



## Patterns and mechanisms of dispersal in a keystone seagrass species



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### ABSTRACT

Mechanisms and vectors of long-distance dispersal remain unknown for many coastal benthic species, including plants. Indications for the possibility for long-distance dispersal come from dispersal modelling and from genetic assessments, but have rarely been assessed with both methods. To this end, we assessed dispersal of the seagrass *Zostera noltei*, an important foundation species of the coastal zone. We investigate whether small scale seed dispersal and long-distance propagule dispersal do play a role for meta-population dynamics, using both genetic assessments based on eight microsatellite markers and physical modelling of ocean currents. Such assessments enhance our understanding of the biology and population dynamics of an important coastal foundation species. They are relevant for large scale conservation strategies as they give insights in the maintenance of genetic diversity and connectivity that may enhance resilience and resistance to stresses associated with seagrass loss.

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### 1. Introduction

Quantifying connectivity in marine populations is a crucial component of the management and conservation of coastal ecosystems (Ruiz-Montoya et al., 2015). Connectivity may confer populations resilience to anthropogenic impact and climate change (Andrello et al., 2015), and changes in patterns of connectivity may affect population persistence, leading to decline and extinction. Habitat loss and fragmentation are among the main causes of population isolation, and further changes in connectivity may represent major threats to all levels of biodiversity (Fahrig, 2003).

Connectivity among populations can be assessed using genetic approaches or modelling movements of dispersal units. In the marine environment, passive dispersal vehicles such as planktonic larvae of benthic organisms or vegetative and sexual propagules of

marine plants disperse with the movement of marine currents in which they occur (Thiel and Gutow, 2005). Genetic assessments are the most straight-forward way to assess realized connectivity, which is the result of dispersal, recruitment success and selection pressures (Sanford and Kelly, 2011). Modelling approaches in contrast can give information on dispersal potential and patterns. Comparing genetic and physical connectivity assessments can be especially useful for discerning the main modes of dispersal as well as relevant time scales (White et al., 2010). With the increasing availability and coverage of operational hydrodynamic models, semi-realistic Lagrangian modelling of physical-biological interactions has become feasible for a wide range of species, the accuracy being limited by uncertainty in the knowledge of the species biology. Recent examples include eco-regionalization in the Mediterranean basin (Serra et al., 2010; Berline et al., 2014), understanding of elusive eel recruitment aspects (Bonhommeau et al., 2009) and physical-biological interaction in spatial fish population models (Christensen et al., 2013). While most oceanographic current assessments are in the range of days to months, genetic

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