

SURVEY OF DISEASES ON MARULA (*SCLEROCARYA BIRREA*), IN  
TSHIKUNDAMALEMA, LIMPOPO PROVINCE, SOUTH AFRICA.

BY

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## ABSTRACT

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Marula (*Sclerocarya birrea*) is an indigenous, drought tolerant multipurpose tree that belongs to the Family Anacardiaceae. The tree species is recognized as an important wild fruit tree that plays a vital role as a source of food, medicine and income for rural communities. *S. birrea* products are widely used in rural areas, including the Tshikundamalema area, Limpopo Province, South Africa. Despite the known uses of *S. birrea* in rural communities, there has been little research on diseases of *S. birrea* in Southern Africa. The study was conducted in Tshikundamalema at two sites approximately 50 km apart to investigate the presence of disease and identify the causal agents of these diseases on *S. birrea*. Symptomatic and asymptomatic plant materials were collected and processed in the laboratory. Isolates obtained were identified based on DNA sequence data of multiple genome regions of the internal transcribed spacer (ITS), beta-tubulin (BT), the translation elongation factor (TEF) and the RNA polymerase II subunit (RPB2) gene regions. Species in the genera *Fusarium* and *Lasiodiplodia* were recovered from diseased *S. birrea* fruits and identified as *F. equiseti*, *F. chlamydosporum*, *L. theobromae* and *L. mahajangana*. Pathogenicity trials conducted showed that *L. theobromae* and *L. mahajangana* were pathogenic to *S. birrea* fruits. Asymptomatic plant materials were processed for the identification of species that occur as endophytes on *S. birrea*. Isolates obtained from endophytic isolations represented species of Botryosphaeriaceae. Phylogenetic analyses distinguished five clades corresponding to *Lasiodiplodia crassispora*, *L. mahajangana*, *L. theobromae*, *L. pseudotheobromae* and *Macrophomina phaseolina*. The results obtained in this study indicate the diversity of fungal pathogens that occur on *S. birrea* in Tshikundamalema. Further studies in different geographical areas are needed to investigate the presence of other disease and the identity of their causal agents.

**Keywords:** *Sclerocarya birrea*, DNA sequence data, pathogenicity, ITS gene region, BT gene region, TEF gene region, RPB2 gene region, *Fusarium*, *Lasiodiplodia*, *Macrophomina*.