

# **Diversity of root nodulating bacteria associated with *Cyclopia* species**

by

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**Submitted in partial fulfilment of the requirements for the degree of**

**PHILOSOPHIAE DOCTOR  
(MICROBIOLOGY)**

in the

**DEPARTMENT OF MICROBIOLOGY AND PLANT PATHOLOGY  
FACULTY OF NATURAL AND AGRICULTURAL SCIENCES  
UNIVERSITY OF PRETORIA  
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SOUTH AFRICA**

February 2004



I certify that the thesis hereby submitted to the University of Pretoria for the degree PhD (Microbiology) has not previously been submitted by me in respect of a degree at any other university.

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Date: 26/02/2004

# OPGEDRA AAN MYP OUERS

## BEDANKINGS

**Ek wil graag my opregte dank aan die volgende persone en instansies uitspreek:**

**Prof P L Steyn** vir al die jare se leiding, belangstelling en ondersteuning. Baie dankie vir al die lekker geselsies en die mooi musiek wat Prof altyd vir my gespeel het.

**Die Universiteit van Pretoria** en die National Research Foundation vir die finansiële ondersteuning tydens die studie.

**Noëlle Amarger** vir die wonderlike ondervinding om saam met haar te kon werk en al die goeie herinneringe wat ek kon saambring huis toe. Ook 'n woord van dank aan **INRA, Dijon** waar ek waardevolle ondervinding kon opdoen.

Baie dankie aan Amy Spriggs en Jacomina Bloem vir die isolate wat hulle voorsien het.

**Julian Jastha** vir sy tegniese advies, vriendskap en ondersteuning.

**Magdaleen** vir haar hulp met die skryf van my literatuurstudie. Ook baie dankie vir haar en haar familie se jarelange ondersteuning en liefde.

My mede-genote van lab 9-37, baie dankie vir julle vriendelikheid en die lekker saamwerk.

'n Spesiale woord van dank aan elkeen van my vriende in die departement . Julle het dit lekker gemaak om daar te wees. Dankie veral aan Raynard, Chris, Boet, Jaco en Sonya vir julle vriendskap en ondersteuning.

Elkeen van my vriende wil ek opreg bedank vir hul aanmoediging, bemoediging, gebede, liefde, ondersteuning en al die terapeutiese lagsessies. Ek is oneindig gesêend met mense soos julle in my lewe.

Elkeen van my boeties en sussies - Frederik, Henry, Sulet, Petrus, Jurgen en Jacomien - baie dankie vir julle onvoorwaardelike liefde en ondersteuning.

Dan die mense sonder wie ek nie hier sou gewees het nie: my ouers. Baie dankie vir Pappa en Mamma se oneindige liefde, geduld, ondersteuning, bystand en al julle gebede. Dankie dat julle albei so 'n wonderlike voorbeeld is en was deur al die jare van my lewe.

En dan my Hemelse Vader sonder wie ek nie kan bestaan nie en wat my gesêen het met soveel gawes en genade. Aan Hom kom toe al die eer.

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# DIVERSITY OF ROOT NODULATING BACTERIA ASSOCIATED WITH *CYCLOPIA* SPECIES

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**DEPARTMENT:** Microbiology and Plant Pathology

**DEGREE:** PhD (Microbiology)

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## SUMMARY

In recent years, the rhizobial taxonomy changed significantly with the discovery of novel symbiotic associations between legumes and nodulating bacteria. This was aided by the focus shift from studying only agricultural crops to legumes indigenous to certain regions, ultimately to discover new inoculant strains and to uncover the secrets of the rhizobium-legume symbiosis. In previous studies on the diversity of South African rhizobia, it has become clear that our country has a wealth of rhizobia.

*Cyclopia* is a legume genus, which belongs to the fynbos biome of South Africa. Honeybush tea is a herbal infusion manufactured from the leaves and stems of certain *Cyclopia* spp. Commercial cultivation of this potentially new agricultural crop is now developed to protect the natural *Cyclopia* spp. populations from harvesting and ultimately extinction. Superior inoculant strains are necessary for these commercial seedlings.

The diversity of root-nodulating strains isolated from 14 *Cyclopia* spp. was determined using 16S-23S IGS-RFLP and partial 16S rDNA base sequencing. Based on 16S-23S IGS-RFLP and partial 16S rDNA base sequencing most of the isolates, with the exception of seven strains, were found to belong to the genus *Burkholderia*. More extensive phylogenetic,

symbiotic and phenotypic studies of selected strains were performed using near full-length 16S rDNA base sequencing, *nodA* base sequencing and substrate utilisation analysis. In the genus *Burkholderia*, the isolates belonged to the novel root-nodulating species *Burkholderia tuberum* and several novel, undescribed *Burkholderia* genotypes. However, no new *Burkholderia* species could formally be proposed, since DNA-DNA hybridisation analysis, which is a prerequisite for the description of new species could not be performed in our laboratory. The seven strains not affiliated with the *Burkholderia* genus belonged to two *Bradyrhizobium* genospecies, *R. tropici* and a possibly new genus in the  $\alpha$ -*Proteobacteria*. The *nodA* sequences of all the *Cyclopia* isolates corresponded to a large extent, indicating that different chromosomal genotypes harbour the same symbiotic genotype. All the isolates of the *Cyclopia* genus appear to be acid-tolerant, which is in agreement with the acidic nature of the soil from which the strains were isolated.

# DIVERSITEIT VAN WORTELNODULERENDE BAKTERIEË GEASSOSIEER MET *CYCLOPIA* SPESIES

deur

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**GRAAD:** PhD (Mikrobiologie)

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## OPSOMMING

Die rhizobium-taksonomie het ingrypend oor die afgelope jare verander met die ontdekking van nuwe simbiotiese assosiasies tussen peulplante en nodulerende bakterieë. Hierdie ontdekings is aangehelp deur die klemverskuiwing van die studie van slegs landbougewasse na inheemse peulplante. Hierdie verskuiwing was om nuwe entstoffrasse te ontdek asook om die geheime van die rhizobium-peulplant simbiose te ontrafel. In die vorige diversiteit studies van Suid-Afrikaanse rhizobia het dit duidelik geword dat ons land ryk is aan 'n verskeidenheid rhizobia.

*Cyclopia* is 'n genus wat deel maak van die fynbos bioom van Suid-Afrika. Heuningbostee is 'n kruietee wat vervaardig word van die blare en stamme van sekere *Cyclopia* spp. Die kommersiële verbouing van hierdie potensiële landbougewas word ontwikkel om die natuurlike *Cyclopia* spp. populasies te beskerm teen uitwissing agt die oes van natuurlike populasies. Effektiewe entstoffrasse is noodsaaklik vir hierdie kommersiële saailinge.

Die diversiteit van wortelnodulerende isolate afkomstig vanaf 14 *Cyclopia* spp. is ondersoek deur 16S-23S IGS-RFLP en gedeeltelike 16S rDNS basis volgorde-bepaling. Al die isolate,