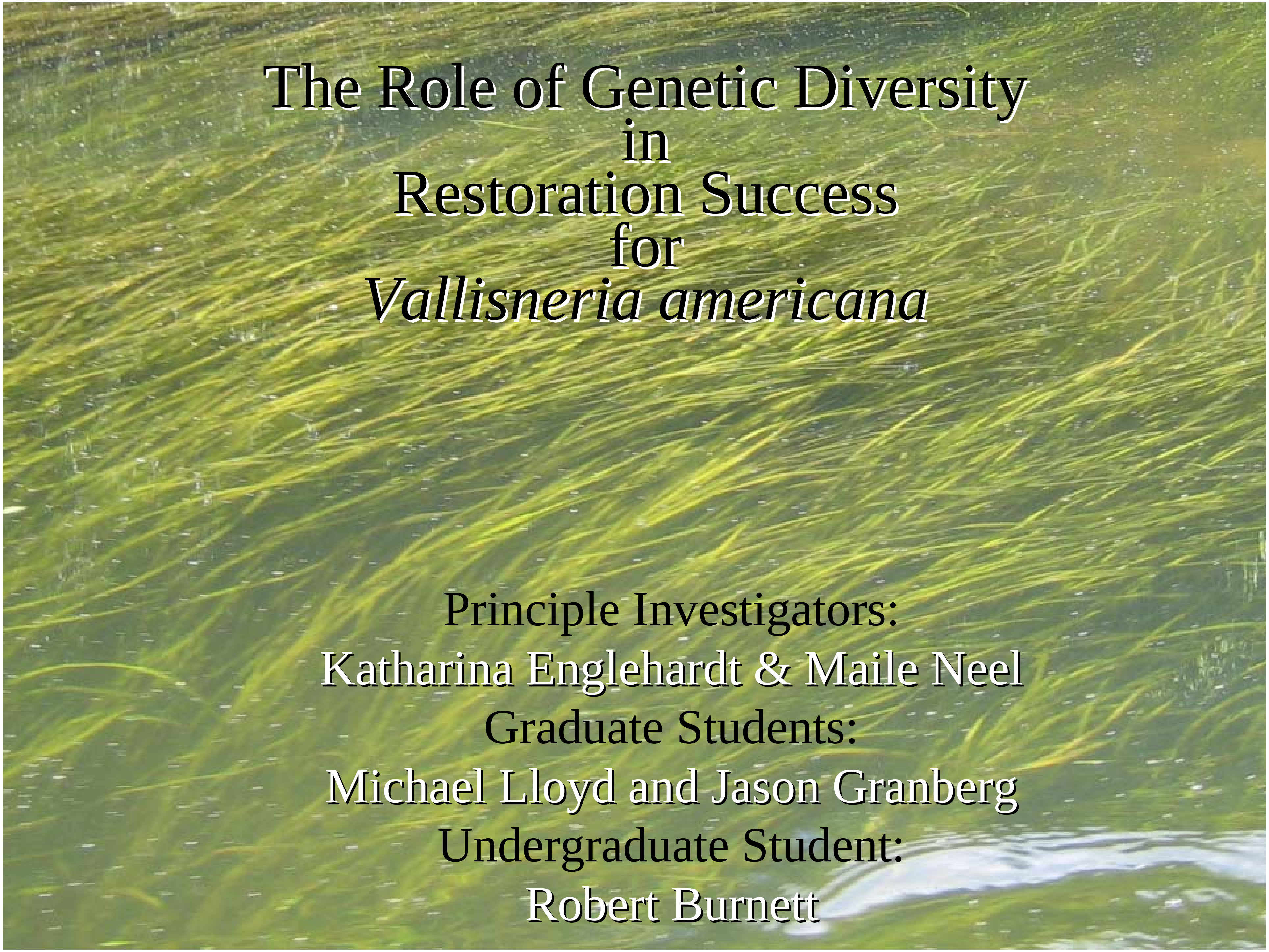


The Role of Genetic Diversity
in
Restoration Success
for
Vallisneria americana

Principle Investigators:
Katharina Englehardt & Maile Neel
Graduate Students:
Michael Lloyd and Jason Granberg
Undergraduate Student:
Robert Burnett

University of Maryland Center for Environmental Science

Appalachian Laboratory

University of Maryland College Park

Goals

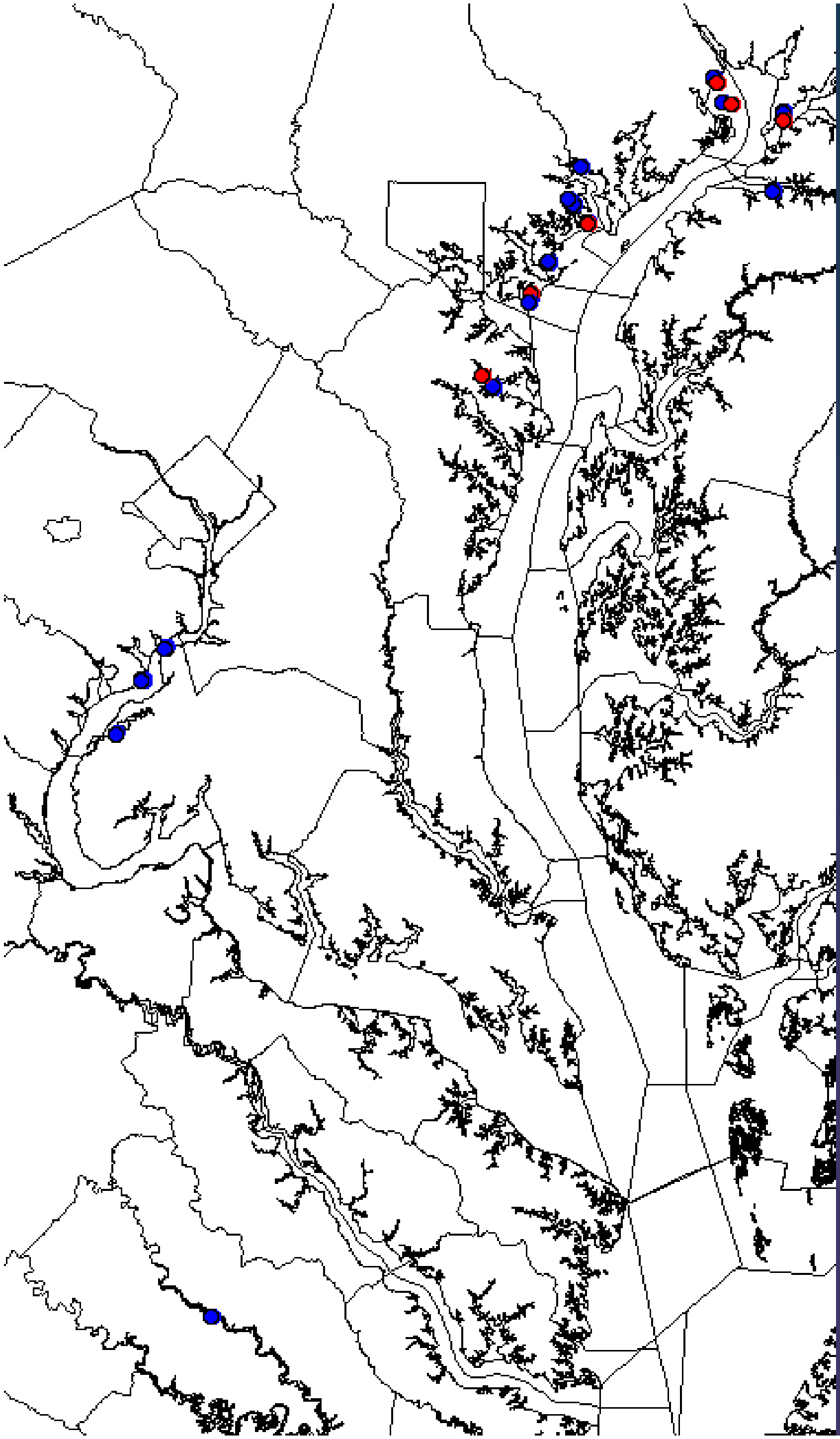
- Describe patterns of genetic diversity within and among native populations of *Vallisneria americana* in the Chesapeake Bay.
- Compare native populations with restored and cultured populations.
- Examine the role of genetic diversity in growth and survival of *V. americana.*
  - High versus low heterozygosity within individuals
  - High genotypic versus low genotypic diversity plantings.
  - Local versus non-local stock.
- Culture distinct genotypes of *V. americana* to serve as a repository of genetic diversity.

Implications for Restoration Practice

- How extensive are clones within locations?
- How many different individuals are there at individual locations?
- Is there any evidence for local adaptation within the Bay?
  - Are occurrences of *Vallisneria* genetically isolated or are levels of gene flow high enough to prevent differentiation?
  - Do collections from different locations perform differently when planted with plants from alternate locations?
- Do cultivated stocks used in restoration efforts represent the genetic diversity in natural populations?
- Does genetic diversity influence survival and growth of *Vallisneria*?

Progress to Date

- Made initial field collections
- Developing microsatellite loci
- Extracting DNA from all collections
- Culturing each of the collections in the greenhouse



🔴 Restored Sites (n=6)

🔵 Natural Sites (n=17)

- Sample sites
  - represent the geographic range of *Vallisneria* in the Bay and its tributaries
  - 6 restored/natural site pairs

Sampling Summary

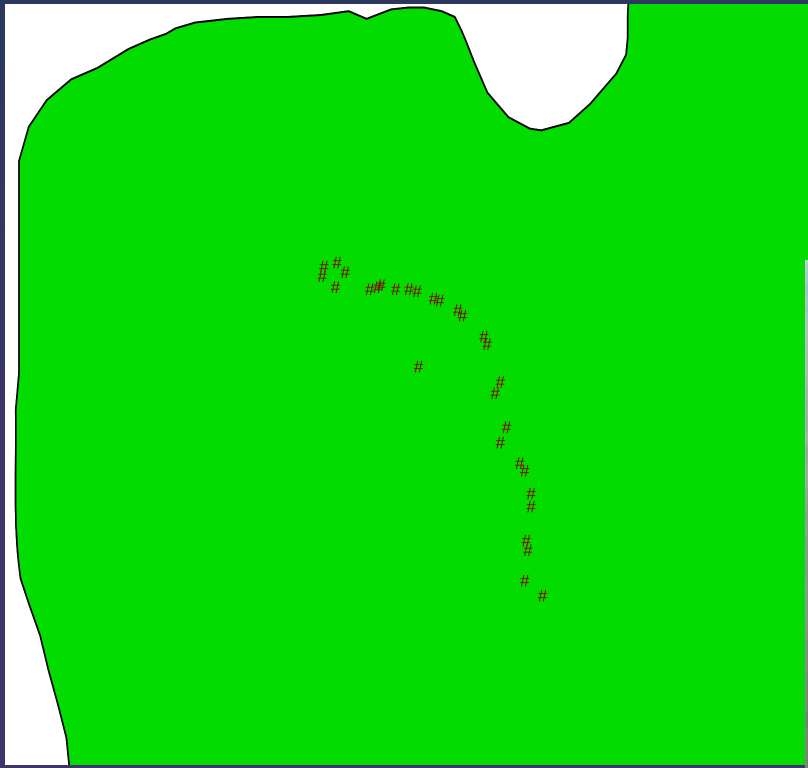
River	**Site Type**	**# Sites**	**# Samples**
Conococheague Creek	Natural	1	11
Gunpowder	Natural	2	60
	Restored	1	15
Magothy	Natural	1	15
	Restored	1	3
Mattaponi	Natural	1	30
Patapsco	Natural	1	30
	Restored	1	15
Potomac	Natural	7	210
	Restored	1	15
Sassafras	Natural	1	30
Susquehanna	Natural	3	90
	Restored	3	90
Grand Total		27	615

Sampling Summary:
From Cultivated Stock

Location	**# Samples**
Kollar Farms	30
Anne Arundel CC (Steve Ailstock)	4
Wisconsin Nursery	5
Grand Total	39

Within-Site Sampling

- Vegetative tissue collected 3-5 meters apart
- ~30 individuals/site
- GPS locations recorded for all samples




This Project Supported by
Chesapeake Bay Trust
Maryland
OUR BAY
www.chesapeakebaytrust.org

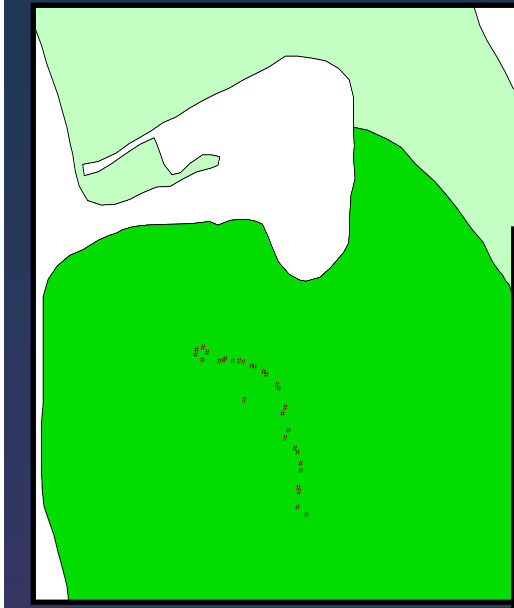
- All collections labeled and split into two

  Material with roots/ rhizomes taken to Appalachian Lab for propagation

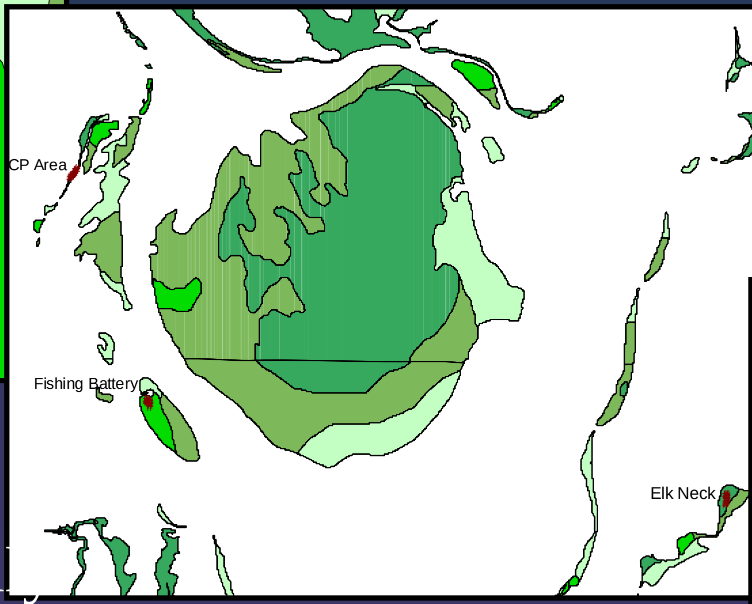
Leaf material taken to UMCP for DNA extraction and genotyping

Sampling strategy allows hierarchical spatial analysis

Within locations

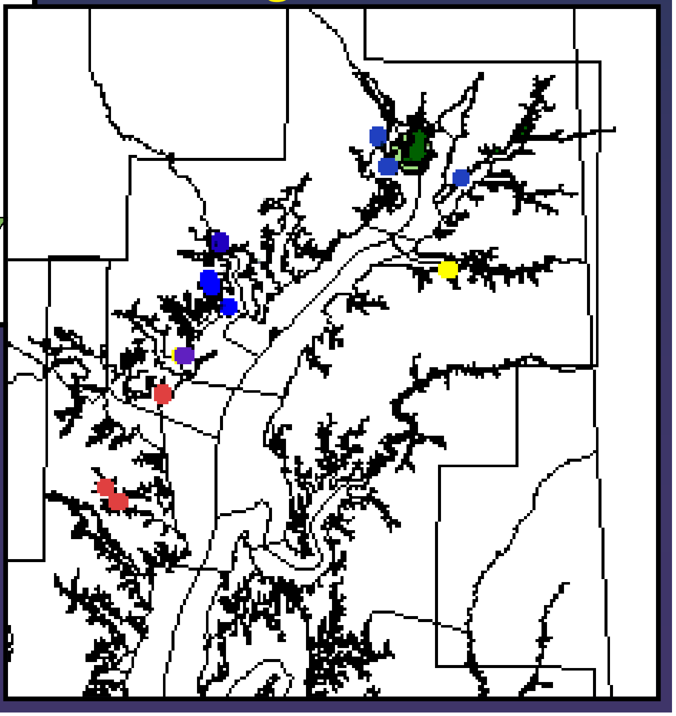


Among locations within tributaries



Allelic diversity
Polymorphism
Inbreeding
Differentiation
Migration

Among tributaries

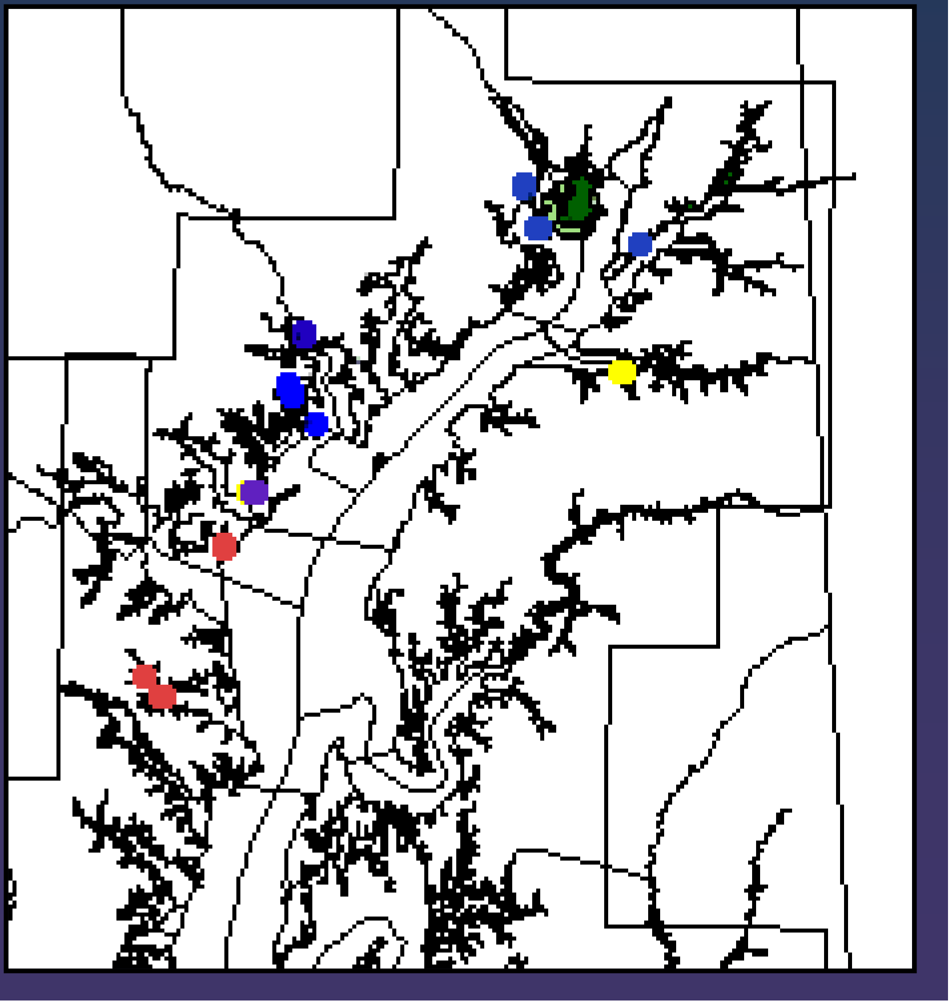


Allows us to estimate spatial extent of genetically distinct individuals within sites

Additional Sampling in 2008

Sampling mothers and their seeds will allow us to determine

- pollen sources
- functional connectivity among sites
- if levels of connectivity have changed



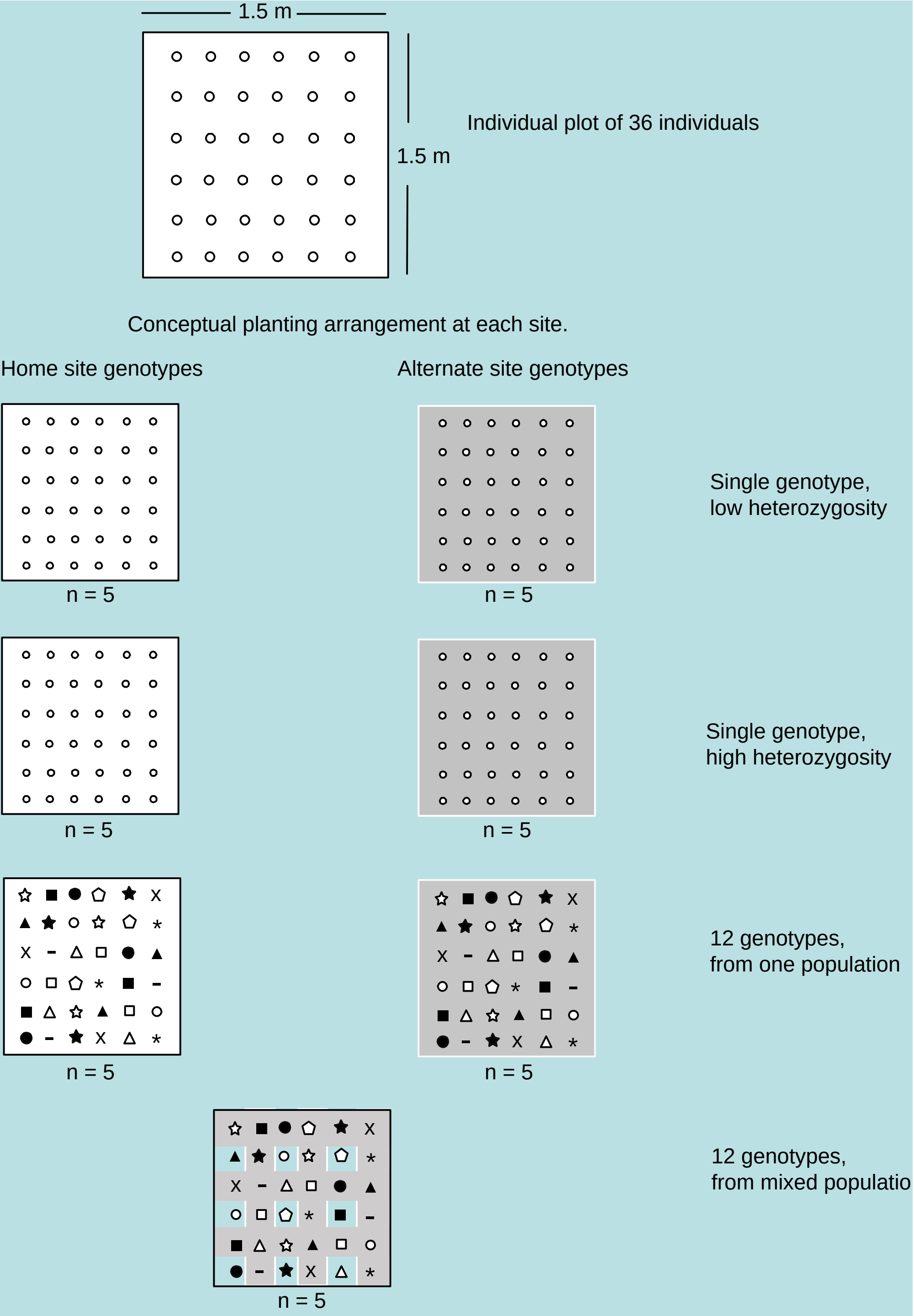
Linking genetic diversity and ecological performance

Factorial planting design allows us to

analyze independent and joint effects of

- heterozygosity (inbreeding)
- genotypic diversity
- local adaptation

on survival and growth of *Vallisneria americana* clones



Outreach

Develop a project Website


Maile C. Neel
Plant Science and Landscape Architecture, and Entomology

Home » Research » Effects of Genetic Diversity on Restoration Success

Research

- Biological Diversity Patterns and Reserve Design
- Effects of Biased and Incomplete Data and Reserve Selection
- Landscape Pattern Analysis
- Evolutionary Distinctiveness of Rare Taxa
- Effects of Genetic Diversity on Restoration Success

Search

Effects of Genetic Diversity on Restoration Success

Human-induced changes declines in submerged aquatic vegetation (SAV) in the Chesapeake Bay have both been caused by and led to declines in water quality. The far-reaching consequences of SAV decline have focused attention on effective ways of restoring the Bay's living resources. Resulting restoration efforts of SAV in the Chesapeake Bay have been impressive; however, success has been undeniably mixed. In collaboration with Dr. Katia Engelhardt at the University of Maryland Appalachian Laboratory, we have been funded by Maryland SeaGrant to assess the role genetic diversity and sources of restoration stock on restoring *Vallisneria. Americana*. At the same time, we are interested in the effect of Large-scale planting and seeding efforts on natural genetic diversity patterns. We are specifically examining three aspects of genetic diversity that have been shown to affect plant fitness and thus have important implications for restoration success: levels of inbreeding within individuals, levels of diversity among individuals), and the adaptation of individuals to local environments.

We are interested in *V. americana* because it was once a dominant species in the Chesapeake Bay, it is considered an important food resource for wildfowl, it does not interfere with recreational uses of waterways, and it is used in restoring freshwater portions of the Bay by a variety of conservation groups. Changes in the distribution of SAV including *Vallisneria americana* are monitored using remote sensing techniques by the Virginia Institute of Marine Science. The remotely sensed locations are ground truthed by a dedicated network of agency personnel and volunteers.

Vallisneria americana is a dioecious submersed aquatic macrophyte that is capable of both clonal growth and sexual reproduction with vegetative expansion often being the dominant form of propagation. Knowledge of the distribution of genetic diversity within and among populations will enable selection of appropriate donor individuals and populations for restoration. For example, quantifying the number and spatial extent of clones within populations will contribute to generating collecting protocols that increase the potential genetic diversity in restoration stock.

Our work focuses on populations growing in freshwater and oligohaline portions of the Chesapeake Bay. During summer 2007 Michael Lloyd (Ph.D student) and Robert Burnett (undergraduate student) are spending lots of time in waders, in boats, and in snorkeling gear sampling both natural and restored populations of *V. americana*.

The sampling design will allow us to assess the spatial and environmental patterns of genetic diversity in natural beds and to compare those patterns with restored beds of varying ages. Additionally, Katia will be growing the same clones we genotype in mesocosm environements, allowing us to link genetic diversity with ecological performance.

When they are not on or in the water, Mike and Robert are in the lab characterizing genetic diversity using microsatellite markers. Katia's lab will use individuals with known genotypes to establish populations in mesocosms. These populations will be used to improve our understanding of linkages between neutral genetic diversity and fitness related characteristics such as sexual reproduction and growth rates and tolerance to adverse environmental conditions.

Organize a workshop on incorporating genetic diversity in aquatic restoration for fall ‘08

Interact with people doing the real work once we have results to share

Thank you for your help!

- For funding:
  - SeaGrant
  - Maryland Agricultural Experiment Station
- For assistance with field sampling:
  - Peter Bergstrom (NOAA)
  - Todd Beser (Aberdeen Proving Grounds)
  - Patricia Delgado (Maryland National Estuarine Research Reserve System)
  - Stan Kolar and students (Harford Community College)
  - Bob Murphy (Ecosystem Solutions)
  - Nancy Rybicki (USGS)
  - Maryland Department of Natural Resources
- For giving us collections:
  - Ken Moore (Virginia Institute of Marine Science)
- For guidance with propagation methods:
  - Steven Ailstock (Anne Arundel Community College)
  - Eva Maria Koch and Byron Crump (UMCES Horn Point Laboratory)