

Population genetic diversity and clonality in the endangered Pepper-bark, *Warburgia salutaris*

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The extent of clonality in threatened plants has important but neglected implications for their management. We propose the use of Amplified Fragment Length Polymorphisms to assess genetic diversity and clonality, which is suspected but remains unconfirmed, in the regionally endangered *Warburgia salutaris* (Bertol.f.) Chiov. Warburgia bark is extensively harvested for subsistence medicine, which has driven population collapse and local extinction outside of protected areas, where illegal harvesting continues. Kruger National Park supports some of the last remaining populations of *W. salutaris* in north-eastern South Africa. By definition, these relicts face significant restrictions in gene flow, which is exacerbated where species are clonal and populations are dominated by ramets, rather than genetically distinct genets. Confirming clonality in Warburgia would elevate the species to a level of concern higher than currently assigned, and would negate all existing demographic data. In order to effectively assess the conservation status, and management needs, of the pepper-bark, an assessment of the distribution of genets within and between populations is vital. Sanparks currently conduct in situ monitoring of populations, and provide source material for ex situ propagation programs, but without knowledge of clonality. The efficacy of these monitor-and-multiply strategies will benefit from an understanding of genetic diversity and structure in this species. By assessing the genetic diversity and structure of 250 Warburgia stems from in situ KNP populations and stock plants from ex situ collections, this project will provide the information needed to 1) Develop strategies for maintaining, or promoting, in situ genetic diversity in the pepper-bark; 2) Ensure effective in situ population monitoring through the development of methodologies appropriate for threatened, clonal species; and 3) Develop ex situ propagation programs which capture maximum genetic diversity.