

Genetic considerations for hatchery-based enhancement of native oyster populations: Are good intentions enough?

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Background



- Oysters provide a wide array of important ecological services
- Historically populations of Olympia oysters were very large and very broadly distributed
- They were heavily exploited and extensively translocated by humans in the mid-late 1800's and early 1900's leading to rapid declines
- Remnant populations persist in some areas
- There's a LOT of interest in bringing them back

Restoration Goals



- Ecological
 - Supplement existing populations
 - Establish new populations
 - Ecological Function/Services
- Genetic
 - Maintain/restore adaptive diversity and evolutionary processes to promote population persistence.
 - Adaptive genetic variation **within** populations
 - Genetic structure **among** populations
- Historical/Cultural
 - Restore the past?
 - Ensure the future?

Options & Consequences



- Wait and see
- Restore habitat
 - Goal is simply to enhance natural recruitment
 - No intended or unintentional genetic impact
- Hatchery-based enhancement
 - Goal is to increase numbers
 - No intentional genetic impacts
 - Unintentional impacts
 - Broodstock source & management
 - Natural genetic structure
 - Locally isolated populations?
 - Regionally connected metapopulation?
- “Genetic Rehabilitation”
 - Goal is to “improve” the genetics of populations
 - Manipulate gene flow
 - Selectively bred or genetically engineered broodstock

Hatchery Supplementation: Good Intentions



- Very limited genetic data
- Conservative “Do no harm” approach?
 - local populations may be genetically distinct
 - this distinctiveness may be adaptive
 - mixing is irreversible
- Questions:
 - Really conservative & harmless?
 - How could we know?
 - Unintended consequences?

Review: Types of Genetic Variation



- **Molecular Genetic Variation**
 - Direct access to genetic-level information (allozymes, microsatellite markers, RAPD, RFLP, AFLP etc.)
 - Statistical analyses describe patterns of differentiation, gene flow, etc.
 - No direct connection to actual traits.
- **Quantitative Genetic Variation**
 - “Indirect” access to genetic and environmental components of phenotypic variance
 - Requires knowledge of levels of relatedness among individuals
 - Controlled matings or pedigreed populations
 - Indirect estimates from genetic markers
 - Statistical analyses for measuring natural selection, local adaptation

Question: Molecules as a short-cut?



- Molecular data can be substituted for quantitative data only if:
 1. Molecular genetic variation **within** populations approximates quantitative genetic variation and evolutionary potential
 2. Structure **among** populations = local adaptation
 3. Boosting numbers also produces improves genetics
 4. Preserving current or historical patterns also preserves future function.

1. Molecular $\sigma^2 \approx$ Quantitative σ^2 ?



Differentiation among populations at some molecular marker loci may not exclusively reflect random genetic processes because of the non-neutrality of the loci (e.g., Watt 1977; Powers et al. 1979), and molecular and metric characters are expected to show differing patterns on a number of theoretical grounds (Lynch 1995). Together, these results portend difficulties in the detection of genetic variation with persistence value based exclusively on molecular marker-based descriptions of the isolation history of populations.

1. Molecular $\sigma^2 \approx$ Quantitative σ^2 ?



- Reed, D.H., Frankham, R., 2001. How closely correlated are molecular and quantitative measures of genetic variation? A meta-analysis. *Evolution* 55, 1095–1103
 - Compiled estimates of molecular and quantitative genetic variation for the same populations; conducted simple correlation analysis to see determine relation
 - Life history traits - if anything, the correlations are negative
 - Heritability - if anything, the correlations are negative

1. Molecular $\sigma^2 \approx$ Quantitative σ^2 ?



- Why is the correlation so bad?
 - Only a small fraction of the genome codes for the relevant traits
 - Neutral markers will only reflect patterns of selection and adaptation if they are tightly linked to these relevant bits
 - Recombination quickly disrupts these linkages
 - So.. There's really no reason to even expect that genome-wide patterns at randomly-selected loci should reflect selection and adaptation.

2. Structure => Local Adaptation?



● Processes structuring molecular variation

- Selection (?????)
- Mating structure
- Genetic Drift/Founder Effect
- Barriers to gene flow

● Processes structuring quantitative variation

- Selection
- Mating structure
- Genetic Drift/Founder Effect
- Barriers to gene flow

● Processes producing local adaptation

- Selection

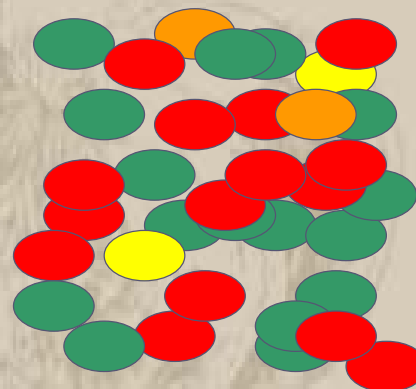
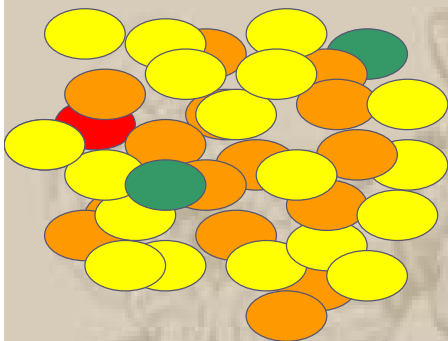
2. Structure => Local Adaptation?



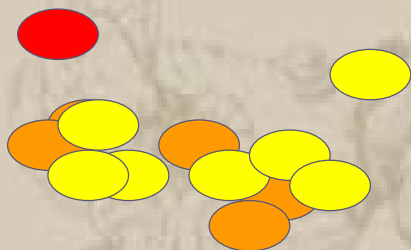
● Gene flow

- Homogenizing force
 - Prevents divergence by drift
 - Limits local adaptation
- Source of adaptive variation
 - Delivers both “good” and “bad” genes to populations
 - Changing environments
- Impact depends on relative strength of gene flow and selection
 - Additive gene effects
 - Non-additive gene effects
 - Recessive genes
 - Co-adapted gene complexes

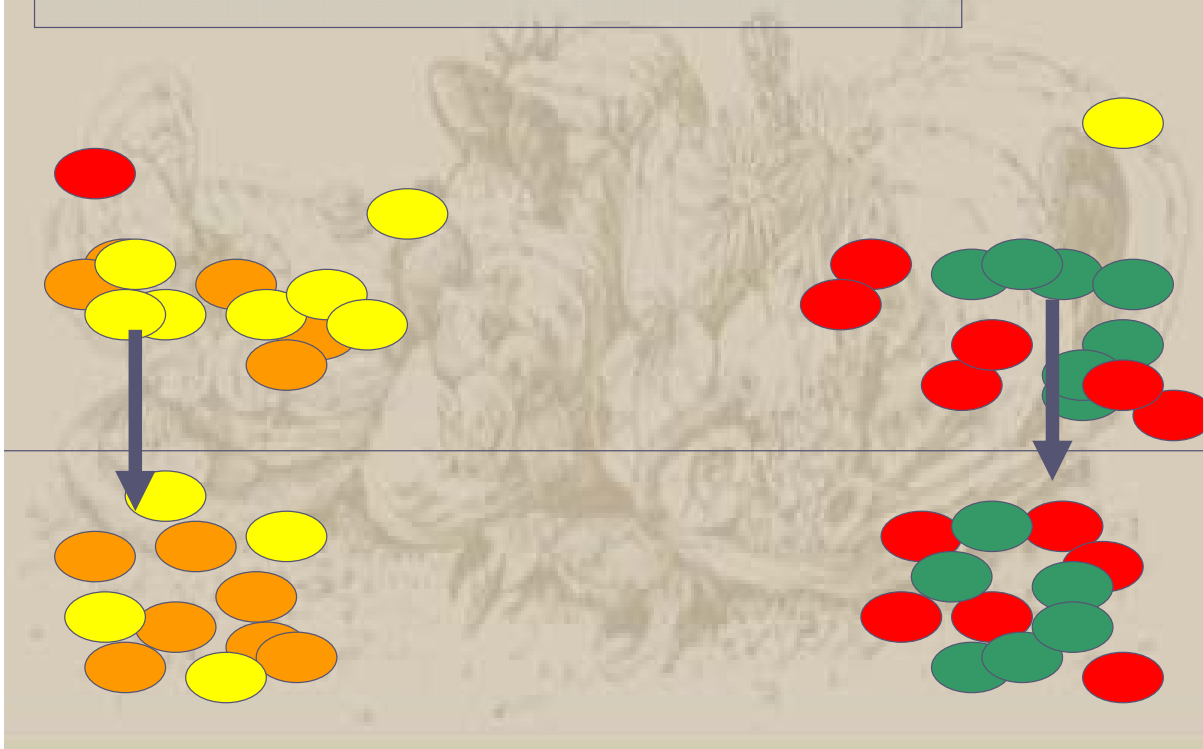
Isolation & Local Adaptation



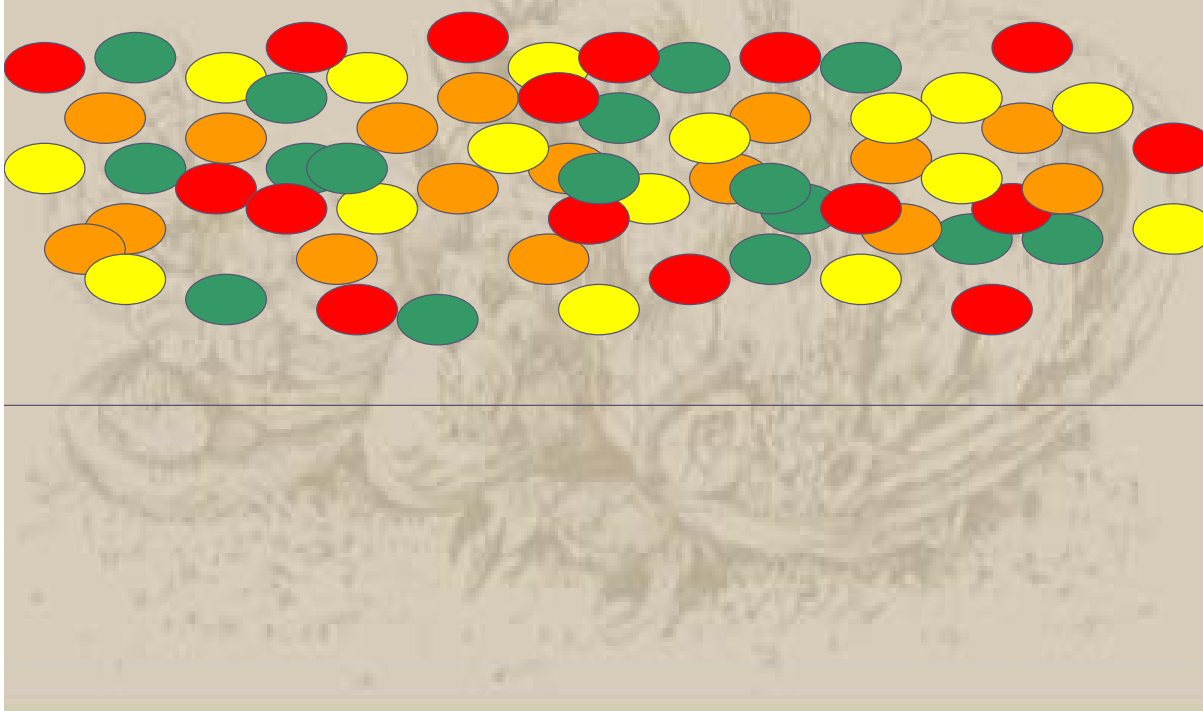
Isolation & Local Adaptation



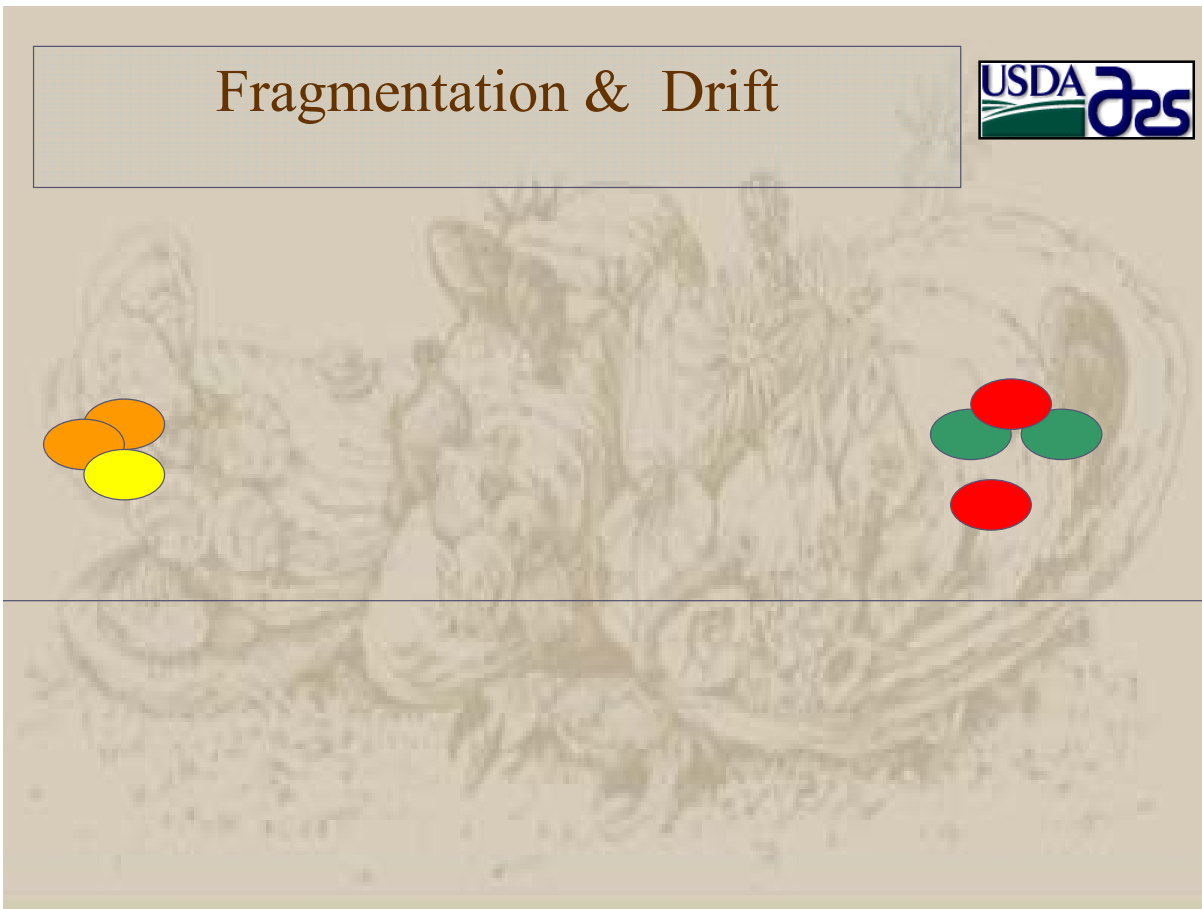
Isolation & Local Adaptation



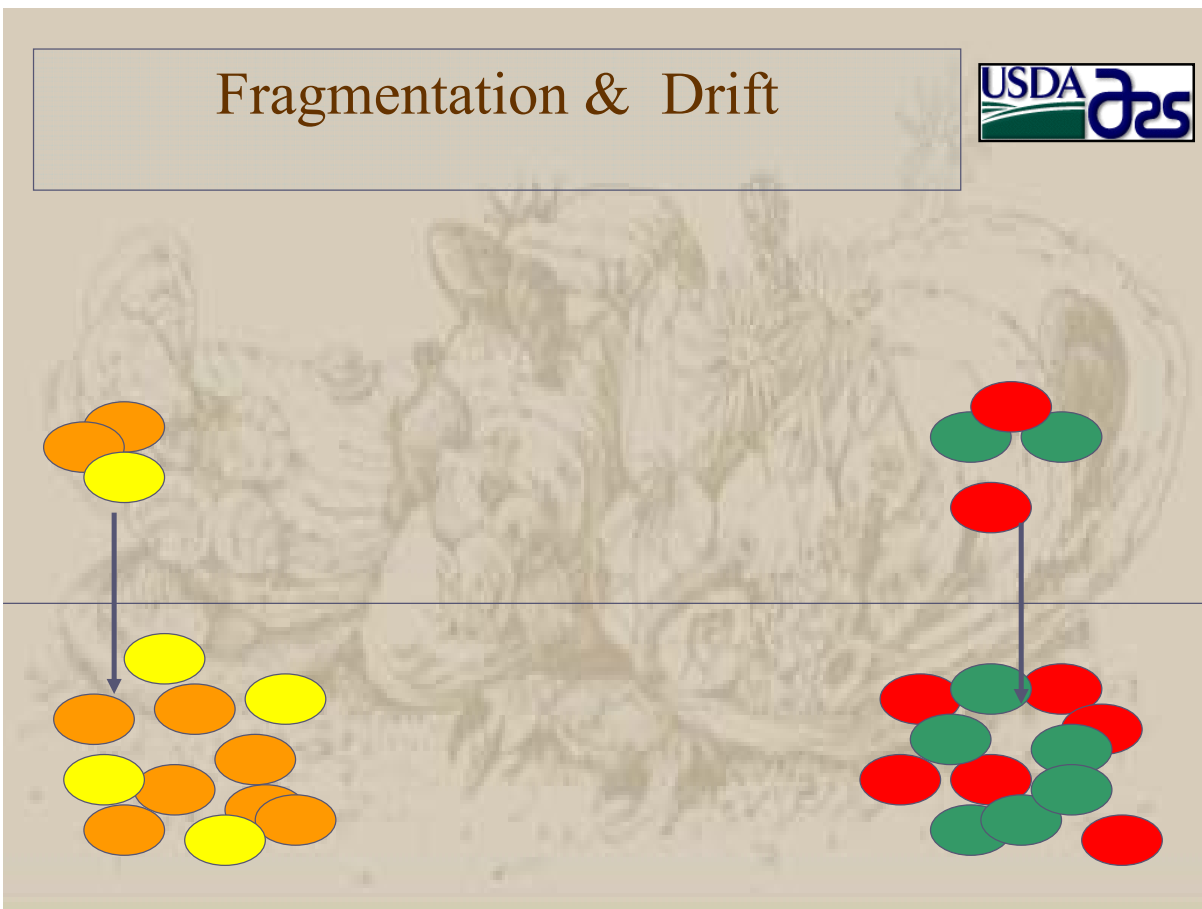
Fragmentation & Drift



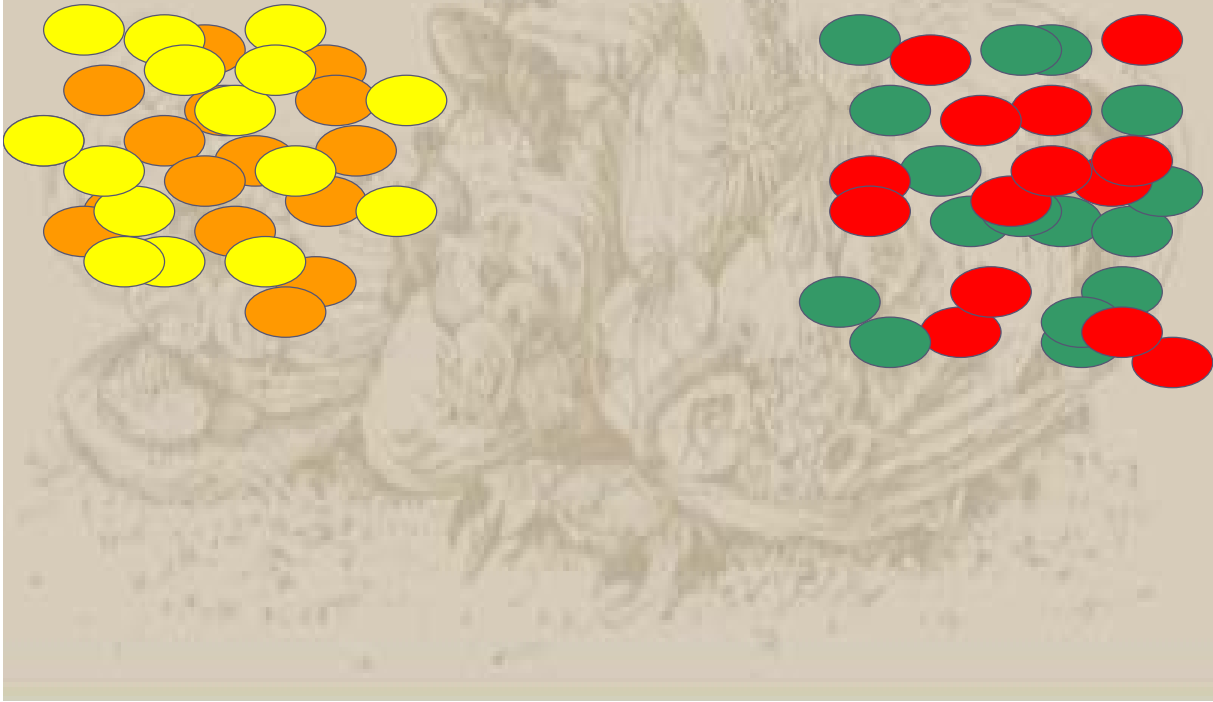
Fragmentation & Drift



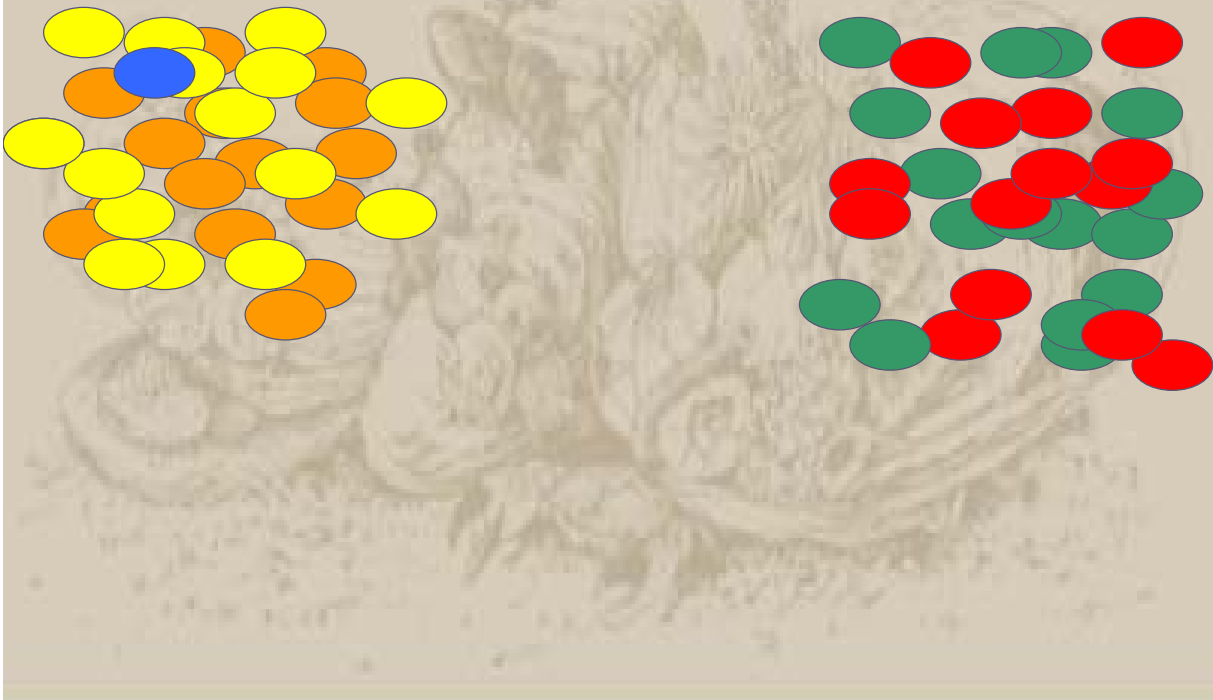
Fragmentation & Drift



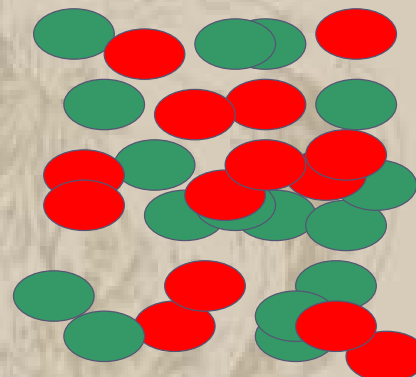
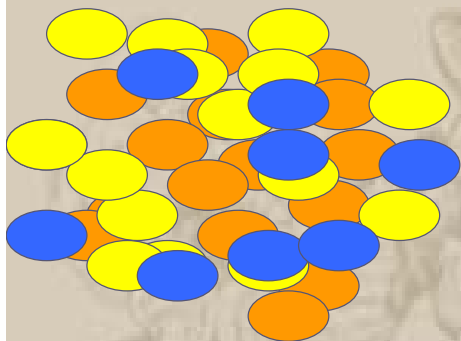
Gene Flow & Adaptive Variation



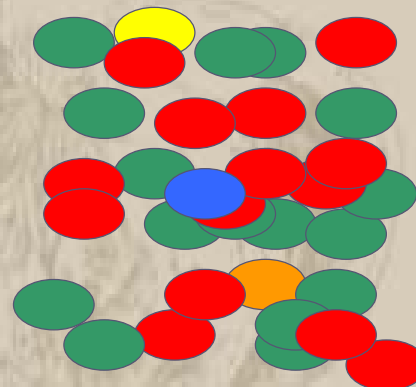
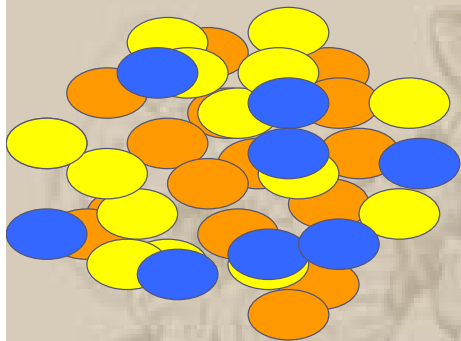
Gene Flow & Adaptive Variation



Gene Flow & Adaptive Variation



Gene Flow & Adaptive Variation



Gene Flow & Adaptive Variation



2. Structure => Local Adaptation?



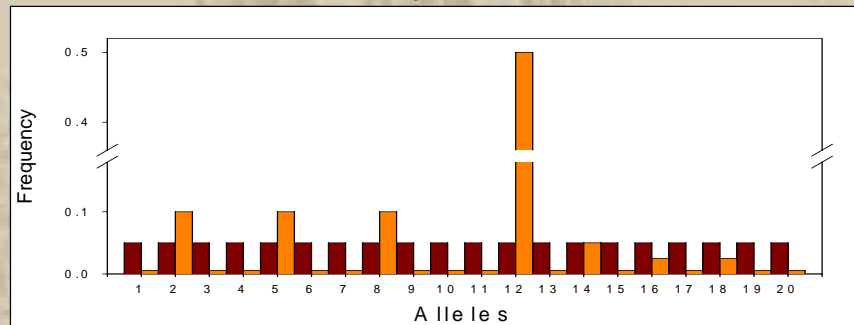
- Empirical Approaches:
 - Direct: Crossing & Transplanting Experiments
 - Pedigreed families
 - Mass spawns
 - Is there a “home team advantage?”
 - Indirect: Comparisons of Q_{st} and F_{st}
 - Molecular structure (F_{st})
 - Quantitative structure (Q_{st})
 - Marker-based relatedness
 - $Q_{st} = F_{st}$ implies no local adaptation
 - $Q_{st} \gg F_{st}$ implies local adaptation

McKay, J.K., Latta, R.G., 2002. Adaptive population divergence: markers, QTL and traits. Trends in Ecology and Evolution 17, 285-291.

3: Large # = Genetically Healthy?



● Effective Population Size (N_e)



● What reduces N_e ?

- Genetic Drift (small populations)
- Variance in reproductive success (small or large)
- Founder effects
- Inbreeding

3: Large # = Genetically Healthy?



● Hatchery supplementation can cause genetic drift by increasing the variance in reproductive success

- small remnant populations easy to impact
 - small # parents
 - related parents
 - unequal parental contributions
- #### ● Hatchery initiation of NEW populations can result in strong bottlenecks/founder effects
- small # parents
 - related parents
 - unequal parental contributions

3: Large # = Genetically Healthy?



- Hatchery production and inbreeding
 - Typically deleterious (inbreeding depression)
 - Recessive deleterious alleles are “exposed” when homozygous. (Dominance hypothesis)
 - Heterozygote advantage lost (Overdominance hypothesis)
 - Sometimes advantageous (outbreeding depression)
 - Maintains integrity of beneficial epistatic combinations
 - These are disrupted by out-crossing
 - Another empirical question!
 - Comparisons between crosses within and among populations

3: Large # = Genetically Healthy?



- Broodstock sampling issues, hatchery techniques, and the relative numbers of wild vs. hatchery-produced animals interact in complex ways to determine the genetic effects of hatchery supplementation.
- Best practices:
 - Large number of parents
 - Unrelated parents
 - Balance contribution of parents to hatchery spawns

4. Past = Present = Future?



- Local adaptation is dynamic
 - Natural changes/cycles in environmental conditions
 - Human impacts
 - Introduced species
- Does restoring historical structure or maintaining current structure also ensure future capacity to respond?
- Would it be better to:
 - Mix populations to maximize future adaptive potential?
 - Match broodstock sources to current conditions?

A Framework for Decisions



Crandall, K.A., Bininda-Emonds, O.R.P., Mace, G.M., Wayne, R.K., 2000.
Considering evolutionary processes in conservation biology. *Trends in Ecology & Evolution* 15, 290-295.

- Developed type of hierarchical arrangement that takes into account both ecological and genetic factors on both historical and current time scales
 - Distinctness/Exchangeability
 - Ecological
 - Genetic
 - Time frames
 - Historical
 - Current

Discussion Points



- Do we know enough to do this right?
- If not, what's the best immediate course of action?
- What else do we need to know?
- How can we get this information?
- Is this all just academic?

References



- McKay, J.K., Latta, R.G., 2002. Adaptive population divergence: markers, QTL and traits. *Trends in Ecology and Evolution* 17, 285-291.
- Crandall, K.A., Bininda-Emonds, O.R.P., Mace, G.M., Wayne, R.K., 2000. Considering evolutionary processes in conservation biology. *Trends in Ecology & Evolution* 15, 290-295
- Reed, D.H., Frankham, R., 2001. How closely correlated are molecular and quantitative measures of genetic variation? A meta-analysis. *Evolution* 55, 1095-1103
- Pearman, P.B., 2001. Conservation value of independently evolving units: Sacred cow or testable hypothesis? *Conservation Biology* 15, 780-783.
- Lynch, M. 1995. A quantitative-genetic perspective on conservation issues. Pages 471-501 in J. C. Avise and J. L. Hamrick, editors. *Conservation genetics: case histories from nature*. Chapman and Hall, New York.
- Doyle, R.M., Perez-Enriquez, R., Takagi, M., Taniguchi, N., 2001. Selective recovery of founder genetic diversity in aquacultural broodstocks and captive, endangered fish populations. *Genetica* 111, 291-304
- Newkirk, G.F., 1978. A discussion of possible sources of inbreeding in hatchery stock and associated problems. *Proceedings of the World Aquaculture Society* 9, 93-100