

Assessing genetic variability of New Zealand seagrass (*Zostera muelleri*, Zosteraceae) at multiple spatial scales

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Background

Zostera muelleri Irmisch ex Asch., is the sole New Zealand representative of the eel grass family Zosteraceae (Figure 1). *Z. muelleri* predominantly inhabits estuarine intertidal sand flats but also can be found on rocky platforms and offshore islands (Figure 2). It is an important element of the estuarine ecosystem because it provides structure to these ecosystems, is a primary producer, and provides habitat for a number of organisms. However, as elsewhere in the world today, New Zealand's seagrasses are in decline resulting from ecosystem degradation and are in need of conservation management (Figure 3).

Objectives

The main objectives of the study were to a) evaluate the genetic variability on a fine scale within two New Zealand estuaries, b) evaluate the genetic variability along a latitudinal gradient of New Zealand, c) assess spatial relatedness, and d) provide information for the establishment of management practices to help in the conservation of this species.



Figure 1. Herbarium specimen of *Zostera muelleri*



Figure 2. *Z. muelleri* bed showing its influence in structuring of estuary bed at Raglan Harbour



Figure 3. Seagrass decline in Otago Harbour, New Zealand. Adapted from World Atlas of Seagrasses (Green & Short, 2003)



Figure 4. New Zealand Map showing study sites

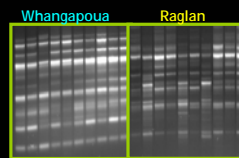


Figure 5. RAPD gel showing banding patterns of ten samples at each of the two intrasite locations Raglan and Whangapoua

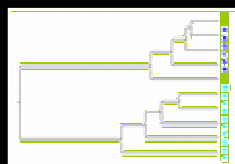


Figure 6. UPGMA of fine scale analysis

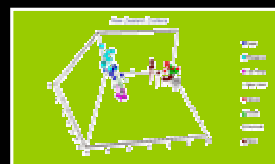


Figure 7. PCA showing intersite variability

Table 1. AMOVA showing partitioning of genetic variability

Intra site study		
Source of variation	d.f.	%Var
Between groups (North Island vs South Island)	1	46.1
Among sites (within islands)	6	31.6
Within sites	71	22.4
Inter site study		
Source of variation	d.f.	%Var
Between sites (Raglan vs Whangapoua)	1	50.8
Among sampling locations (within sites)	6	21.0
Within sampling locations	71	28.2

Methods

Intrasite sample sets consisted of five transects of ten samples 500m-5km distance and inter-site sample sets consisted of ten random samples per site (Figure 4). DNA extraction was followed by RAPD PCR and gel electrophoresis (Figure 5), and analysis was carried out using the software programmes UPGMA, PCA and AMOVA.

Results

The intrasite study showed that RAPDs is an appropriate technique to provide data on population genetic structure of seagrasses giving distinctive variable data.

Intrasite variability Both estuaries showed each transect distinctly but showed a higher distinction between estuaries than within estuaries (Figure 6).

Intersite variability The inter-site data showed a very strong relationship between geographical locations, with several smaller groupings seen within islands and clear demarcation between North and South island populations (Figure 7).

Amovas Genetic variability shows high percentage of variation between sites (Table 1) with strong relation to dominant New Zealand current patterns (Figure 8).

Conclusions

Each *Z. muelleri* site should be managed on an individual basis due to genetic distinctness of each site. Population augmentations/restorations should be locally ecosourced BUT as ecological studies suggest that re-establishment of populations has low probability of success, the focus must be on the maintenance of extant populations.

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Figure 8. Genetic variability shows relation to dominant New Zealand ocean currents

