

Poster Genetic diversity of Vetiver clones (*Chrysopogon zizanioides* and *Chrysopogon nigritana*) available in South Africa based on sequencing analyses

V. Diedericks^a, K. Conradie^b, S. Barnard^a

^aSchool of Environmental Sciences and Development, North-West University, Private Bag X6001, Potchefstroom 2520, South Africa,

^bCentre of Excellence in Nutrition, North-West University, Private Bag X6001, Potchefstroom 2520, South Africa, e-mail: Karin.conradie@nwu.ac.za

Keywords: sequencing, 5.8SrDNA, *ndhF* gene, phylogenetic analyses

Abstract

The awareness of Vetiver as a solution to erosion control and mine-rehabilitation in South Africa was created by Tony Tantom, who moved to South Africa during the 1980's. The current use of Vetiver in South Africa includes erosion control in sugarcane plantations, as well as disrupted areas for example next to highways, mines, next to railways, next to steep road embankment as well as to prevent soil loss in firebreaks. Vetiver currently has a bright future as rehabilitation agent and phyto-mitigator in South Africa. The Vetiver System is relatively low in cost and is an efficient system for erosion control, water conservation, soil stabilization, pollution control, waste water treatment, mitigation and prevention of storm damage, as well as cultural applications.

Currently Hydromulch is the leading company in South Africa supplying Vetiver to the industrial- and mining sectors. The Vetiver supplied for rehabilitation is in the form of slips because this organism is supposedly non-fertile. The collection is known locally as the "Roley collection" and it consists of different Vetiver lines collected from all over the world by Mr Roley Nöffke. Hydromulch consists of a Vetiver Nursery close to Johannesburg and is able to supply slips to South African as well as International clients. In request of Hydromulch, this study aim to distinguish phylogenetically between the different lines in the collection and to verify the difference between the organisms listed as *Chrysopogon zizanioides* and *Chrysopogon nigritana*. We aim to accomplish this with the phylogenetic analyses of predetermined gene sequences.

During the first phase of this study we used the ITS1, 5.8S ribosomal and ITSII gene fragment as well as the *ndhF* chloroplastic gene. Both genes are regularly used in phylogenetic analyses. The gene fragments were isolated via PCR and then sequenced. The ITS gene fragment was isolated and sequenced using the same primers to yield a fragment of ±600 bp. The *ndhF* fragment was isolated using primers obtained from Pascal -Antoine Christin, et al, 2008. The sequencing was done using internal primers also obtained from Pascal -Antoine Christin, et al, 2008.