

MOLECULAR PHYLOGENETIC STUDIES ON ARMILLARIA WITH SPECIFIC REFERENCE TO SOUTHERN HEMISPHERE SPECIES

BY

MARTIN PETRUS ALBERTUS COETZEE

Submitted in partial fulfillment of the requirements for the degree

PHILOSOPHIAE DOCTOR

in the Faculty of Natural and Agricultural Science

University of Pretoria

Pretoria

November 2003

PROMOTOR: PROF. B.D. WINGFIELD

CO-PROMOTORS: PROF. M.J. WINGFIELD AND PROF. P. BLOOMER



DECLARATION

I the undersigned hereby declare that the thesis submitted herewith for the degree Philosophiae Doctor to the University of Pretoria, contains my own independent work as hitherto not been submitted for any degree at any university or faculty.

Martin Petrus Albertus Coetzee

November 2003



TABLE OF CONTENTS

ACKNOWLEDGMENTS	1
PREFACE	ii
CHAPTER ONE	
Literature review	
Armillaria (Fr.:Fr.) Staude: Taxonomy, species concepts and phylogenetic relationships	1-1 to 1-71
CHAPTER TWO	
Phylogenetic relationships of Australian and New Zealand Armillaria species	2-1 to 2-22
CHAPTER THREE	
Molecular identification and phylogeny of Armillaria isolates from South America and Indo-	
Malaysia	3-1 to 3-23
CHAPTER FOUR	
A global view of the phylogeny and origin of the root rot pathogen Armillaria	4-1 to 4-39
CHAPTER FIVE	
Phylogenetic relationships between African Armillaria species	5-1 to 5-31
CHAPTER SIX	
Discovery of two Northern Hemisphere Armillaria species on Proteaceae in South Africa	6-1 to 6-23
CHAPTER SEVEN	
Identification of Armillaria isolates from Bhutan based on DNA sequence comparisons	7-1 to 7-34
CHAPTER EIGHT	
RFLP Identification tool for Armillaria species	8-1 to 8-30
SUMMARY	9-1 to 9-2



ACKNOWLEDGMENTS

I wish to express my sincere gratitude towards the following people and institutions that have made this work possible:

- My study leaders Profs. Brenda Wingfield, Mike Wingfield and Paulette Bloomer for their guidance, advice, patience (when needed) and endless support;
- Drs. Jolanda Roux, Pedro Crous, Sandra Denman, Geoff Ridley, Glen Kile, Thomas Kirisits and B. Chhetri who have, as co-authors, contributed to some of the studies;
- The members of the Tree Pathology Co-operative Programme (TPCP); the National Research Foundation (NRF); the THRIP initiative of the Department of Trade and Industry, South Africa; and the Mellon Foundation for financial support;
- The Department of Genetics for providing the facilities to undertake this study;
- Mark Banik and Drs. Kari Korhonen, Ottmar Holdenrieder and Caroline Mohammed who provided me with cultures of Armillaria;
- My brother Marius-Gert Coetzee who wrote and re-wrote the code for the computer program "RFLP Identification Tool for Armillaria species";
- · Leo van Straten for translating to English species descriptions published in French;
- Vivienne Clarence for ensuring that all my needs in the laboratory were being provided for;
- My family, friends and colleagues;
- · My parents for their unconditional love and support to fulfil my dreams;
- Jan Perold for challenging my ideas, reading my manuscripts, pointing out problems, and providing bottomless cups of coffee along with emotional support.



PREFACE

Armillaria spp. are plant pathogenic fungi that cause the disease known as Armillaria root rot. Species in the genus are distributed throughout temperate and tropical regions of the world and have a broad range of plant hosts. Armillaria spp. from the Northern Hemisphere have received much attention in the past and their phylogenetic relationships are well resolved. There is, however, a dearth of information pertaining to phylogenetic relationships between Armillaria spp. from the Southern Hemisphere and their relationships with those from the Northern Hemisphere. This lack of knowledge has prompted the studies presented in this thesis.

The first chapter of this thesis presents a review of literature regarding Armillaria. The review is arranged in three sections. The first of these deals with the taxonomic history of Armillaria. This is followed by a broad discussion on species concepts and their application in Armillaria taxonomy. The last section is concerned mainly with the known phylogenetic relationships between species from the Northern Hemisphere and Africa; but also includes discussion on possible relationships between Australasian Armillaria spp.

Chapter Two of this thesis deals with the phylogenetic relationships between Australian and New Zealand Armillaria spp. Various species have previously been identified based on their basidiocarp morphology. A large volume of information about the distribution and the host ranges of these species is currently available. However, information pertaining to the phylogenetic relationships among these species has been conspicuously absent in systematic literature.

Chapter Three concerns the identity and phylogeny of Armillaria isolates from South America and Indo-Malaysia. Armillaria root rot is well known in South America and Indo-Malaysia but very little is known regarding the Armillaria spp. responsible for the disease. Studies presented in this chapter were, therefore, intended to add to the limited information regarding the species in these areas. Isolates were collected from infected trees with symptoms of Armillaria root rot in Chile, Indonesia and Malaysia. Basidiocarps were not present at the time of collection and field identification was, therefore, not possible. Isolates from basidiocarps with uncertain taxonomic status but resembling A. novae-zelandiae and A. limonea from Chile and Argentina, respectively, but with uncertain taxonomic status were also included in this study. The identities of all isolates



were determined by means of sequence comparisons, with those available for known Armillaria spp. The phylogenetic relationships among isolates of Armillaria spp. from the Southern Hemisphere were also determined.

Chapter Four of this thesis addresses the possible origin of Armillaria by investigating the phylogeny of Armillaria spp. from various floral kingdoms of the world. Earlier investigations revealed the phylogenetic relationships among Armillaria spp. from the Holarctic floral kingdom. Likewise, those from the Australian, Indo-Pacific and South American floral kingdoms were considered in chapters two and three of this thesis. The global phylogeny of the species in the genus, however, remained unresolved. The work presented in this chapter was, therefore, designed to determine the phylogenetic relationships between the Armillaria spp. from Africa, Australia, Europe, New-Zealand, South America and North America. In addition, the hypothesis that the genus originated in Gondwana was tested by estimating the date of divergence between non-Holarctic and Holarctic Armillaria spp.

Chapter Five deals with the phylogeny of African Armillaria isolates. One of my earlier studies showed that isolates thought to represent A. fuscipes reside in two monophyletic groups. The one group was suggested to represent A. fuscipes and the second group either A. heimii or an unknown species. Some isolates from the two monophyletic groups have, however, been found to represent the same biological species based on mating studies. The contradiction observed between phylogenetic studies and mating tests rendered the taxonomic position of the two African monophyletic groups refutable. The research presented in this chapter attempts to resolve the taxonomic status of isolates within two monophyletic groups.

Chapter Six deals with the identity of Armillaria isolates found on native Protea spp. and Leucadendron spp. in Kirstenbosh Botanical Gardens in the Western Cape Province of South Africa. Root rot disease on Proteaceae in this botanic garden is generally ascribed to Phytophthora cinnamomi infection. However, an investigation in 2000 revealed the presence of white mycelial fans between the bark and wood of dying plants, which are typical symptoms of Armillaria root rot. Basidiocarps were not found in the vicinity of the infected plants; consequently identification of the causal species based on morphology was not possible. The identity of the species was, therefore, determined based on DNA sequence data, their phylogenetic relationships with other Armillaria spp. and sexual compatibility tests.



Chapter Seven deals with identification of Armillaria isolates from Bhutan. Armillaria root rot is commonly encountered in fir and mixed forests in this mountain Kingdom. With the exception of one unsubstantiated record of A. ostoyae, virtually nothing is known about the species causing the disease in Bhutan. During a survey of tree diseases in 2001, isolates were collected from infected conifers showing typical symptoms of Armillaria root rot at four locations. Basidiocarps of the species causing the disease were, however, not found during the course of the survey. The identity of these isolates was therefore determined based on RFLP and DNA sequence data, their phylogenetic relationships with other Northern Hemisphere Armillaria spp. and sexual compatibility tests.

The last chapter of this thesis describes the development of an electronic RFLP identification tool for Armillaria spp. RFLP based methods provide a rapid and highly effective means for identification of Armillaria spp. The extensive use of this method has yielded a large number of PCR-RFLP profiles for various species. These profiles are currently available from a substantial and continuously growing set of publications. Identification using RFLP profiles, therefore, usually requires a cumbersome procedure of comparing profiles from unknown isolates with those that have been published. The software application described in this chapter circumvents this difficulty by providing all this information in a single database and employing an automated procedure for comparing RFLP profiles. The programme also allows for the addition of new information as it becomes available.

This thesis presents a collection of studies conducted over six year period that treat various aspects of Armillaria systematics. Three chapters deal with identification and phylogenetic relationships of unknown isolates from different locations in the world. Two chapters are specifically focussed on phylogenetic relationships among species from the Southern Hemisphere. One chapter deals with the global phylogeny of species from the Northern and the Southern Hemispheres. Each chapter is written in such a way that it can be read independently of the others; some repetition has, therefore, been unavoidable. It is my sincere hope that the work presented in thesis will advance our knowledge regarding Armillaria spp., their distribution and their relationships with one another.





"It is a strange fate that we should suffer so much fear and doubt over so small a thing."

BOROMIR

THE LORD OF THE RINGS,

THE FELLOWSHIP OF THE RING (THE MOVIE)



SUMMARY

Species of Armillaria are plant pathogens that cause the disease known as Armillaria root rot. Studies on the taxonomy and systematics of these fungi render a vital contribution to our ability to accurately identify them, as well as to our understanding of their distribution and ecology. This thesis represents an assemblage of studies that pertain to the taxonomy and phylogenetics of Armillaria species. The literature review presents an overview of the taxonomic history of the genus, the species concepts employed in fungal taxonomy, and the relevance of these concepts to Armillaria. It also discusses the phylogenetic relationships among Armillaria spp., to the extent that these were known prior to the studies constituting this thesis.

The major focus of the studies presented in this thesis was an investigation of the phylogenetic relationships between Armillaria spp. Armillaria hinnulea from Australia and New Zealand was shown to be closely related to the Northern Hemisphere Armillaria spp. The remainder of the Armillaria spp. from the two countries form a monophyletic group, thus confirming their separation based on morphology. A subsequent phylogenetic analysis for a global collection of Armillaria spp. suggests that species from the non-Holarctic floral kingdoms may be the ancestors of those from the Holarctic. Results also suggest that the genus probably originated in Gondwana. Phylogenetic and genetic analyses of isolates from Africa, which were previously considered to represent the same biological species, revealed two distinct phylogenetic species: A. fuscipes and an undescribed species.

Mating tests as well as RFLP and DNA sequence analyses were employed to determine the identity of vegetative isolates obtained during disease surveys from infected trees and shrubs. Isolates from South America and Indo-Malaysia were identified as A. novae-zelandiae and A. luteobubalina based on phylogenetic analyses. The Northern Hemisphere species, A. gallica and A. mellea, were shown to be the causal agents of Armillaria root rot on Proteaceae in Kirstenbosch Botanical Gardens, South Africa. Isolates from Bhutan were identified as A. mellea subsp. nipponica and an apparently undescribed species that we have referred to as Bhutanese Phylogenetic Species (BPS I).

Identification of Armillaria isolates is increasingly based on DNA sequence and RFLP data.

There are currently a number of separate studies that present a confusing array of data for this



genus. To resolve this problem, a computer program was developed to provide an electronic database for managing RFLP profiles. It also includes an automated search algorithm for rapid identification of *Armillaria* isolates.

This thesis includes seven research chapters in addition to a comprehensive literature review. The collection of studies undoubtedly represents one of the most intensive efforts ever undertaken to identify Armillaria spp. This has been made possible through opportunities to collect isolates in many different countries and the availability of isolates from the collections of colleagues. New species have thus been recognised and intriguing patterns pertaining to the phylogeography of these fascinating fungi have begun to emerge. Additional evidence has emerged that, contrary to expectation, these soil-borne fungi have at least to some extent been dispersed across the globe by humans. This information and a considerably enhanced knowledge of the identity of Armillaria spp. should improve quarantine procedures to prevent their further spread.