Confirmation of Western Port seagrass species using genetic markers

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Western Port science review high priority research need '19'.

Seagrasses are major ecosystem engineers in Western Port, influencing the biodiversity and ecosystem functions within the bay. Extensive seagrass loss in the past, lack of subsequent recolonisation and poor condition of some of the bay's existing seagrass beds has prompted actions to identify and manage threats to the bay's seagrass communities (Walker 2011). Research into potential threats including water quality (sedimentation, nutrients and toxicants) requires the species of seagrass being studied to be accurately identified because species can differ in their sensitivity to physical conditions. Species-specific information enables effective water quality standards to be identified that meet the environmental requirements of seagrass.

Until now, the identity of *Zostera* seagrass species in Western Port has been somewhat confused. Visually, *Zostera* species can be difficult to tell apart. Observations of morphological differences in the same seagrass species at deep and shallow sites, together with recent revisions to the taxonomy of the *Zostera*/*Heterozostera* complex of seagrass species (Les *et al*. 2002, Kuo 2005, Jacobs and Les 2009) has resulted in uncertainty in the classification of the seagrass assemblages in Western Port. Identifying Western Port seagrass species has, therefore, been highlighted as an immediate research need (Keough *et al*. 2011). An effective way to resolve this question is to use molecular genetic tools to examine specimens from main seagrass areas around Western Port, at several depths.

Seagrass samples were collected from shallow and deep sites at Flinders, Crib Point, Newhaven and Charing Cross (south of Tooradin) (Figure 1). Genetic markers - chloroplast (*matK*) and nuclear genes (microsatellites; Sherman *et al*. 2012) – were analysed in order to clarify the taxonomic status of samples. Molecular markers were used to test the hypothesis that 3 different *Zostera* species - *Z. muelleri* , *Z. tasmanica* and *Z. nigricaulis* - are present in the area rather than two (*Z. muelleri* and *Z. tasmanica*) as previously thought. Historically, *Zostera muelleri* was considered the dominant intertidal species in the bay and morphologically distinct from the main subtidal species, *Heterozosetera* *tasmanica*. *H. tasmanica* has since been reclassified into four *Zostera* species including *Z. tasmanica* and *Z. nigricaulis* (Jacobs and Les 2009, Kuo 2005).

Genetic analysis of the Western Port seagrass samples was consistent with morphological identifications of samples being *Z. muelleri* (intertidal – shallow subtidal) and *Z. nigricaulis* (shallow – deep subtidal). There was no molecular evidence for two species of the plant formerly classified as *H. tasmanica*. Rather, it appears that a single species *Z. nigricaulis* occurs in deep and shallow sites with any morphological differences at different depths likely to be environmentally driven.

In addition to correctly identifying seagrass species in Western Port, this work is important because it enables knowledge from seagrass studies elsewhere to be applied to Western Port. For example, a recent study of seagrass resilience (*Z. nigricaulis*) in Port Phillip Bay has potential implications for this species in Western Port (Jenkins *et al*. 2015). Part of the Port Phillip Bay study used microsatellites (Sherman *et al*. 2012) to examine the genetic and genotypic diversity of *Z. nigricaulis* and showed the overall genetic diversity for this species in Port Phillip Bay to be comparable to that in Western Port.

Resolution of seagrass species identity also means that other high priority research projects can progress, such as the determining the capacity for *Zostera* species to recover and colonise new areas (Research need No. 26 (Keough *et al*. 2011)). Such studies require information on species biology, reproductive strategies, and environmental tolerances.

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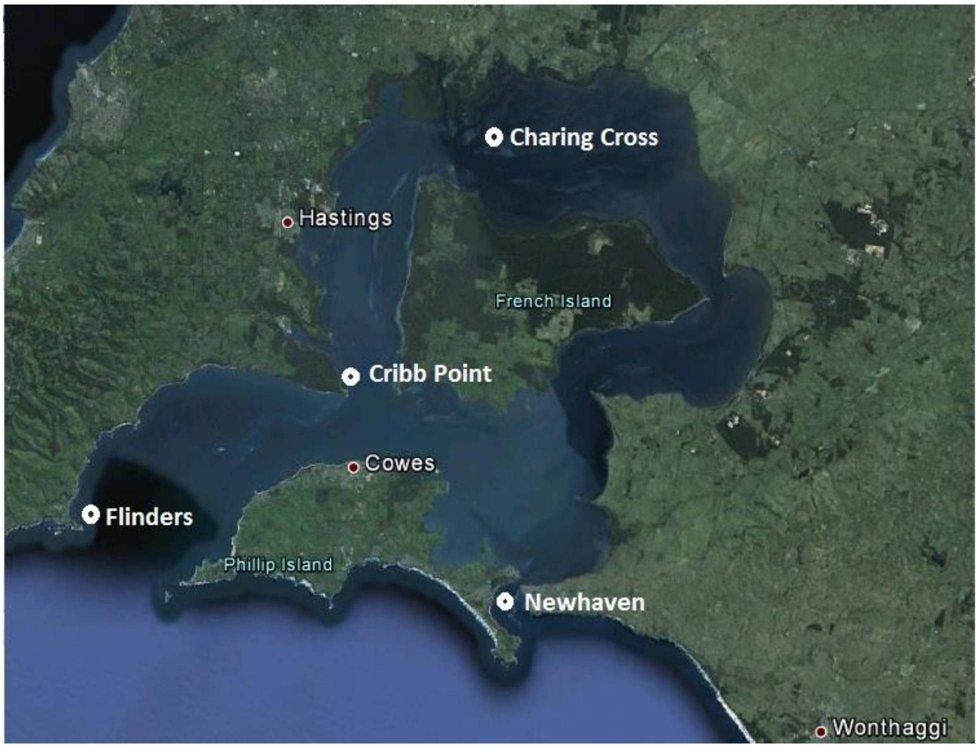

Figure 1: Collection sites for seagrass samples for genetic analysis.