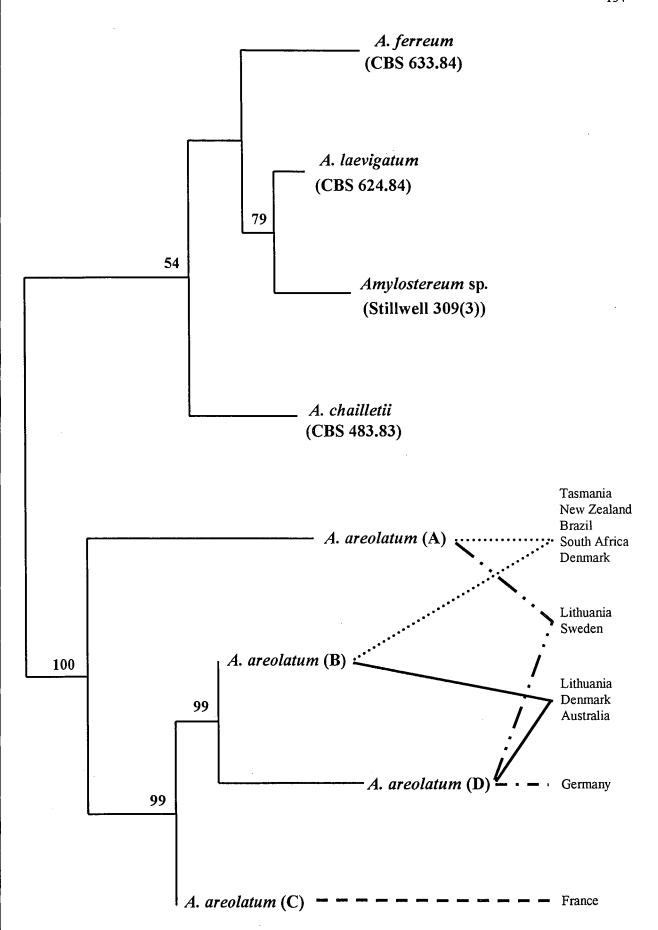


Figure 5: Restriction maps for the restriction enzymes AluI (a) and CfoI (b) for the nuc-IGS-rDNA region of different species of Amylostereum. Specific restriction sites ($\frac{1}{V}$) and fragment sizes (numbers indicate sizes in bp) were inferred from sequence data.

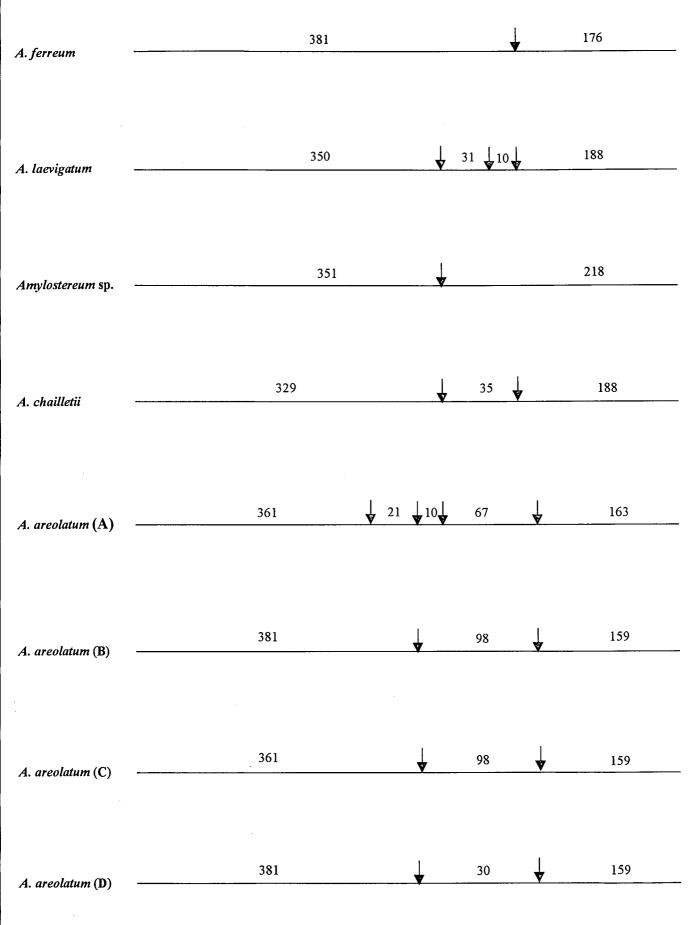


Figure 5(a)

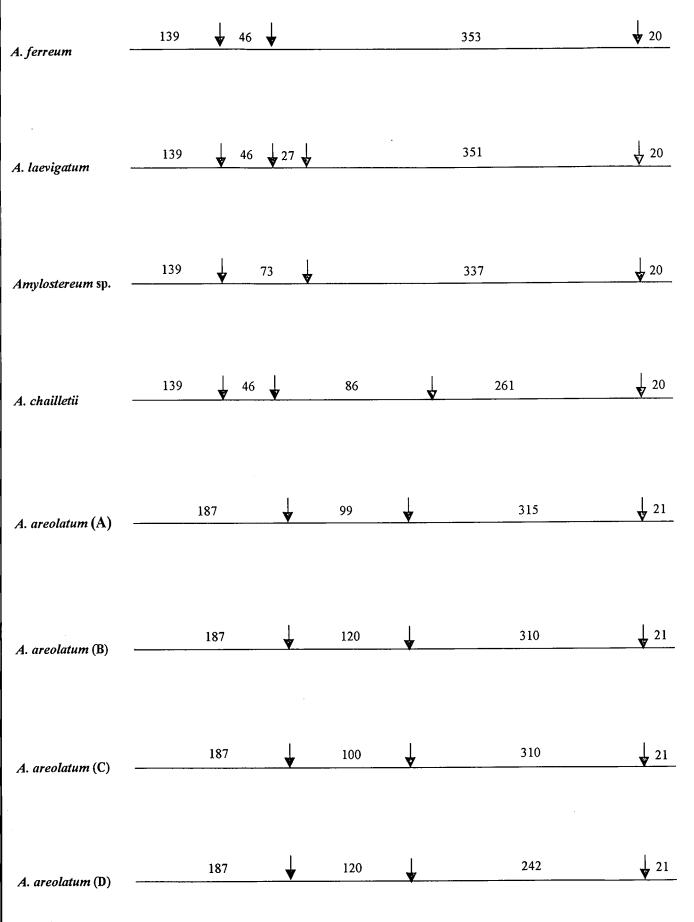


Figure 5(b)

Figure 6: A 2 % agarose gel stained with ethidium bromide showing AluI (a) and CfoI (b) restriction fragments of the IGS PCR products of different species of Amylostereum. Lanes marked a marker contain a 100 bp size marker. Isolates S19A, Br60, Waite Inst. 6195, DAOM 21785, CBS305.82 and CBS334.66 represent A. areolatum. Isolate Stillwell 309(3) represents an Amylostereum sp. Isolates CBS483.83, 54-95 and DAOM 21327 represent A. chailletii, isolate CBS624.84 A. laevigatum and isolate CBS633.84 A. ferreum.

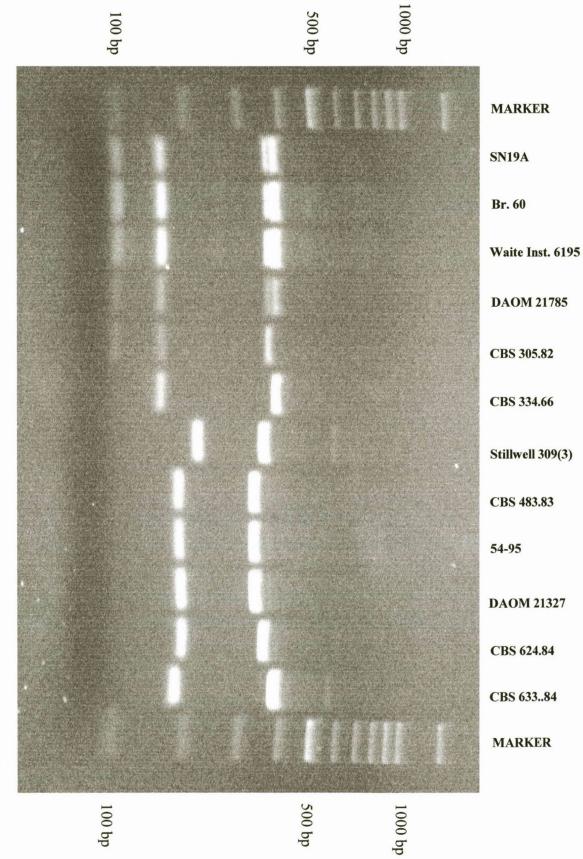


Figure 6(a)

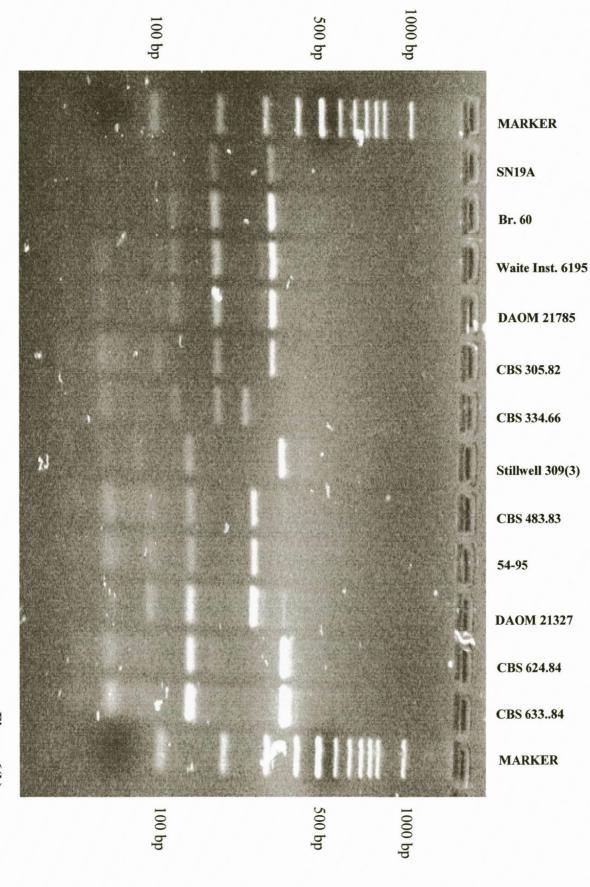


Figure 6(b)

Figure 7: AluI (a) and CfoI (b) restriction fragment patterns of the IGS PCR products of different isolates of A. areolatum, visualised on a 2 % agarose gel stained with ethidium bromide. Marker lanes contain a 100 bp size marker.

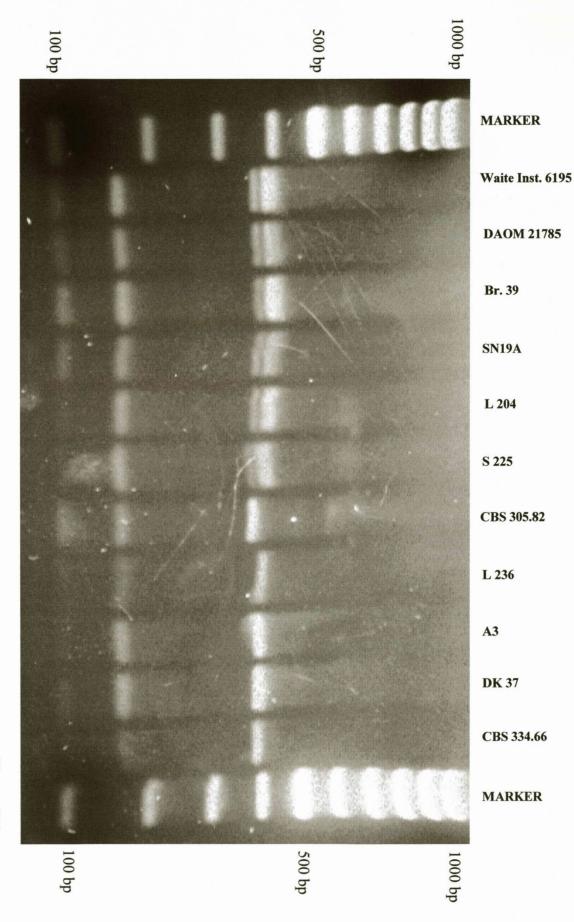
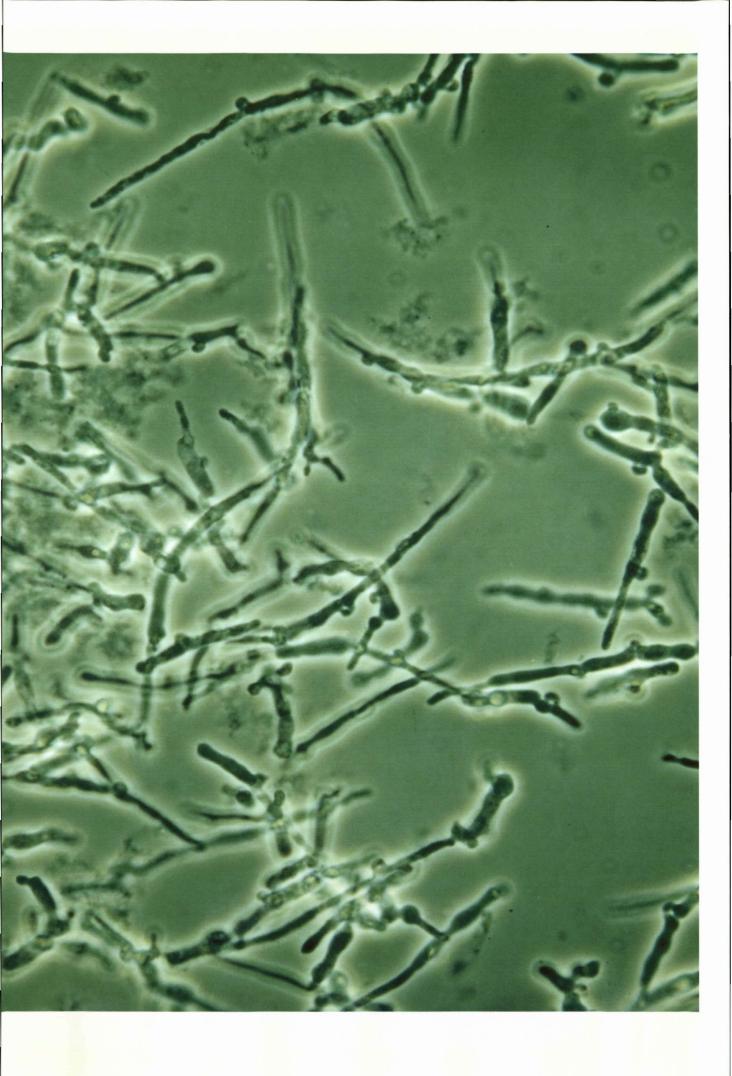


Figure 7(a)

Figure 7(b)



THE GENUS AMYLOSTEREUM AND ITS ASSOCIATION WITH WOODWASPS: A CONTEMPORARY REVIEW

ABSTRACT

A fascinating symbiosis exists between the fungi, Amylostereum chailletii and A. areolatum, and various species of Siricid woodwasps. These intrinsic symbioses and their importance to forestry have stimulated much research activity in the past. The fungi have, however, often been confused or misidentified. Similarly, the phylogenetic relationships of the Amylostereum spp. with each other, as well as with other Basidiomycetes, have been unclear for a long period. Recent studies based on molecular data have, however, given new insight into the taxonomy and phylogeny of the genus Amylostereum. Molecular sequence data have shown that A. areolatum is most distantly related to other Amylostereum spp. Of the three remaining species, A. laevigatum and A. ferreum are most closely related. Sequence data have also made it possible to develop PCR RFLPfingerprints to delineate Amylostereum spp., which presents a solution to the difficulties that are generally experienced identifying these fungi using traditional methods. Furthermore, sequence data suggest that there is an evolutionary relationship between Amylostereum spp. and such divergent species as Echinodontium tinctorium, Russula compacta, Heterobasidion annosum and Peniophora nuda. Recent studies, investigating the population structure of A. areolatum and A. chailletii, have also substantially increased our understanding of the ecology of these species that are associated with woodwasps. Clonal lineages have been shown to occur in both A. areolatum and A. chailletii. These genetic lines, that arise as a result of the association with woodwasps, are spread over large distances and are preserved over time. This character of the populations, now presents an opportunity to trace the geographical origin of these fungi and their associated wasps. The occurrence of heterogenic sequences in the nuc-IGS-rDNA region of isolates of A. areolatum also gives insight into the structure and relationship between populations of this fungus that are isolated as a result of its association with different woodwasp species. In this review an overview is given of these recent developments and the opportunities for future research.

INTRODUCTION

Amylostereum represents a fascinating genus of Basidiomycetes, of which two species live in a highly evolved symbiosis with Siricid woodwasps. Internal glands in some woodwasp species that contained fungal oidia were first reported in the 1920's (Buchner, 1928; Chrystal, 1928; Cartwright, 1929). The presence of clamp connections suggested that these fungi belonged to the Basidiomycetes, but their identities were uncertain. Subsequently, these fungi were identified as Stereum sanguinolentum (Alb. & Schw.:Fr.) Fr., S. chailletii (Pers.:Fr.) Fr., Stereum sp., Peniophora sp., among others (Thomsen, 1996). Eventually it was, however, conclusively shown that these fungi should reside in the genus Amylostereum (Talbot, 1964; Gaut, 1969 & 1970). Today it is known that two Amylostereum spp., A. chailletii (Pers.:Fr.) Boid. and A. areolatum (Fr.) Boid., are symbionts of a variety of woodwasp species (Gaut, 1970).

The relationship between *Amylostereum* spp. and woodwasps is highly evolved and has been shown to be always species specific (Gaut, 1970; Talbot, 1977). The principle advantage of the relationship for the fungus is that it is spread and effectively inoculated into new wood during wasp oviposition (Gilmour, 1965; King, 1966). In turn the fungus rots and dries the wood, so providing a suitable environment, nutrients and enzymes that are important for the survival and development of the insect larvae (Francke-Grosmann, 1939; Morgan, 1968; Madden & Coutts, 1979; Kukor & Martin, 1983; Martin, 1987).

The burrowing activity of the Siricid larvae and rot of the wood by *Amylostereum* spp., makes this insect-fungus symbiosis potentially harmful to host trees, which include important commercial species. In the Northern Hemisphere, where the Siricidae are native, the insect is, however, of little economic importance (Hanson, 1939; Hall, 1978; Spradbery & Kirk, 1978). Here a natural balance exists between the insect-fungus complex, its natural parasites and trees. In contrast, *Sirex noctilio* Fabr. and *A. areolatum*, that have been introduced into various countries of the Southern Hemisphere, have caused extensive mortality in exotic pine plantations in this region (Neumann, Morey & McKimm, 1987; Madden, 1988; Haugen, 1990; Neumann & Marks, 1990; Chou, 1991).

The association between woodwasps and Amylostereum and their importance to forestry in the Southern Hemisphere, has stimulated much research in this field. This work has been reviewed a number of times in the past (Morgan, 1968; Talbot, 1977; Neumann & Minko, 1981; Madden, 1988; Bedding, 1995; Thomsen, 1996; Chapter 1). Much of this research has, however, concentrated on the woodwasps and especially their control in the Southern Hemisphere. Recent studies on the fungal symbionts of Siricidae, has given new insight into the taxonomy, phylogeny and ecology of these fungi. The aim of this review is, therefore, to provide a contemporary view of Amylostereum and its symbiosis with woodwasps.

TAXONOMY AND PHYLOGENY

AMYLOSTEREUM SPP.

The genus Amylostereum was established in 1958 by Boidin to accommodate species of Stereum that have, among other characteristics, smooth amyloid basidiospores, hyaline encrusted cystidia and resupinate to effuso-reflexed fruiting bodies (Boidin, 1958). The genus then included A. chailletii (Pers.:Fr.) Boid., the type species, A. areolatum (Fr.) Boid. and A. laevigatum (Fr.) Boid. Boidin and Lanquetin (1984) added a fourth species in the genus, namely A. ferreum (Berk. & Curt.) Boid. & Lanq. (= Stereum ferreum) (Boidin & Lanquetin, 1984).

In a recent review Thomsen (1996) notes many misidentifications of isolates of Amylostereum, especially the species associated with woodwasps, have been made in the past. This can in most cases be ascribed to the rarity or absence of the sporocarps of these fungi and the fact that the sporocarps of A. chailletii and A. areolatum are very similar (Thomsen, 1998). However, spore size and the colour and texture of the sporocarps can also be used to distinguish these species (Thomsen, 1998). The symbionts of woodwasps often had to be studied entirely in culture or from the mycangia of the wasps, where A. chailletii and A. areolatum are morphologically similar. These species can, however, be separated by the fact that only A. areolatum forms arthrospores in culture (Gaut, 1970; Boidin & Lanquetin, 1984; Thomsen, 1998). A. laevigatum and A. ferreum cause less confusion, as neither of these species are associated with woodwasps. Unlike the other species, A. laevigatum has a monomytic hyphal system and A. ferreum has been isolated

only from *Podocarpus* species (Boidin & Lanquetin, 1984; Breitenbach & Kränzlin, 1986).

Despite the fact that it is possible to distinguish the species of Amylostereum morphologically (Boidin & Lanquetin, 1984; Thomsen, 1998), the many misidentifications in the past show that the small differences that delineate species such as A. chailletii and A. areolatum still present difficulties to the non-specialised researcher. Another method that have been shown to successfully distinguish the species of Amylostereum is PCR RFLP fingerprinting of the nuc-IGS-rDNA region (Chapter 4). As has been shown for other Basidiomycetes fungi, this method has the potential to serve as a quick, yet precise, identification tool to distinguish these morphologically similar fungal species in culture (Harrington & Wingfield, 1995).

Boidin and Lanquetin (1984) used mating studies and the Buller phenomenon (Buller, 1931) to evaluate the phylogenetic relationships among the Amylostereum spp. The results from this study show an unusual triangular mating system. A. chailletii and A. laevigatum were completely incompatible, but both species were partially compatible with A. ferreum. Amylostereum areolatum was, however, not compatible with any of these species. The conclusion was that A. areolatum, which is morphologically close to A. chailletii, must have diverged earlier. Furthermore, the other three species are more closely related, although their specific relationship to each other is not clearly defined. Following these observations, Boidin and Lanquetin (1984) concluded that a more complete study, including a wider range of isolates that are associated with gymnosperms, would provide a more lucid view of the speciation process in lignicolous fungi.

Sequence data from the mt-SSU- and nuc-IGS-rDNA complexes support previous hypotheses regarding the phylogeny of Amylostereum spp. and give new insight into previously unclear relationships (Chapter 3 & 4). Both these studies support the hypotheses (Boidin & Lanquetin, 1984) that A. areolatum is the most clearly defined species. Furthermore, these studies show that, of the three remaining species, A. laevigatum and A. ferreum are the most closely related. This finding leads to more comprehensive understanding of the results of sexual matings (Boidin & Lanquetin,

1984), which showed that A. ferreum and A. laevigatum were partially compatible more often (60 %) than were A. chailletii and A. ferreum (44 %).

Only A. chailletii and A. areolatum have been associated in symbioses with woodwasps (Gaut, 1970). An isolate from the wasp S. areolatus, that is believed to carry A. chailletii, has, however, been shown to be more closely related to A. laevigatum and A. ferreum (Chapter 3 & 4). This isolate might represent a new species or alternatively a sub-group of one of the known species. It might also represent a link between the latter species and the species associated with woodwasps.

Amylostereum areolatum are carried by a number of different wasps species (Gaut, 1970). The association with different wasp species and predominance of asexual reproduction, separates populations of this fungus genetically. The occurrence and combination of heterogenic sequences of the nuc-IGS-rDNA in isolates of A. areolatum, makes it possible to determine the relationship between such separated populations of the fungus (Chapter 4). At least four such heterogenic sequences of the nuc-IGS-rDNA region have been shown to occur in five different combinations in isolates of A. areolatum (Chapter 4). A preliminary study using this data have shown that isolates of A. areolatum associated with S. noctilio and S. juvencus did not, however, form two distinct genetic groups (Chapter 4). These populations rather shared some of these heterogenic sequences.

RELATEDNESS TO OTHER BASIDIOMYCETES

The relationship of Amylostereum to other Basidiomycetes has been uncertain in the past. Before Boidin (1958) described the genus Amylostereum, species resided in Stereum, as S. chailletii (Pers.:Fr.) Fr., S. areolatum (Fr.:Fr.) Fr., S. juniperi (Karst.) Boid. and S. ferreum Berk. & Kurt. Amylostereum laevigatum was, however, better known as Peniophora laevigata (Fr.) Karst. This classification and the general macromorphological similarities between some Amylostereum spp. and species of Stereum (e.g. A. chailletii and S. sanguinolentum), supported the view that Amylostereum is closely related to Stereum. Boidin and Lanquetin (1984), however, argue that the presence of gloeocystidia positive in sulfuric-aldehyde, normal nuclear behaviour and a tetrapolar mating system in all four Amylostereum spp. makes this genus more closely related to Peniophora than to the family Stereaceae. Parmasto (1995), using 86 morphological and physiological characters

in a cladistic study of the genera of Corticoid fungi, found that A. chailletii forms a sister group to Stereum and Xylobolus, while this clade groups basal to Peniophora.

In a study including 89 Basidiomycete species, Hibbett et al. (1997) showed that morphological characters can be misleading and that molecular data might give a clearer view of the true phylogeny of these fungi. From this study it became clear, for example, that a major character such as gills might have evolved as many as six times. In a study using mt-SSU-rDNA sequence data of a number of Basidiomycetes fungi, Hsiau (1996) found that A. chailletii grouped more closely to Stereum, than to Peniophora. When mt-SSU-rDNA sequence data of all four Amylostereum spp. were included in the extended database of Hibbett et al. (1997), these species grouped with neither Stereum nor Peniophora, but strongly with the wood decay fungus Echinodontium tinctorium Ell. & Ev. (Chapter 3).

Despite obvious macro-morphological differences between the Amylostereum spp. and E. tinctorium, all these species have amyloid basidiospores and form encrusted cystidia (Gross, 1964, Boidin & Lanquetin, 1984). Furthermore, it has been hypothesised that E. tinctorium is closely related to Stereum based on morphological data (Gross, 1964, Stalpers, 1978). Hibbett et al. (1997), however, groups Russula compacta Frost and E. tinctorium together and this clade more closely to Peniophora than to Stereum. Slippers (Chapter 3) groups R. compacta and Heterobasidion annosum (Fr.) Bref. together and more closely to the Amylostereum/Echinodontium group, than to Stereum and Peniophora. Hsiau (1996) also showed that R. compacta and Heterobasidion annosum group together and close to A. chailletii. Various studies (Hsiau, 1996, Hibbett et al., 1997, Chapter 3), thus, support the view that there is a close relationship between Amylostereum, Echinodontium, Russula and Heterobasidion, and that this group might be more closely related to Peniophora than to Stereum.

POPULATION STRUCTURE

Amylostereum spp. are heterothallic and have a tetrapolar nuclear state (Boidin & Lanquetin, 1984). The heterokaryotic isolates that are, thus, derived from the pairing of primary mycelia arising from basidiospores, will give rise to genetically different entities.

Both A. areolatum and A. chailletii are, however, also spread by woodwasps in the form of asexually produced oidia in a very strict symbiosis (Talbot, 1977).

In the Northern Hemisphere, is has been shown that, as a result of the spread of oidia of A. areolatum and A. chailletii by woodwasps, clonal lines of these fungi are preserved over time and are spread over large areas (Vasiliauskas, Stenlid & Thomsen, 1998; Thomsen & Koch, 1999; Vasiliauskas & Stenlid, 1999). These studies also showed that the presence of clones was very frequent among isolates of A. areolatum, but more rare among isolates of A. chailletii. It can be concluded from these studies that A. areolatum is predominately spread by woodwasps with which it is associated, while A. chailletii is regularly spread both via basidiospores and by woodwasps. This is in accordance with the fact that the sporocarps of A. areolatum are much less common than those of A. chailletii (Thomsen, 1998).

Amylostereum areolatum has been introduced, together with S. noctilio, into various pine growing regions of the Southern Hemisphere during this Century. It was reported in New Zealand around 1900, Tasmania in the early 1950's, on mainland Australia in 1961, in South America in the 1980's and more recently in South Africa in 1994 (Madden, 1988; Chou, 1991; Baxter, Rong, & Schutte, 1995; Reardon, Eav, & Wetterberg, 1995; Tribe, 1995). Large vegetative compatibility groups (VCG) have been shown to occur in isolates of A. areolatum associated with S. noctilio in the Southern Hemisphere (Chapter 2). Isolates from South Africa represent a single genetic entity. Furthermore, Brazil and Uruguay also share the same VCG, and this VCG is the same as the one in South Africa. Partial vegetative compatibility was also observed between isolates representing this VCG and isolates from New Zealand and Tasmania. This suggests that the spread of Sirex through the Southern Hemisphere during this century has taken place among the continents and countries of the Southern Hemisphere, rather than based on introductions from the Northern Hemisphere. The clonal nature of populations of A. areolatum in the Southern Hemisphere further indicates that the fungus mainly spreads asexually through its association with S. noctilio in this region. This is also confirmed by the fact that sporocarps of A. areolatum have never been found in the Southern Hemisphere.

Vegetative compatibility groups do not necessarily constitute clonality (Worrall, 1997). Vasiliauskas et al. (1998) have, however, shown that VCG's of A. areolatum found in Northern Europe, represent clonal lines. Molecular markers, such as those that have been used in the Northern Hemisphere (Vasiliauskas et al., 1998), must be applied to studies investigating the population structure of A. areolatum from the Southern Hemisphere, in order to establish the true genetic structure of these isolates.

The nematode, *Deladenus siricidicola*, sterilises female *S. noctilio* wasps during a parasitic phase of its life cycle (Bedding, 1995). This nematode is used extensively in biological control programmes in the Southern Hemisphere (Bedding, 1995). For this purpose the mycetophagous phase of the life cycle of the nematode, during which it feeds on *A. areolatum*, is used to mass rear the nematode. Isolates of *A. areolatum* that are used to rear *D. siricidicola*, have, however, been shown to be genetically distinct from other field isolates from South Africa, Brazil, New Zealand and Tasmania (Chapter 2). This nematode has been imported and released in both South Africa and Brazil as part of a biological control initiative against *S. noctilio*. A different genetic entity of the fungus has thus been introduced into these countries along with the *D. siricidicola*. This has the potential to influence the population structure of *A. areolatum* in these countries. The efficacy of *D. siricidicola* as biocontrol agent might also be negatively influenced by a strain of the fungus in South Africa and Brazil, that is different to the one on which it was reared (Chapter 2).

The predominance of asexual reproduction and spread of A. areolatum in its symbiosis with woodwasps, has led to the preservation of heterogenic sequences of the nuc-IGS-rDNA region, in this fungus (Chapter 4). The distribution of such heterogenic sequences among isolates of the fungus can be useful in characterising populations of the fungus. Isolates from the Southern Hemisphere, for example, share the same combination of these sequences (Chapter 4). This supports the hypothesis, based on VCG studies (Chapter 2), that the isolates from different regions in the Southern Hemisphere are genetically related.

CONCLUSIONS

- 1. Molecular techniques, particularly those based on DNA sequencing, have only recently been applied to questions pertaining to *Amylostereum*. These have clarified previously hypotheses, that were based on morphological and mating studies, regarding the relationships among *Amylostereum* spp. They have also raised new and challenging questions, such as the identity of the fungal isolates associated with woodwasps such as *S. areolatus*. Furthermore, these techniques can now be used to determine other phylogenetic relationships, such as the one between the two types of *A. laevigatum* thought to exist on different hosts in Europe.
- 2. PCR RFLP fingerprinting can be used to differentiate between the various Amylostereum spp. This technique provides a useful tool to overcome difficulties in identifying the morphologically similar Amylostereum symbionts of woodwasps.
- 3. There is a phylogenetic relationship between Amylostereum spp. and E. tinctorium, that has previously not been recognised using traditional methods. Furthermore, there is a relationship between these species and other Basidiomycetes such as Russula, Heterobasidion and Peniophora. Further studies, combining both molecular and morphological data, are needed to resolve the exact evolutionary relationship between these morphologically disparate fungi.
- 4. Extensive clonal lineages exist among isolates of A. areolatum and A. chailletii that are associated with Siricid woodwasps. A study of the population structure of these fungi, using both VCG's and molecular markers, from many parts of the world will give valuable insight into the geographical origin and spread of these fungi, as well as their associated Siricid wasps.
- 5. Heterogenic sequences in the nuc-IGS-rDNA region of isolates of A. areolatum make it possible to compare and characterise populations of these fungi that are associated with different wasp species. The occurrence and combination of these sequences provides insight into both the geographical distribution and evolutionary relationships of populations of the fungus.

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SUMMARY

In Chapter 1 of this thesis, the literature pertaining to the symbiosis between Sirex noctilio and Amylostereum areolatum in the Southern Hemisphere, is reviewed. It is evident from this review that S. noctilio and A. areolatum have become established throughout the pine growing regions of the Southern Hemisphere, despite measures to prevent its introduction. Unlike its relative unimportance as a pathogen in the Northern Hemisphere, this fungal-insect complex has resulted in great losses to softwood industries during a number of severe outbreaks in the Southern Hemisphere. The use of biological control agents in combination with preventative silvicultural practices, has been shown to be very effective in controlling Sirex in Australasia. It is, however, also evident from this review that despite the rather large collection of knowledge concerning the wasp and its control, information regarding the population structure and phylogenetic relationships of the fungal symbiont of Sirex, is scarce.

The recent introduction of *S. noctilio* into South Africa and its confinement to a rather small area in this country provided the opportunity to study the population of its fungal symbiont in detail. Results from Chapter 2 suggest that the fungus has a very narrow genetic base in South Africa and that the introduction of *Sirex* into this country was limited. The genetic base of *A. areolatum* in Brazil and Uruguay is similarly uniform. Of even greater interest is the fact that South Africa and Brazil share a common vegetative compatibility group and, thus, a common origin of *A. areolatum* and *S. noctilio*. Moreover, field isolates from the Southern Hemisphere appear to be closely related, which indicates that *Sirex* might have spread among countries of the Southern Hemisphere and were not necessarily new introductions from the Northern Hemisphere. Isolates of the fungus associated with the biocontrol nematode, *Deladenus siricidicola*, are, however, distinct from isolates from other Southern Hemisphere populations of the fungus. This could negatively influence the efficacy of the nematode as biocontrol agent in countries to which the nematode has been distributed.

Boidin and Lanquetin (1984) report triangular mating incompatibility between isolates from the different Amylostereum spp. Results of Chapter 3 support their

conclusions by clearly showing that A. areolatum is more distantly related to A. chailletii, A. laevigatum and A. ferreum, than these three species are to each other. The relationship between the latter three species is, however, more clearly defined in Chapter 3 where it is shown that A. ferreum and A. laevigatum are most closely related to each other. One isolate collected from Sirex areolatus, and, therefore, expected to be A. chailletii, was most closely related to A. laevigatum and A. ferreum. Neither of the latter species has, however, been implicated in associations with woodwasps. Furthermore, the data from this study show that Amylostereum spp. group with neither Stereum nor Peniophora, as has been previously hypothesised, but rather with Echinodontium tinctorium. This grouping was included in a larger clade that included species of Russula, Heterobasidion, Lentinellus and Auriscalpium.

Analysis of DNA sequence data derived from the nuc-IGS-rDNA in Chapter 4 supported the phylogenetic relationships of the Amylostereum spp. inferred in Chapter 3. Similarly, the isolate obtained from S. areolatus, did not group with any of the four species of Amylostereum and might represent a new species or a distinct group in of one of the current species. Isolates of A. areolatum associated with both S. noctilio and S. juvencus contained four heterogenic sequences in the DNA region analysed. These heterogenic sequences were contained in each isolate of the fungus in one of five combinations. Neither the heterogenic sequences included in the fungal isolates, nor the different combinations of these sequences, separated the populations of A. areolatum associated with different wasp species. Despite the heterogenic nature of this DNA region in some isolates, RFLP analysis was used effectively to distinguish between the different species of Amylostereum.

The work presented in this thesis represents the first molecular view of the phylogeny of the genus Amylostereum, as well as that of some of the Amylostereum spp. associated with woodwasp species. It is clear from Chapter 5 that these findings now provide a powerful tool to give a clearer picture of the taxonomy and evolution of these fungi, as well the ecology of their symbiosis with woodwasps. The study of the genetic structure of the fungal populations associated with woodwasps also gives new insight into the geographical origin and history of both the insects and their associated fungi.

OPSOMMING

In Hoofstuk 1 word 'n oorsig gegee van die literatuur aangaande die simbiose tussen Amylostereum areolatum en Sirex noctilio. Uit hierdie oorsig blyk dit dat S. noctilio en A. areolatum deeglik gevestig is in dié areas van die suidelike halfrond met kommersiële denneplantasies, ten spyte van pogings om dit te verhoed. In die noordelike halfrond het hierdie wesp/swamkompleks min ekonomiese invloed, maar in die suidelike halfrond was dit verantwoordelik vir groot finansiële verliese vir dennehout-industrieë. 'n Kombinasie van biologiese beheermaatreëls en voorkomende beheer deur deeglike bosboupraktyke is egter effektief in die bekamping van Sirex in Australasië. Verder is dit duidelik uit die oorsig dat, ten spyte van die groot databasis oor die wespe en sy beheer, min inligting beskikbaar is oor die populasiestruktuur en filogenetiese verwantskappe van die simbiont van Sirex.

Die onlangse aankoms van S. noctilio in Suid Afrika en die redelik beperkte verspreiding van die pes in die land, bied 'n geleenthied om die populasiestuktuur van die swam-simbiont deeglik te bestudeer. Die resultate in hoofstuk 2 toon aan dat die genetiese basis van A. areolatum in Suid Afrika baie klein is en dat S. noctilio die land dus in 'n beperkte getal binnegekom het. Net so het die swam ook 'n klein genetiese basis in Brasilië en Uruguay. Van meer belang is dat die isolate van die swam van Suid Afrika and Suid Amerika een vegetatiewe verenigbare groep vorm en dus 'n oorsprong van beide A. areolatum en S. noctilio het. Verder blyk die isolate van die suidelike halfrond naby verwant te wees aan mekaar Dit beteken dat die beweging van Sirex na nuwe areas in die suidelike halfrond moontlik tussen die lande van die halfrond is en nie noodwendig nuwe aankomelinge van die noordelike halfrond nie. Isolate van die swam, afkomstig van kulture van die nematode (Deladenus siricidicola) wat gebruik word in biologiese beheer, was egter geneties baie verskillend van die isolate van ander suidelike halfrond lande. Dit kan die effektiwiteit van die nematode as biologiese beheeragent beïnvloed, sowel as die populasies van die swam in lande waar die nematode bekend gestel is.

Die resultate in hoofstuk 3 toon duidelik dat A. areolatum minder verwant is aan A. chailletii, A. laevigatum en A. ferreum, as wat die laasgenoemde drie spesies aan

mekaar is. Van hierdie laaste drie spesies is A. laevigatum en A. ferreum die naaste verwant. Die verwagting was dat een isolaat wat afkomstig is van S. areolatus saam met ander isolate van A. chailletii sou groepeer. Dit het egter saam met A. laevigatum en A. ferreum gegroepeer, alhoewel nie een van die laasgenoemde spesies al ooit in simbiose met wespes gevind is nie. Verder het die studie getoon dat Amylostereum spesies die naaste verwant is aan Echinodontium tinctorium van al die spesies wat by die analise ingesluit is, en nie aan Peniophora of Stereum, soos wat vroeër voorgestel is nie. Hierdie groepering was ingesluit in 'n groter groepering wat ook spesies van Russula, Heterobasidion, Lentinellus and Auriscalpium ingesluit het.

Basisopeenvoling analise van die nukluêre intergeen spasiëring van die ribosomale DNS kompleks (nuk-IGS-rDNS) in hoofstuk 4, ondersteun die bevindings in hoofstuk 3 aangaande die filogenetiese verwantskappe van die Amylostereum spesies. Die isolaat afkomstig van S. areolatus het apart van die bestaande Amylostereum spesies gegroepeer en verteenwoordig moontlik 'n nuwe spesie of 'n afsonderlike groep binne een van die spesies. Vier heterogeniese DNS basisopeenvolgings is geidentifiseer vir die nuk-IGS-rDNS gebied in isolate van A. areolatum afkomstig van beide S. noctilio en S. juvencus. Hierdie heterogeniese opeenvolgings het in een van vyf kombinasies voorgekom in elke isolaat. Nie die heterogeniese opeenvolgings, of die verskillende kombinasies daarvan kon egter die populasies van die swam skei volgens hul assosiasie met die verskillende wesp spesies nie. Desnieteenstaande hierdie variasie, kon die verskillende Amylostereum spesies suksesvol onderskei word met beperkingsfragment lengte-polimorfisme (RFLP) analise van die DNS gebied.

Die resultate van hierdie tesis verteenwoordig die eerste molekulêre analise van die genus Amylostereum, sowel as die filogenie en taksonomie van sekere Amylostereum spesies geassosieer met wespes. Uit hoofstuk 5 is dit duidelik dat hierdie ontwikkelinge nou 'n kragtige tegniek bied wat 'n duideliker beeld kan gee aangaande die taksonomie en evolusie van hierdie swamme, asook die ekologie van hul simbiose met wespes. Verder gee die bestudering van die genetiese stuktuur van die swampopulasies, geassosieer met wespes, nuwe insig oor die geografiese oorsprong en geskiedenis van beide die swam en die insek.