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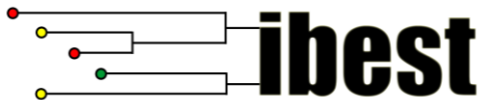
Long-lived marine fish employing broadcast spawning may be resilient to environmental variability: selective sieve hypothesis

*And other insights into Pacific ocean perch (POP) biology
through genomic analysis*

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³JISAO, University of Washington and NOAA PMEL (Pacific Marine Environmental Lab)

Next Generation DNA sequencing

DNA sequences contain information on the spatio-temporal dynamics of populations.



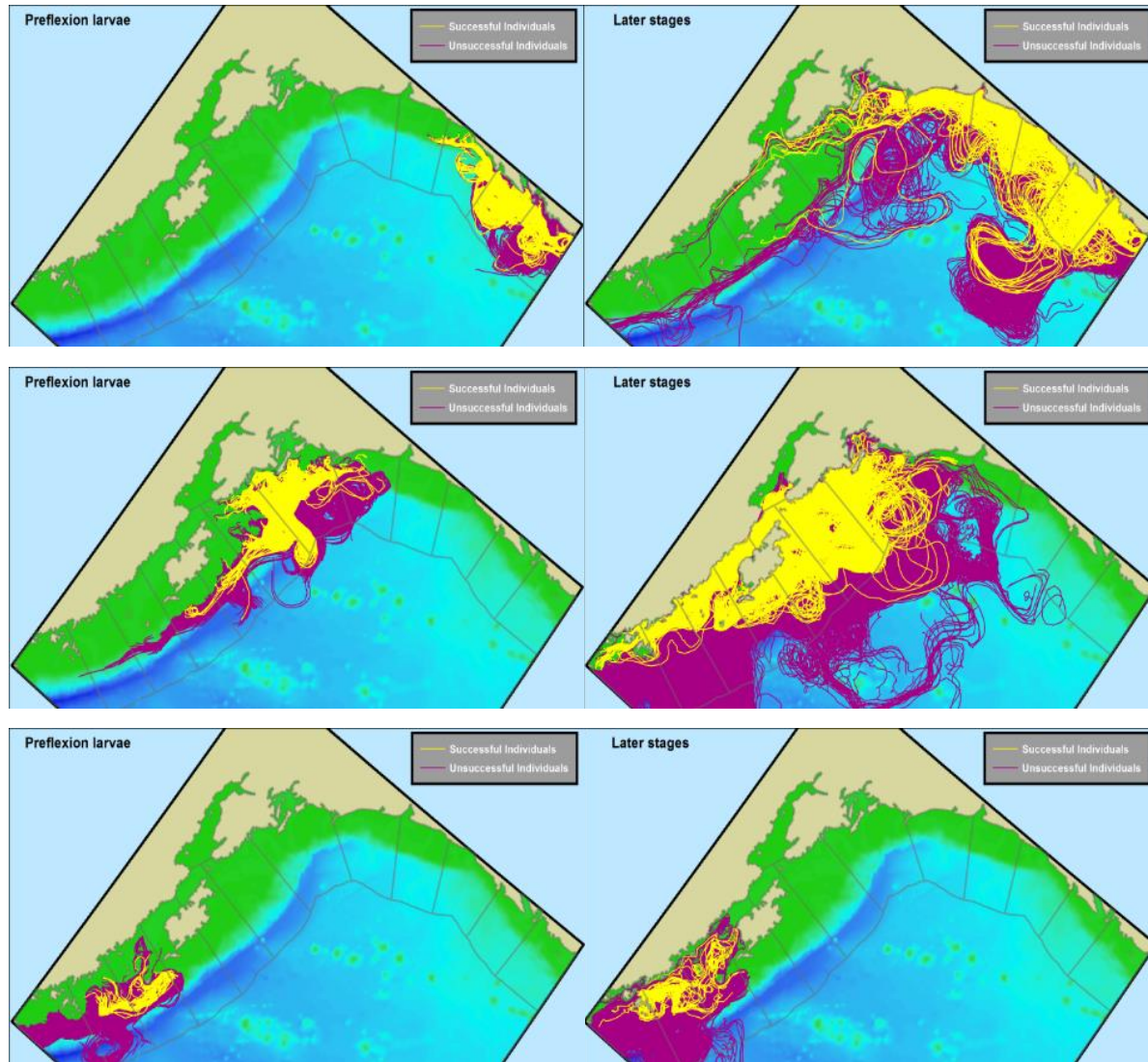
Next Generation DNA sequencing

DNA sequences contain information on the spatio-temporal dynamics of populations.



Q: How can we leverage this information to answer old questions and pose new ones?

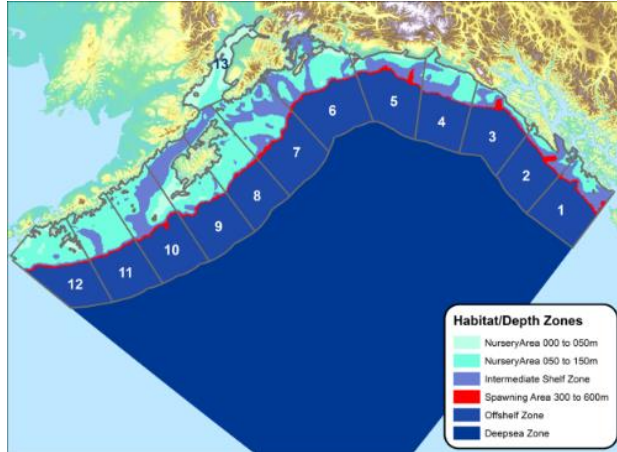
Dispersal model of Pacific ocean perch (POP) larvae



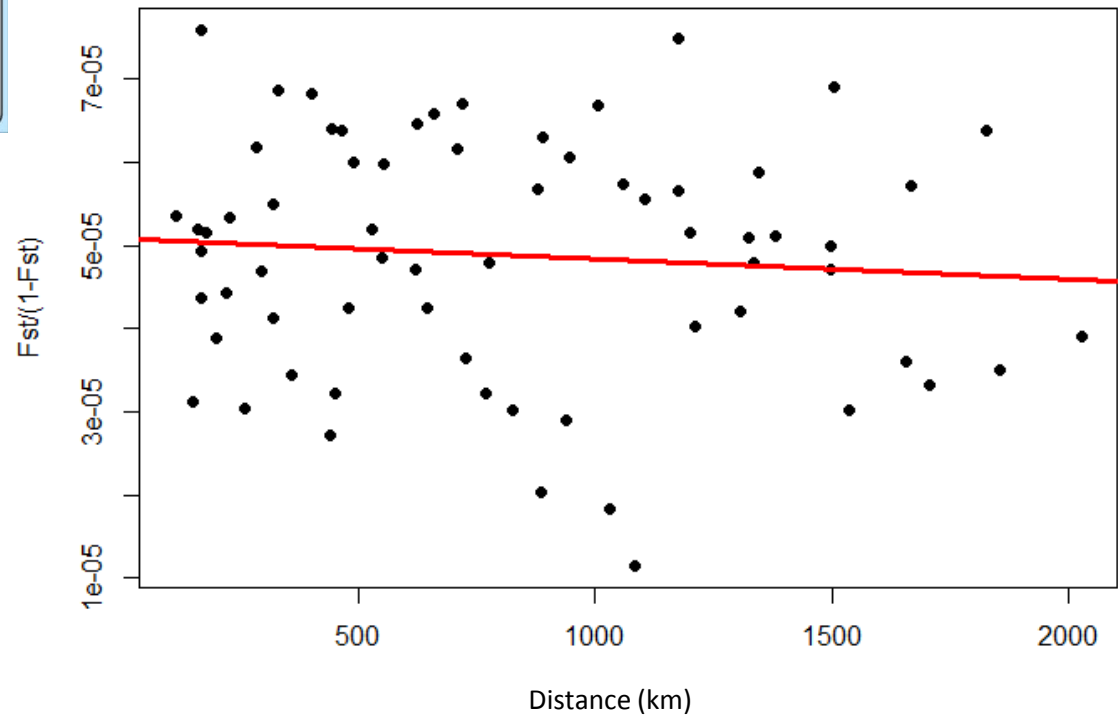
*DisMELS (Dispersal Model for Early Life History Stages),
a ROMS based IBM particle movement model*

DisMELS predicted high lifetime dispersal

Predicted population structure = Panmixia



*In silico Wright-Fisher simulation study:
12 isolated populations subject to DisMELS derived
Transition matrix.*



Observed limited lifetime dispersal

Observed population structure = Isolation by Distance (~100 km scale)

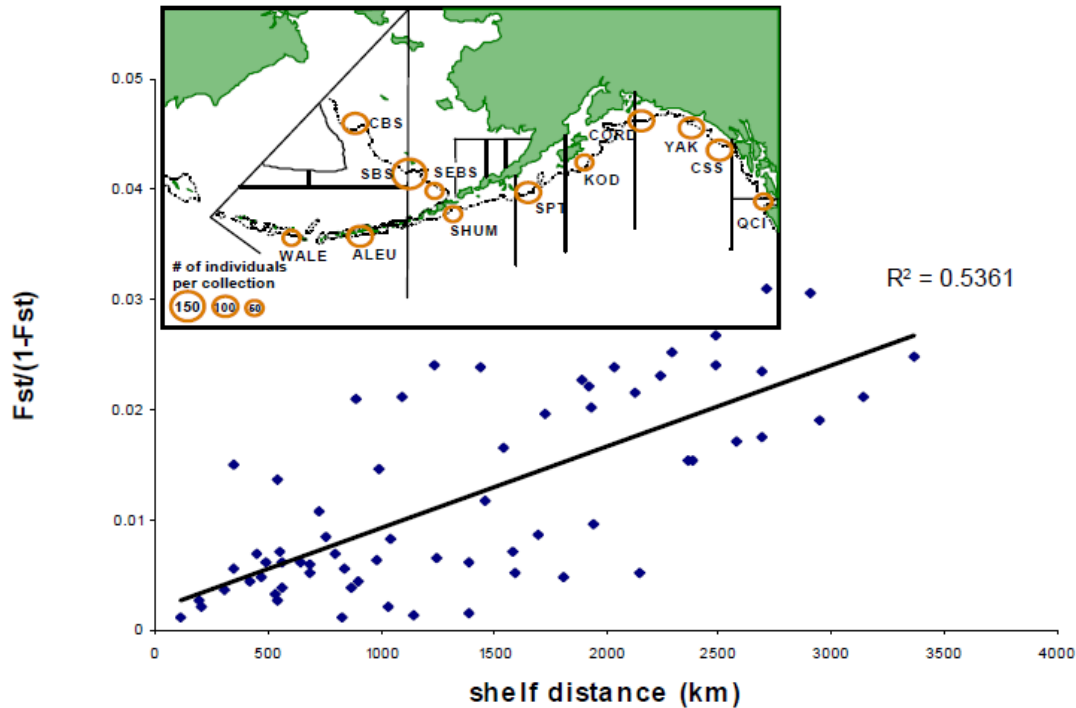


Figure 10. Isolation by distance pattern for Alaska Pacific ocean perch and map of collection sites
Adapted from Palof et al. (2011).

Observed limited lifetime dispersal

Observed population structure = Isolation by Distance (~100 km scale)

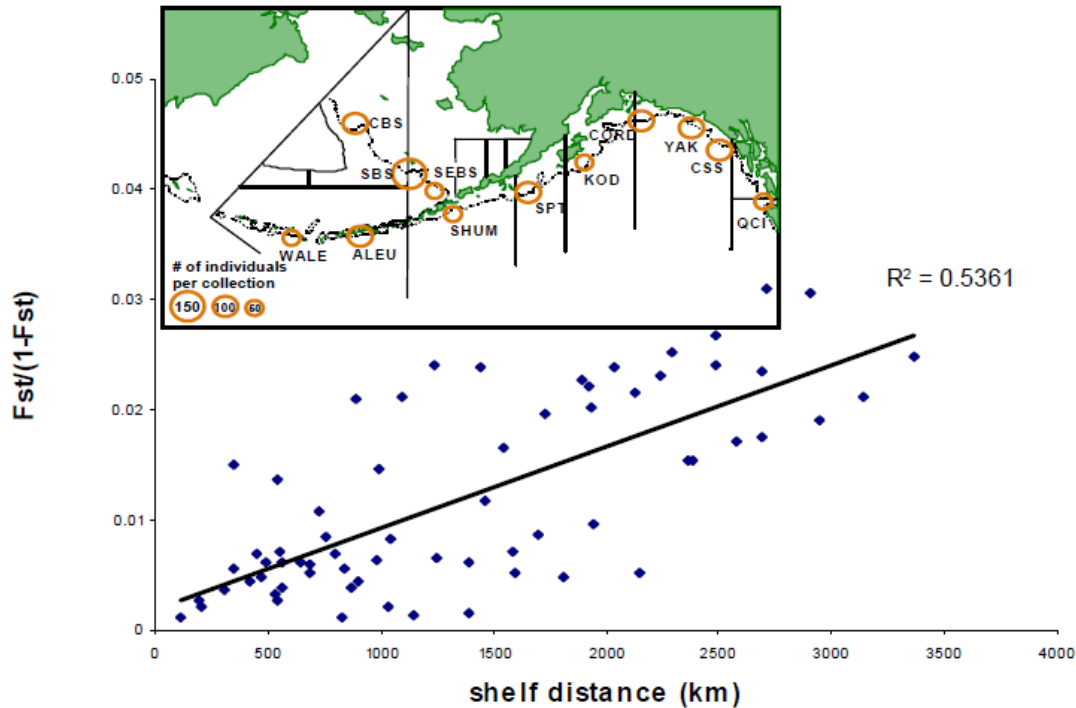
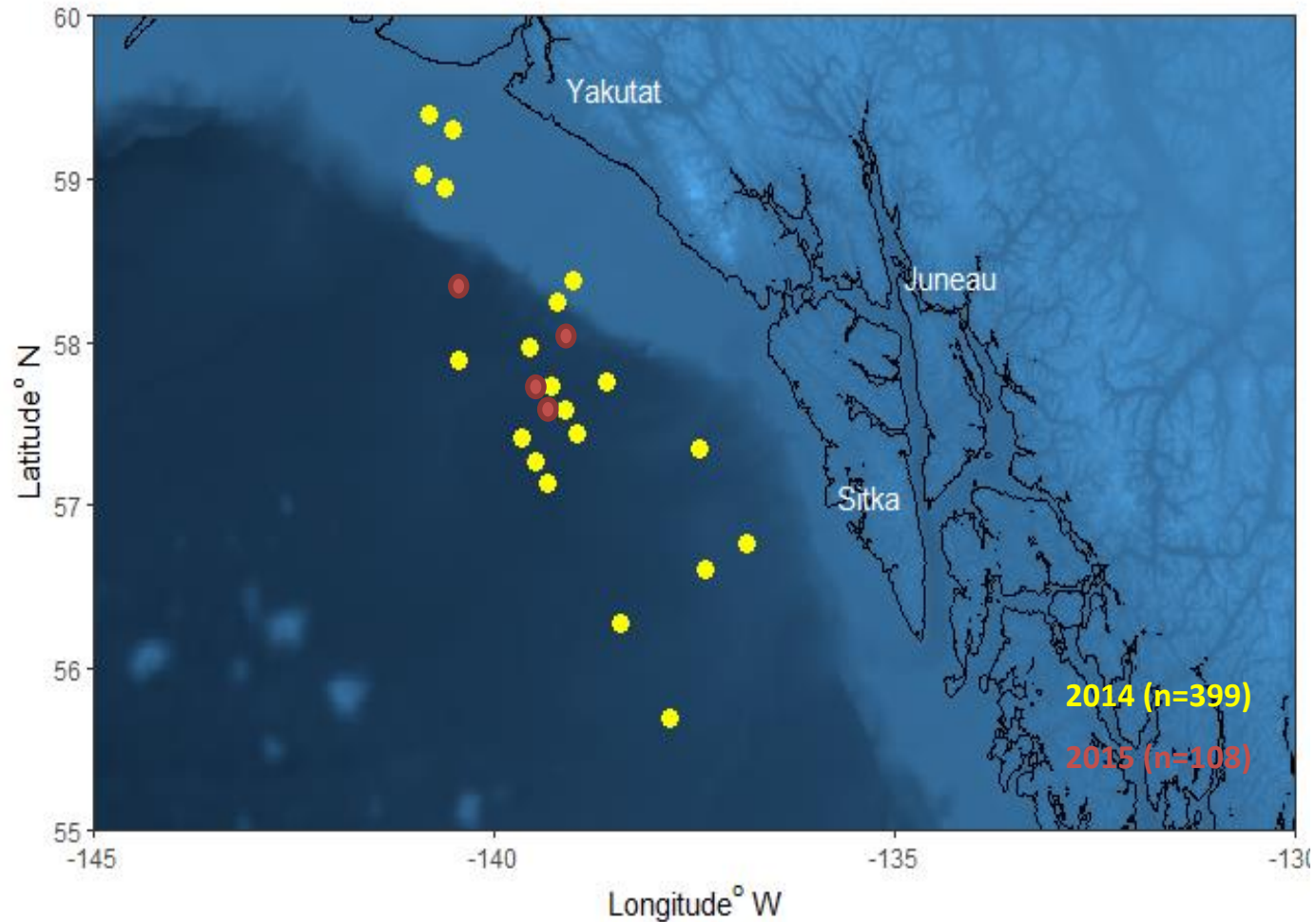


Figure 10. Isolation by distance pattern for Alaska Pacific ocean perch and map of collection sites
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Q: How is this population structure maintained under strong dispersal?

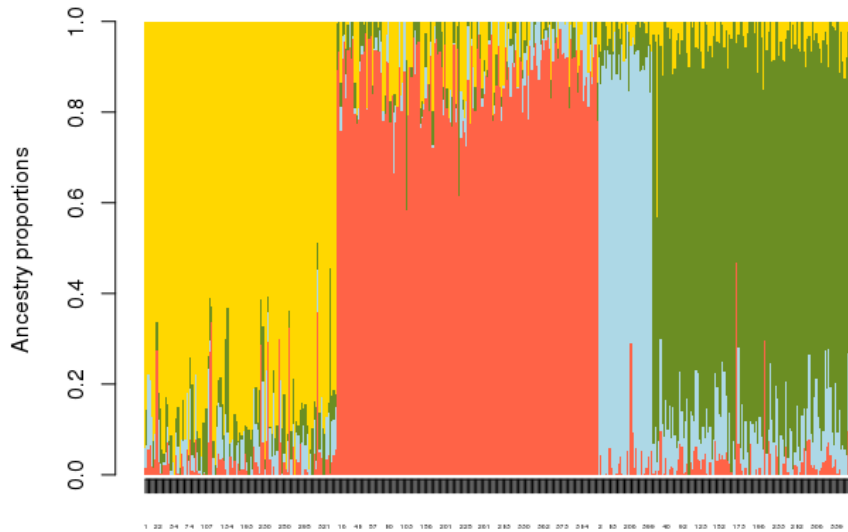
Young of the Year POP collections



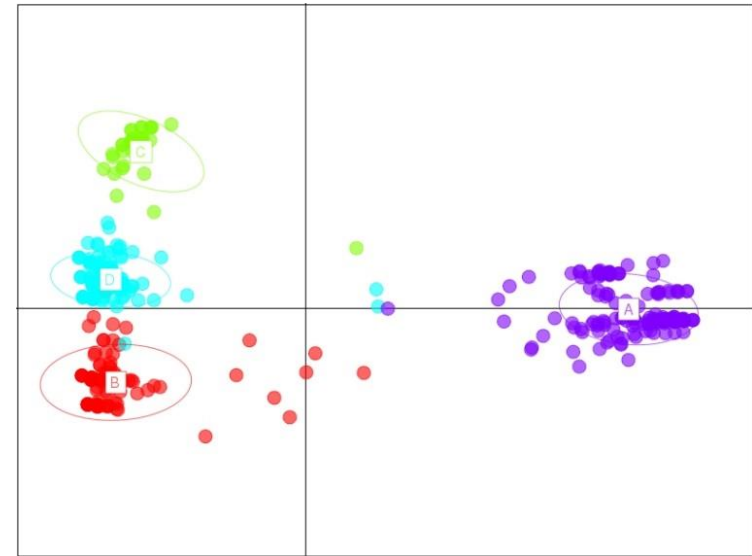
- **RAD seq** analysis of **507 POP** individuals.
- **11,146 SNPs** and **398 individuals** after filtering.

Group assignments based on STRUCTURE analysis revealed 4 populations in the 2014 and 2015 YOY collections

Ancestry matrix



Individuals



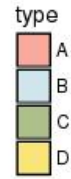
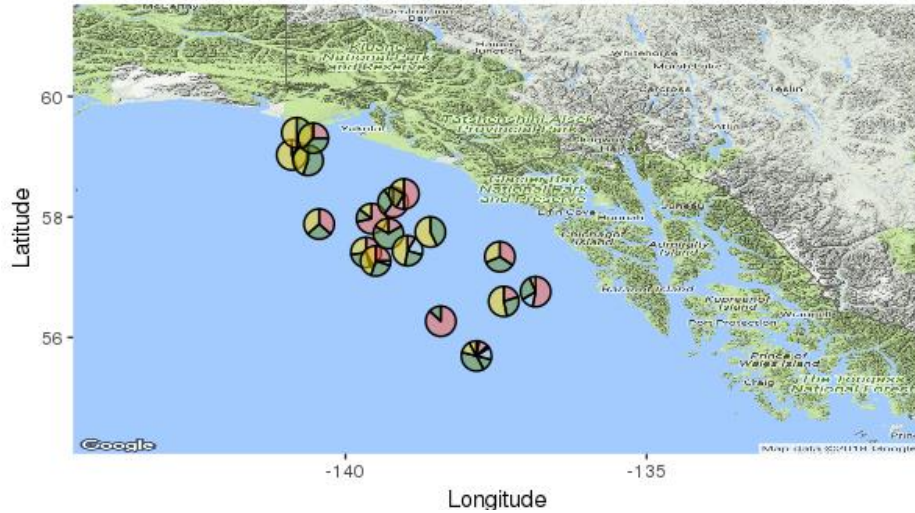
PCA (1st vs 2nd component)

Pairwise Fst

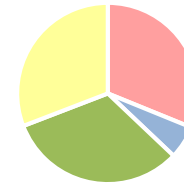
	2014-A	2014-B	2014-C	2014-D	2015-A	2015-B	2015-C
2014-B	0.0232						
2014-C	0.0301	0.0138					
2014-D	0.0229	0.0085	0.0116				
2015-A	0.0008	0.0263	0.0321	0.0259			
2015-B	0.023	0.0001	0.0128	0.0067	0.026		
2015-C	0.0303	0.014	-0.0003	0.0112	0.0321	0.0132	
2015-D	0.0234	0.0085	0.0112	0.0001	0.0264	0.0079	0.0117

Spatial pattern of the population distribution in 2014 and 2015

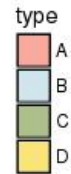
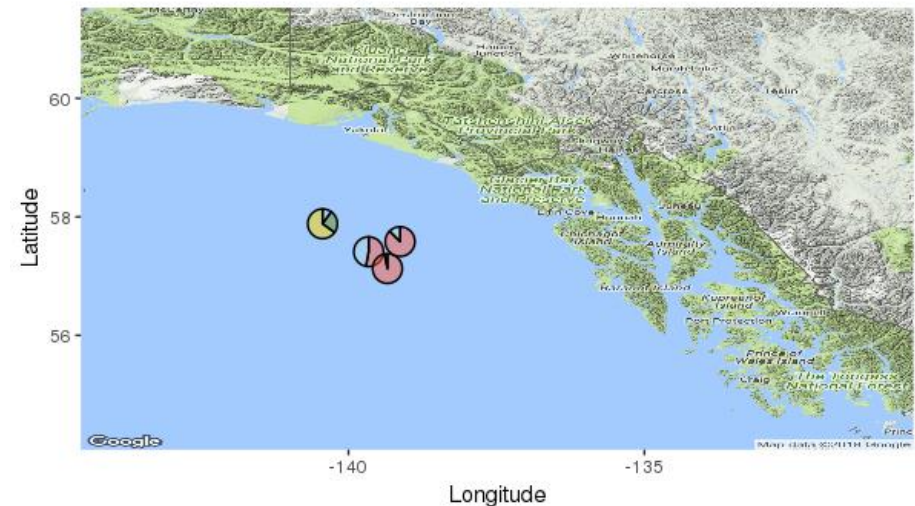
Distribution of POP Populations in YOY catch in 2014



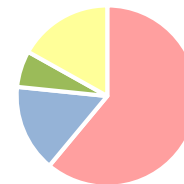
2014



Distribution of POP Populations in YOY catch in 2015



2015



Genome-phenotype and environment association

<i>Environmental Gradient</i>	<i>2014 Candidate Selected Loci</i>	<i>2015 Candidate Selected Loci</i>
Latitude only	19	57
Collection Date only	67	71
Latitude & Date	27	73
Temperature	1	19
Chlorophyll concentration	16	159
<i>Phenotype</i>		
% Lipid	1	58
Weight~Length Residual	6	13

Selection along temporal and latitudinal gradient

<i>Environmental Gradient</i>	<i>2014 Candidate Selected Loci</i>	<i>2015 Candidate Selected Loci</i>
Latitude only	19	57
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- *Selection may be balancing the effects of gene flow due to dispersal.*

Conclusions

Part 1, DisMELS dispersal and population structure

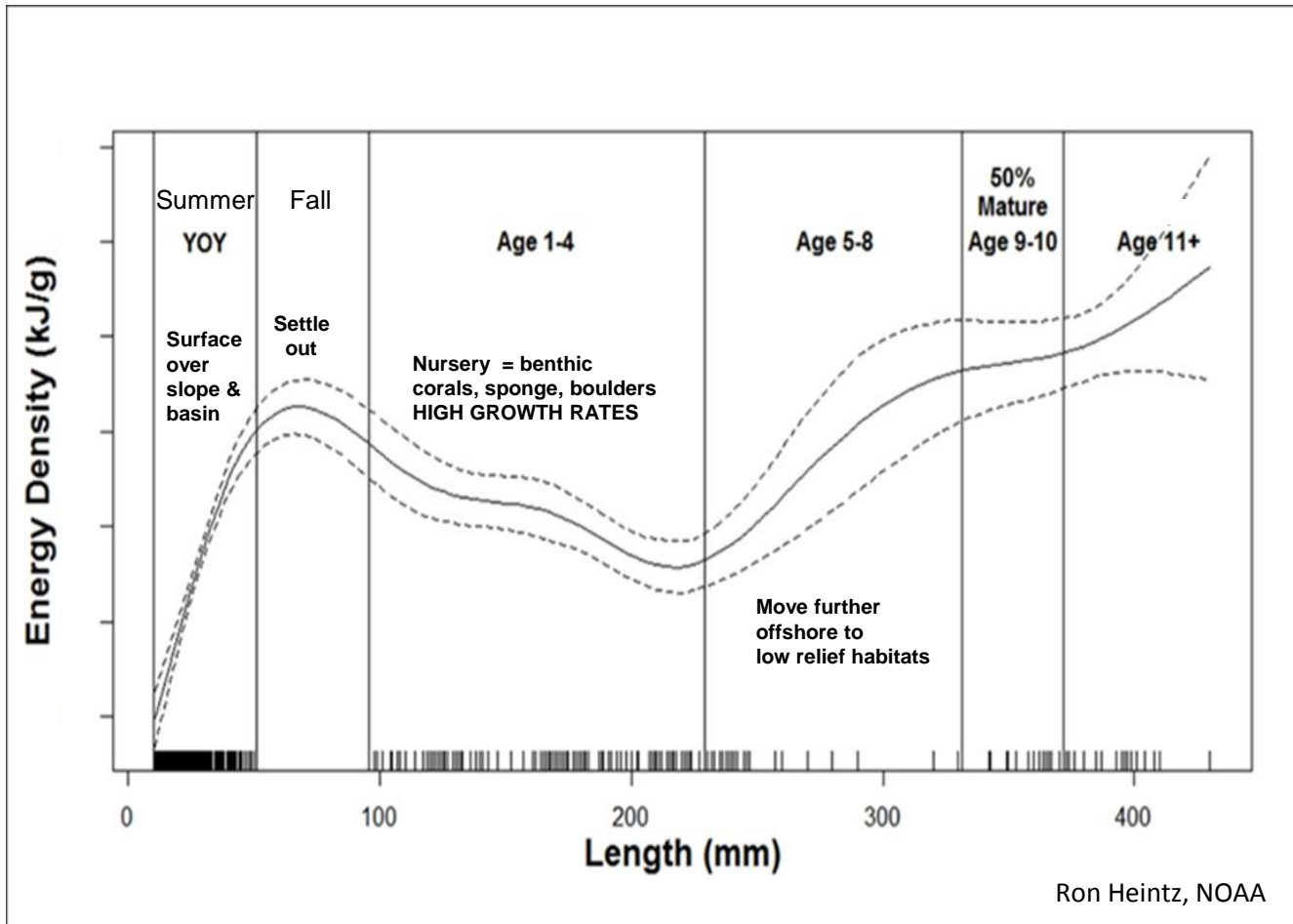
- Wide ranging dispersal is consistent with DisMELS model.
- POP larvae/YOY aggregates are mixtures of spawning populations consistent with DisMELS model.
- Selection along spatio-temporal gradients may be balancing dispersal resulting in the observed population structure.

Annual differences in patterns of selection

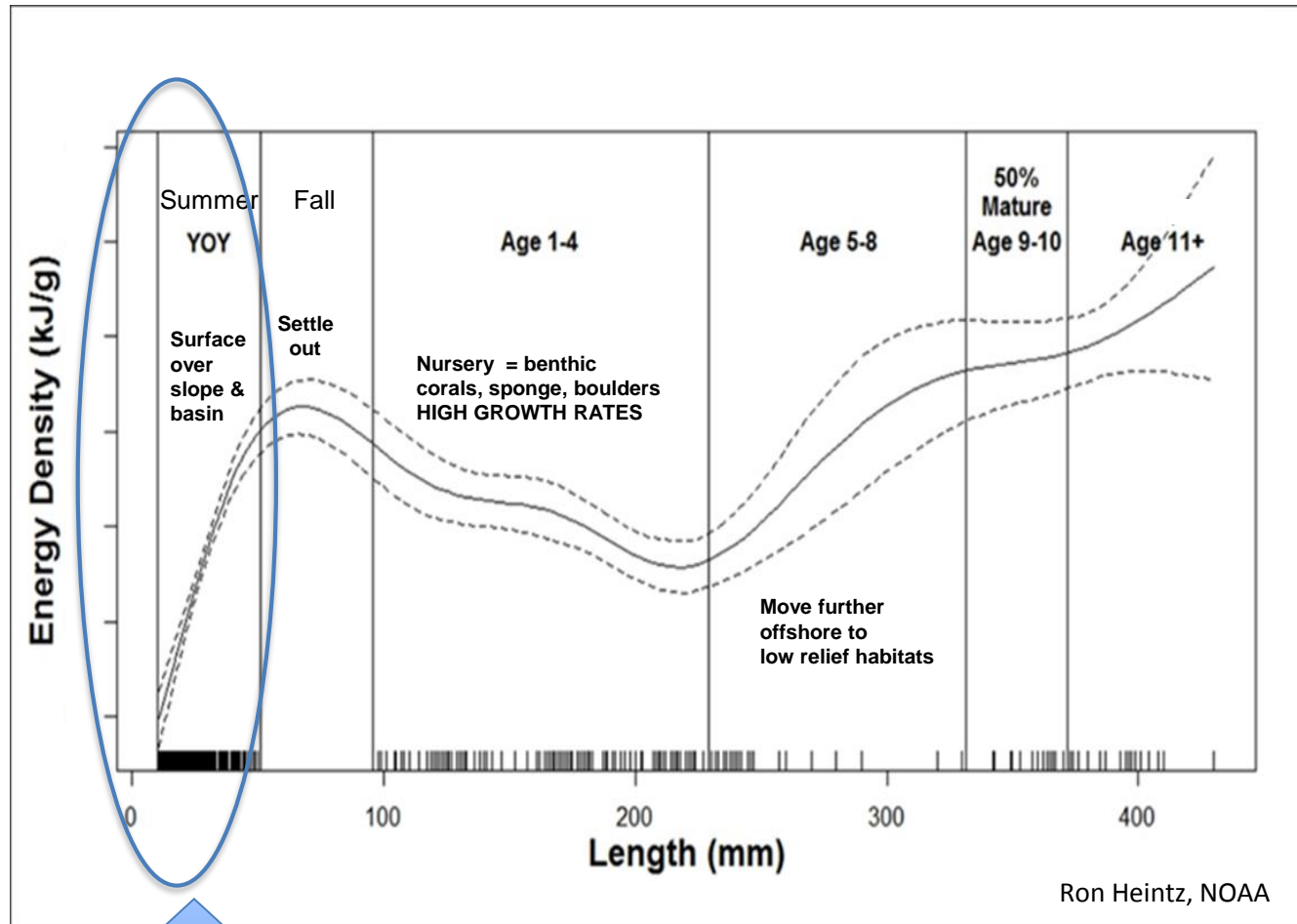
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- *More candidate selected loci in 2015 than in 2014*
 - *Stronger selection in 2015.*
 - *2015 was a warm anomaly year with large sea bird die-offs*

POP life history through energy density

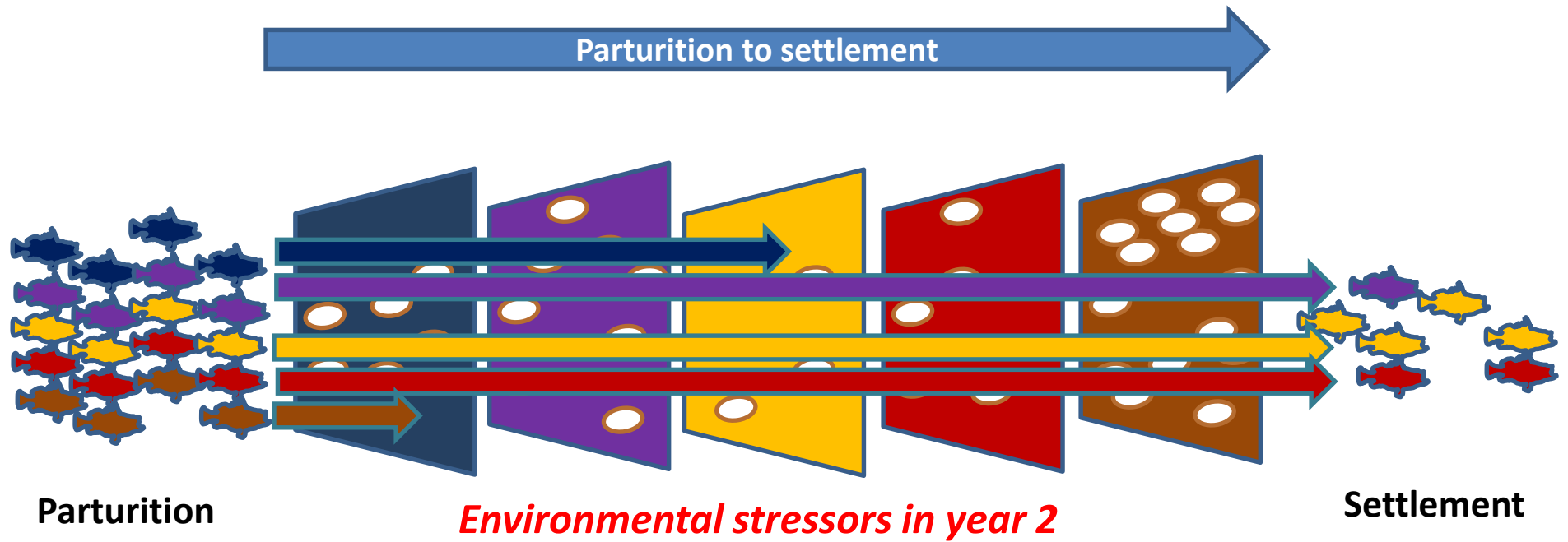
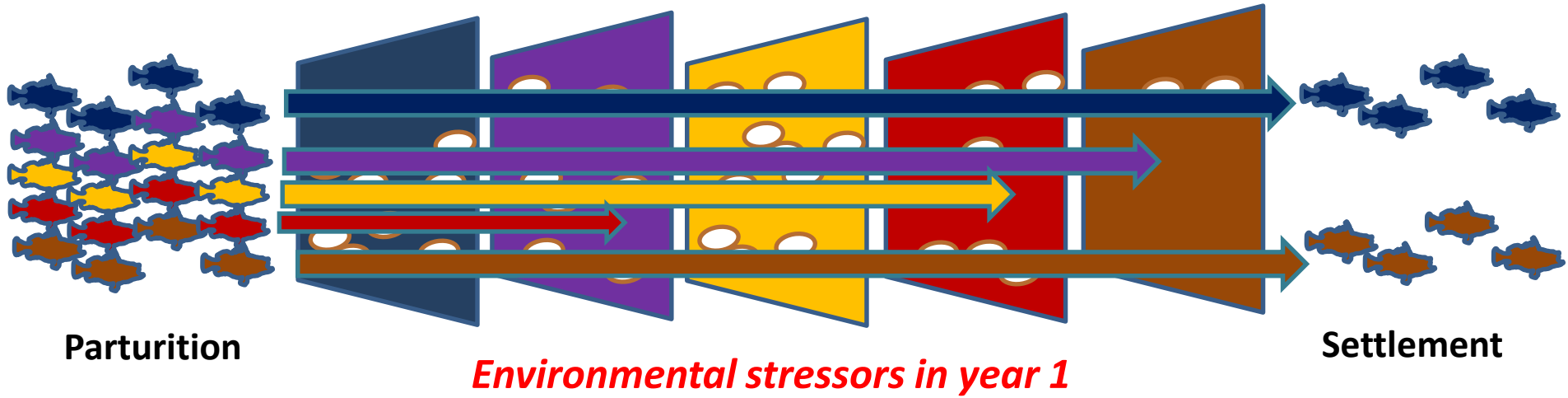


Selection may be strongest during larval/YOY stage



Most vulnerable life stage

Selective sieve hypothesis



Conclusions

Part 2, selective sieve hypothesis

- Selection pressure varies annually (selective sieve):
 - Cohort specific molecular selection signatures may possibly be used to estimate ages of adults.
- Possibly able to reconstruct environmental selection forces (i.e. temperature) based on patterns of selected alleles:
 - What were the environmental conditions 100 years ago based on the alleles found in 100 year old fish?
- Long lived species with multiple cohorts spawning over many years may be particularly resilient to environmental variability by maintaining a portfolio of adaptive alleles.

Thank you

