Estimating Genetic Variability Among Antarctic *Bryum* Species

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Introduction

Dispersal of mosses in Antarctica is thought to be largely by vegetative propagules. As these asexual structures are less easily dispersed than spores, the expected gene flow between areas is thought to be low. For this reason the population genetics of Antarctic mosses is of interest. It is also of interest whether present-day populations are relicts from a warmer time or whether they are from recent colonisation events. Moss-specific microsatellite markers are being developed for the genus *Bryum* due to fungal DNA contaminating the moss samples. Length polymorphisms of the microsatellites will be analysed using the developed markers, to investigate the questions posed above.

Fungal Contamination

Presence of fungi on Antarctic *Bryum* has led to the DNA extracted from the moss samples being contaminated with fungal DNA, thus creating a need for moss-specific markers.

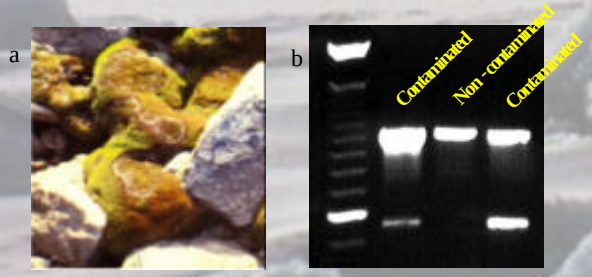

Fig. 2. (a) Moss with fungal growth rings. (b) Agarose gel of ITS amplification from fungal contaminated and non-contaminated DNA samples.

Fig. 1. *Bryum argenteum* on Beaufort Island, Antarctica.

Preliminary Results

Positive dot blots indicate the presence of microsatellite sequences in *Bryum* species allowing further development of these markers.

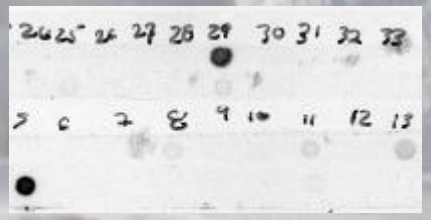

Fig 3. Dot blot showing positive microsatellite clones.

Fig. 4. *Bryum argenteum* at Cape Crozier, Ross Island, Antarctica.

Materials and Methods

DNA was extracted following the protocol out-lined in Rogers and Bendich (1985)[2]. Microsatellite development[3] will follow this flow chart:

Extract total DNA

⇩

Prepare insert DNA

⇩

Ligate size-selected DNA into plasmid vector

⇩

Transform XL-1 Blue competent cells

⇩

Screen colonies for putative positive clones

⇩

Screen putative positive clones for microsatellites via dot blots

⇩

Generate ssDNA containing microsatellites

⇩

Isolate plasmids with microsatellite repeat inserts

⇩

Sequence plasmid inserts using M13 universal primers

⇩

Screen populations for variation

⇩

Score Loci and Analyse Data

Further Work

Identification of positive microsatellite clones will allow us to sequence the microsatellite regions, screen populations for genetic variation and finally score loci and analyse the data.

References

1. Hunger, S. A. (2000). MSc. Thesis, University of Waikato.
2. Rogers, S. O. & A. J. Bendich (1985). *Plant Molecular Biology* **5**: 69-76.
3. Glenn, T. C. 2001. Microsatellite Manual, Version 7.0.1. (http://www.uga.edu/srel/DNA_lab). Extracted from website Jan, 2001.

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