



GENETIC DIVERSITY OF *SERIPHIMUM PLUMOSUM*- A GRASSLAND ENCROACHER

Mzamose Hadebe, Peter Stegmann,
Naser Aliye & Michael Pillay,

Vaal University of Technology, Private
Bag X 021, Vanderbijlpark, 1900, South
Africa

Vaal University of Technology

Your world to a better future

Introduction



Fig 1. Habit picture of *Seriphium plumosum*

- Invasive plants such as *S. plumosum* (Fig. 1) ('slangbos', 'Vaalbossie', 'bankrupt bush') cause damage amounting to millions of rand annually (Snyman 2009).
- The invasiveness of species is often related to their genetic diversity.

Objectives

1. To determine the genetic diversity of a sample of 10 plants within and between five populations of *S. plumosum* using RAPD analysis.
2. To relate the genetic diversity of the plant to its success as an invader.

Materials and Methods



Leaf material was collected from 50 plant samples from 5 sites shown in the map (Fig. 2)

Frankfort
Parys
Senekal
Thaba Nchu
Zastron

Fig. 2: A Google Earth map of localities (shown with a yellow pin) that were used for sampling.

M and M



Fig. 3. Invasion of *Seriphum plumosum* in Thaba Nchu

Materials and Methods

DNA Extraction

DNA was extracted according to the CTAB protocol.

DNA was amplified using 30 RAPD primers

The amplified PCR products were separated on a 1% (w/v) agarose gel.

Data analysis

RAPD data was scored as a 1, 0 matrix indicating presence or absence of a band.

The data matrix was analyzed using POPGENE v. 1.31 (Yeh *et al.* 1999) to determine:

Shannon's information index (H_o),

polymorphic percentage of bands (P),

Nei's genetic diversity among populations (G_{st}),

Estimate of gene flow (Nm),

Nei's genetic diversity index (H),

Results

DNA amplification:

Typical RAPD amplification banding patterns are shown in Fig 4.

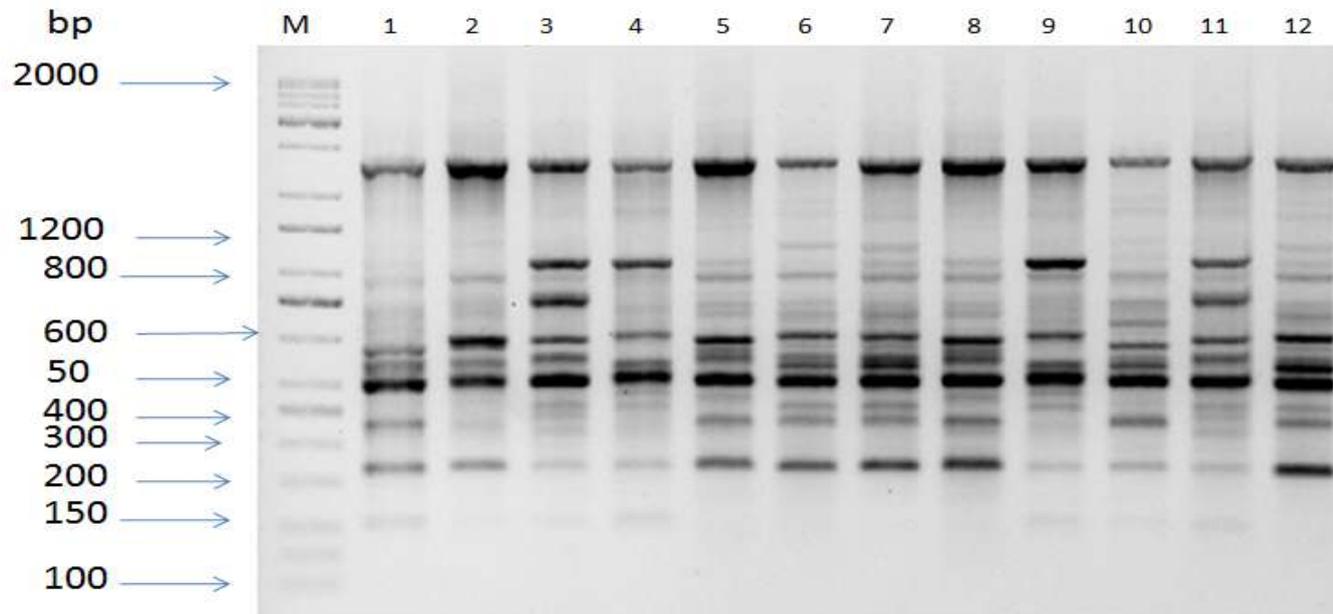


Figure 4: RAPD amplification patterns obtained with primer OPB01 of the samples (lanes 1 to 12) from Thaba Nchu. M represents the 100bp molecular weight marker (Fermantas, S.A) and the arrows indicate specific band sizes.

Results

- Table 3. Nei's analysis of genetic diversity in subdivided populations (Nei 1973).

Set	H_T (SD)	H_s (SD)	Gst (SD)	Nm
OPA	0.3828 (0.0196)	0.1813 (0.0132)	0.5264	0.4499
OPB	0.3828 (0.0196)	0.2350 (0.0110)	0.4175	0.6977
OPC	0.3650 (0.0232)	0.1835 (0.0205)	0.4175	0.5055
OPC	0.4042 (0.0074)	0.1835 (0.0205)	0.4175	0.5667

H_T = Total genetic diversity; H_s = Mean genetic diversity within populations;
Gst = Coefficient of genetic differentiation between populations;
Nm = Estimate of gene flow from Gst [$Nm = 0.5 (1 - Gst)$]; SD = Standard deviation

Results

Table 2. Genetic diversity parameters of *Seriphium plumosum* populations

Sites	Number of polymorphic bands	P (%)	H(SD) ^Y	H ₀ (SD) ^X
Frankfort	29	56.20	0.1969	0.2932
Parys	39	70.82	0.2379	0.3595
Senekal	35	66.65	0.2277	0.3419
Thaba Nchu	29	51.37	0.1819	0.2706
Zastron	28	53.70	0.1735	0.2616

P = Polymorphic percentage; *H* = Nei's genetic diversity index; *H*₀ = Shannon's index.

Discussion

First study that examined genetic diversity of *S. plumosum* at the molecular level.

High levels of genetic variation within and between the 5 populations of *S. plumosum*.

High genetic diversity observed in *S. plumosum* is a probable reason for its adaptability to new environments
Factor in the successfulness of this encroacher.

But?

Thank You!