

**Taxonomy and population biology of selected
Ceratocystis spp. with hat-shaped ascospores.**

by

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DECLARATION

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



Marelize van Wyk

February 2003

**I dedicate this thesis to my two late grandmothers Elisabeth Marè and
Marie Wilkie**

“To laugh often and much; to win the respect of intelligent people and the affection of children; to earn the appreciation of honest critics and endure the betrayal of false friends; to appreciate beauty, to find the best in others; to leave the world a little better; whether by a healthy child, a garden patch or a redeemed social condition; to know even one life has breathed easier because you have lived. This is the meaning of success.”

Ralph Waldo Emerson

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PREFACE

The genus *Ceratocystis* includes some of the most devastating pathogens particularly of woody plants. In forestry, *C. fimbriata* is a well-known pathogen of *Eucalyptus* spp.; *C. albofundus* is a serious pathogen of *Acacia* spp., while *C. polonica* and *C. laricicola* infect *Picea* and *Larix* spp., respectively. During the past 10 years, reports of *Ceratocystis* spp. from commercial hardwood forestry species have doubled. These fungi thus represent a serious threat to forestry globally and they require further study.

In the first chapter of this dissertation, a broad overview of the literature pertaining to the genus *Ceratocystis* is presented. A retrospective consideration of the controversial taxonomic history establishes the background for the research in this dissertation. Morphological, biochemical as well as phylogenetic studies have been reviewed to illustrate the basis for best discriminating between species. The mode of reproduction as well as the distribution, host range, infection, dispersal, disease development and symptoms are also presented. This chapter has a special focus on *Ceratocystis* spp. with hat-shaped ascospores because the research in this dissertation is predominantly on members of this group of *Ceratocystis* spp.

Discovering and describing new species is fundamental to understanding fungi. In chapters two, three and five of this dissertation, I consider the taxonomy of three new *Ceratocystis* spp. from Bhutan, Sulawesi and Sumatra, respectively. These fungi were discovered on *Picea spinulosa*, *Syzygium aromaticum* and *Quercus* trees, respectively. In these chapters the new species are characterized and described using morphological and DNA sequence data. In the studies using sequence data, three different gene regions; the Internal Transcription Spacer regions (ITS), the beta-tubulin (β -tubulin) region and the Transcription Elongation Factor-1 α region (EF1- α) are used to compile multi gene genealogies. The isolates requiring characterisation were compared with other *Ceratocystis* spp. in order to determine their identity.

One of the fastest growing DNA-based tools used to derive and understanding of the origin, mode of reproduction and other population based characteristics in plant

pathology is the use of polymorphic DNA markers or microsatellites. Understanding the population structure of pathogens represents an important aspect of disease management. Microsatellites are often very specific and can only be used on a single species. However, in some cases, closely related species include similar repetitive regions and the primers developed for one species can be used on others. A new species discovered as a result of research presented in Chapter 3 is phylogenetically closely related to *C. fimbriata*. The primers developed for the amplification of repetitive regions in *C. fimbriata*, were thus applied to a population of isolates of this fungus in Chapter 4.

In chapter five of this dissertation, the non-pathogenic species *Ceratocystis moniliformis* was studied to determine whether it is a monophyletic or polyphyletic. Historically, a variety of descriptions exist for this species, suggesting that it probably represents a species complex. DNA sequence and morphological characteristics of a wide range of *C. moniliformis* isolates were, thus used to compare them. For the DNA sequence studies, data from three different gene regions were used to provide strong support for the comparisons.

Studies presented in this dissertation were undertaken during the course of approximately two years. They have relied on an important collection of isolates from diverse parts of the world and I believe that they represent a useful milestone in *Ceratocystis* taxonomy and ecology. Chapters are presented as manuscripts intended for publication. The fact that they have been written sequentially has meant that some redundancy between chapters has been unavoidable.