Estimating migration rates between populations of Zostera marina in the San Francisco Bay

Elizabeth S. Gutierrez, 2 Molly Moritzburke, 3 and C. Sarah Cohen 1
1 Romberg Tiburon Center and Department of Biology, San Francisco State University; 2 Graduate School of Education, University of California, Berkeley; 3 Redwood High School, Larkspur, California

Contact Information
Elizabeth Gutierrez: elizabeth2015@berkeley.edu
C. Sarah Cohen: csarahcohen@gmail.com

Zostera marina: an Ecological Foundation Species
- Ecological importance—provide habitat and essential nutrients to many marine organisms.
- Varied use of sexual and asexual reproduction; occurs in intertidal and subtidal

Restoration and population genetics in SF Bay
- Worldwide population declines call for restoration efforts, generally carried out without prior genetic information on population relatedness
- Restoration and management efforts benefit from knowledge of genetic relatedness for decisions on source populations, restoration methodology, and tracking probability of long population viability
- Spatial genetic comparison (2006, 6 populations, 7 microsatellite loci) found subpopulations were genetically distinct, but linked to varying degrees in SF Bay (Ort et al, 2012)

Temporal Variability in Genetic Relatedness?
- Focused on a single population in SF Bay over 4 years, found differences associated with a strong demographic reduction in 2006 (Point Molate (PM), (Tang, 2012)
- Analyzed connectivity among largest and adjacent subpopulations in the northern SF Bay (4 populations, 7 loci)
- Found 2008 PM sample showed higher genetic relatedness to neighboring populations using standard FST analysis (Tang, 2012)

Bayesian Connectivity Analysis to estimate connectivity in space and time
- F-statistics operate under problematic assumptions of 1. equal population sizes and 2. symmetric migration between populations
- MIGRATE-n (Beerli, 2009) estimates theta (θ) and M values to determine number of immigrants per generation between populations
- 4 temporal analyses: Point Molate sampled 4 different years spanning the die-off (PM05, PM07, PM08 and PM09) versus 3 neighboring subpopulations (PSP, KB, PO) each sampled once in 2006 or 2009.
- Predicted a significantly large number of immigrants per generation from PSP to PM in the 2008 analysis

Results Indicate Temporal Variability in Connectivity
- Point Molate and Point Orient received more genetic input from other subpopulations in 2007 than in any other year
- Point San Pablo and Keller Beach received more genetic input from other subpopulations in 2008 than in any other year
- Genetic connectivity varies spatially and temporally → metapopulation model

Future Research
- Conduct longer, repeated MIGRATE runs with optimized priors for more robust results
- Add 2009 and 2014 Point Molate population samples to analysis
- Add subpopulations from just north of the bay to the spatial genetic comparison study, i.e. 2014 Tomales Bay and Drakes Estero, to look at connectivity across a greater distance in areas with less human impact

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References

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Population connectivity

Bayesian estimates of migration rates between subpopulations of Z. marina in Richmond, California: 1. Point San Pablo (PSP) 2. Point Orient (PO) 3. Point Molate (PM) and 4. Keller Beach (KB).

Figure 5. MIGRATE-estimated number of immigrants per generation from one subpopulation to another from three analyses: PM 2005 v. PSP, PO, and KB; PM 2007 v. PSP, KB, and PO; and PM 2008 v. PSP, KB, and PO.

Figure 3. Four neighboring subpopulations of Z. marina in Richmond, California: 1. Point San Pablo (PSP) 2. Point Orient (PO) 3. Point Molate (PM) and 4. Keller Beach (KB).