Genetic Diversity in Morro Bay Eelgrass: A System in Collapse
Julia Harencar, Greg Lutgen, Zachary Taylor, Dr. Jenn Yost
California Polytechnic State University, San Luis Obispo, CA

Introduction
• Eelgrass, Zostera marina, is a keystone species: purifies water and stabilizes sediment (Short & Wyllie-Echeverria, 1996), and is a nursery environment for invertebrates and fish (Hemminga & Daurte, 2000)
• Morro Bay has lost 95% of its eelgrass population in the last 8 years. Only 7 beds of eelgrass remain (S of Bay, 2014)
• All restoration efforts have failed (over 22,000 plants in 115 unique plots) (Merkel, 2015)
• Genetic diversity has not been assessed in Morro Bay
• Numerous studies have shown that genetic diversity affects eelgrass health and ecosystem function (Hughes and Stachowicz, 2009)

Hypothesis
H1: Each of the 7 beds in Morro Bay is genetically distinct
H0: There is no genetic differentiation among the 7 beds

Overall, we expect genetic diversity in Morro Bay eelgrass to be low due to the recent population bottleneck.

Results and Discussion
• Diversity values were higher than expected (Fig. 1)
• No population structure was found, indicating high connectivity throughout the bay (Fig. 2)
• Next, we will analyze data from Bodega Bay eelgrass to compare diversity levels, and to determine if Morro Bay is genetically isolated
• While there is homogeneity among Morro Bay plants, we don’t know yet how this compares to other eelgrass populations on the West Coast
• These results suggest that any existing eelgrass bed can be used for future restoration efforts and it will contain all of the diversity found within the bay
• These results will be used for future outplanting efforts in 2017-2018

Methods
• Collected 20-50 samples from each of the remaining 7 beds in Morro Bay
• Extracted DNA from 86 individuals
• Ran PCR using 11 microsatellite primers to assess fragment size differences among individuals
• Scored microsatellite peaks with software program “Geneious”
• Used software “STRUCTURE” to estimate number of genetic lineages and population structure in Morro Bay

Figure 1: Diversity values calculated using diveRsity package in R.

<table>
<thead>
<tr>
<th>Locus population size (N)</th>
<th>79.36</th>
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<tbody>
<tr>
<td>Allele number (A)</td>
<td>52.00</td>
</tr>
<tr>
<td>Allelic richness (Ar)</td>
<td>4.12</td>
</tr>
<tr>
<td>Observed Heterozygosity (Ho)</td>
<td>0.54</td>
</tr>
<tr>
<td>Expected Heterozygosity (He)</td>
<td>0.52</td>
</tr>
<tr>
<td>Test for HWE (p-values from chi²)</td>
<td>0.659</td>
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</tbody>
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Figure 2: STRUCTURE output across 7 sampled populations revealed that there were three distinct genetic lineages and no population structure.

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References