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VIU Broodstock Enhancement Program (BEP)

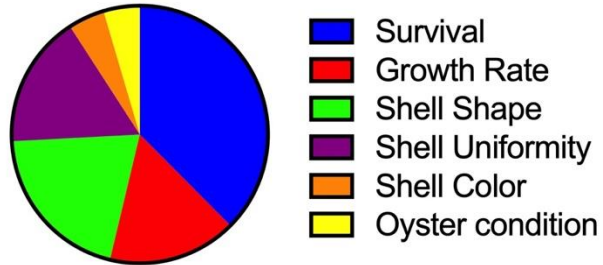


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VIU Broodstock Enhancement Program (BEP)

BCSGA Feedback on Breeding Objectives



Selective breeding is cyclical and consists of:

1. Selecting broodstock based on scientific data.
2. Spawn selected broodstock and raise larvae and spat in the hatchery.
3. Send progeny to field/laboratory sites and collect phenotypic data.
 - a) Ocean acidification resistance as larvae.
 - b) Growth, survival and shell characteristics in field trials.
 - c) Vibrio and marine heatwave challenge in laboratory.
4. Analyze data using quantitative genetics.
 - i. **Animal model: BLUP** -> estimated breeding values (EBVs)
 - ii. **Allocate.Mate**: mate allocation based on EBVs and Wright's inbreeding coefficient (F)
5. Repeat cycle for next generation of oysters.



Oyster Phenotypic Variation



Phenotype = Genetics x Environment

Genetic architecture of a phenotypic trait

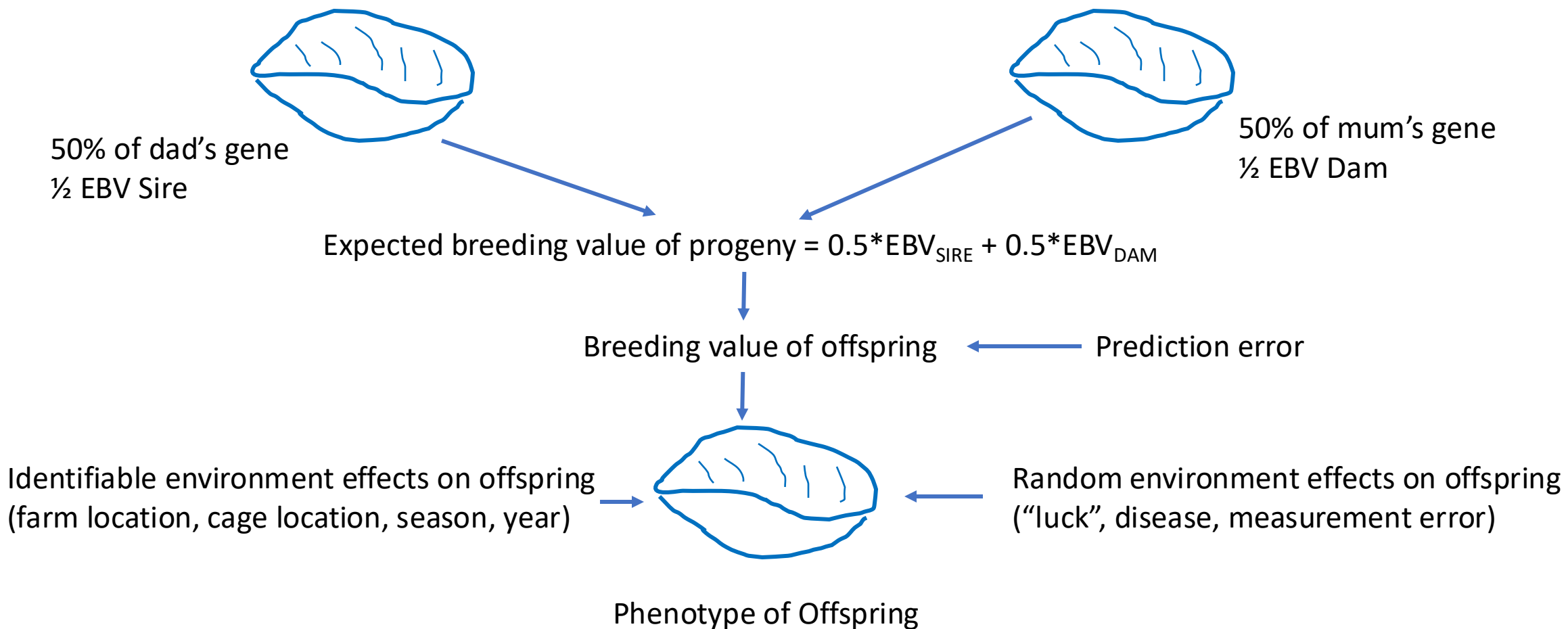
- Complex: many genes influence the trait, such as disease resistance.
- Simple: small number of genes influence a trait (major effect loci), such as shell colour.

Animal Model: Best Linear Unbiased Prediction

$$y_i = u + a_i + e_i$$



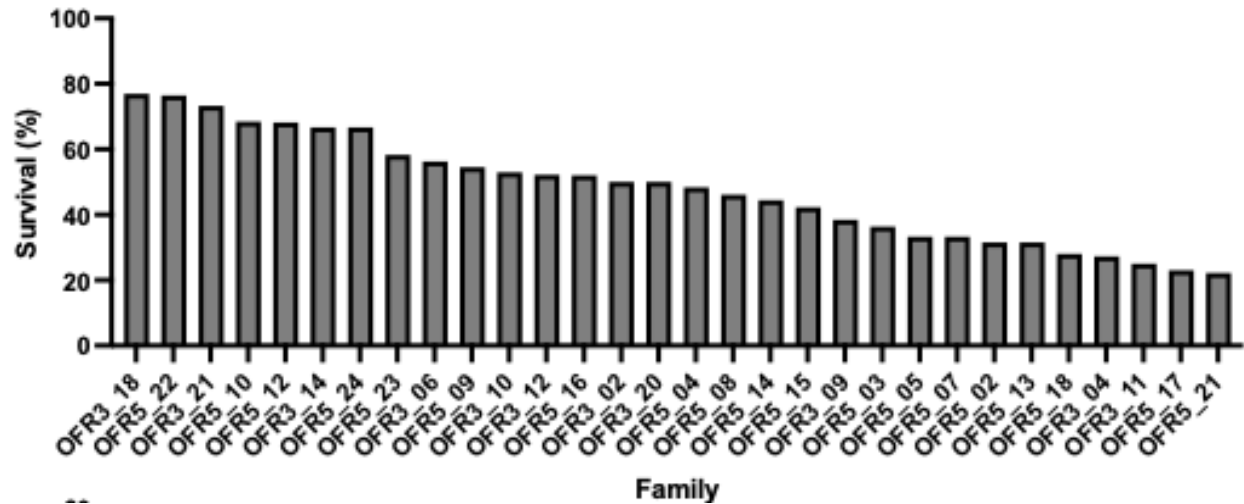
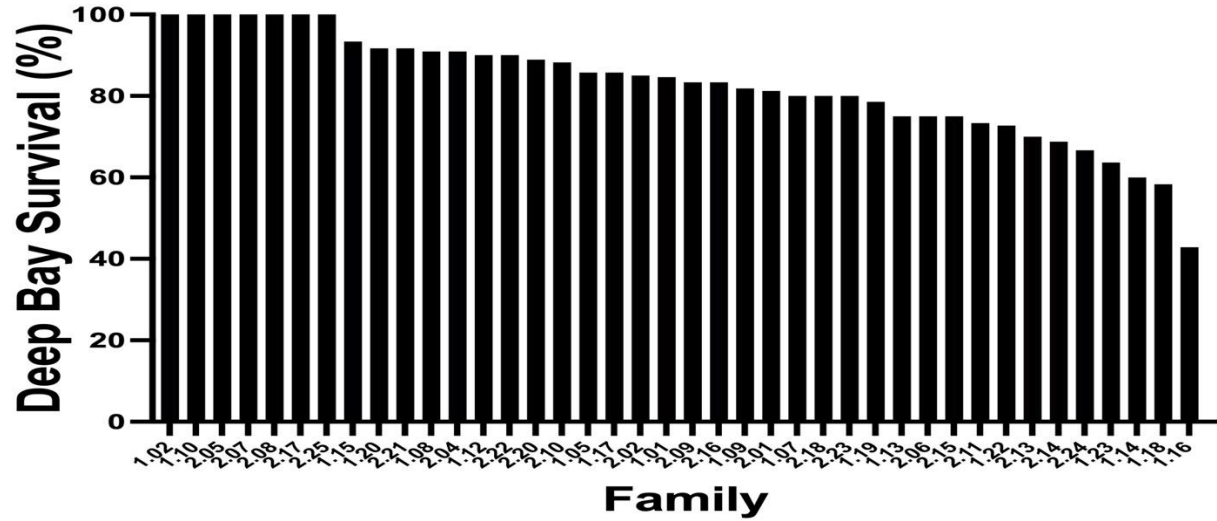
Genetic and environmental factors influencing an offspring genotype



Farm Survival Data



$h^2 = 0.385$, 95% CI = 0.054 - 0.723





Summer mortality is a complex phenomenon



Genetic divergence of selected and wild populations of Pacific oysters (*Crassostrea gigas*) on the West Coast of North America

Dennis Hedgecock Francis T.C. Pan

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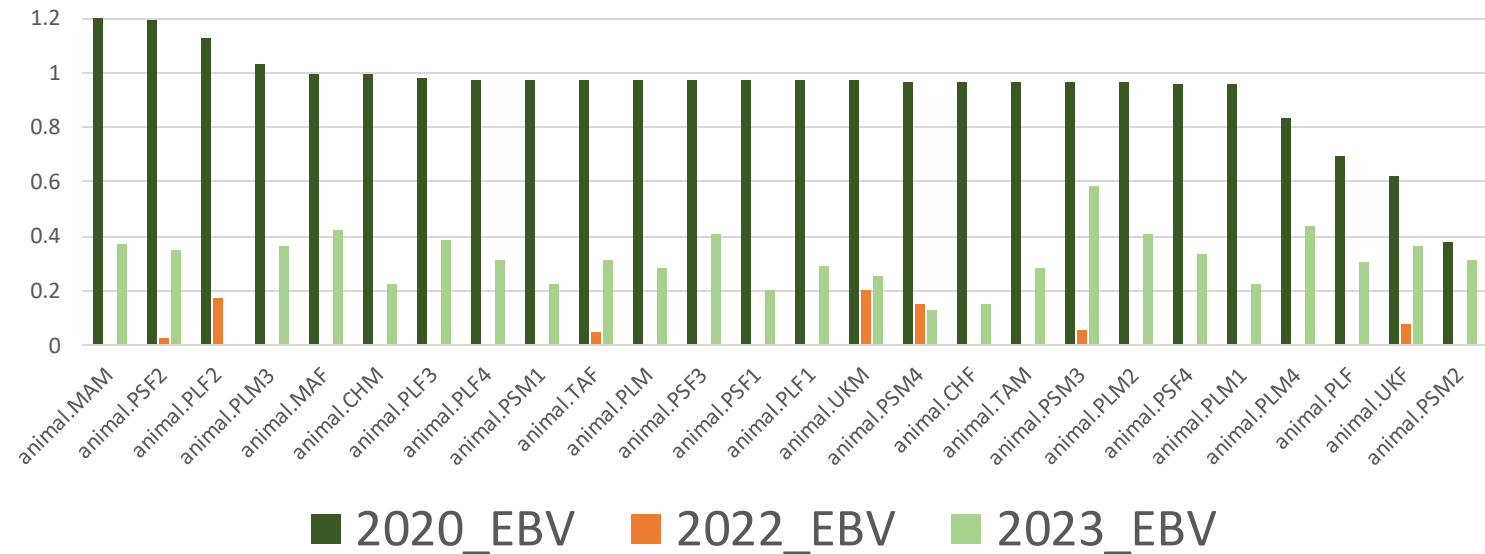
<https://doi.org/10.1016/j.aquaculture.2020.735737>

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Highlights

- “Selected oysters = wild controls” does not explain zero realized gain in yield.
- Selected stocks and wild populations have diverged by random genetic drift.
- Genetic analyses of selected oysters and their parents reveal pedigree errors.
- Zero gain likely explained by pedigree errors, inaccurate and inefficient selection.
- Genetic markers are needed for pedigree control in shellfish breeding programs.

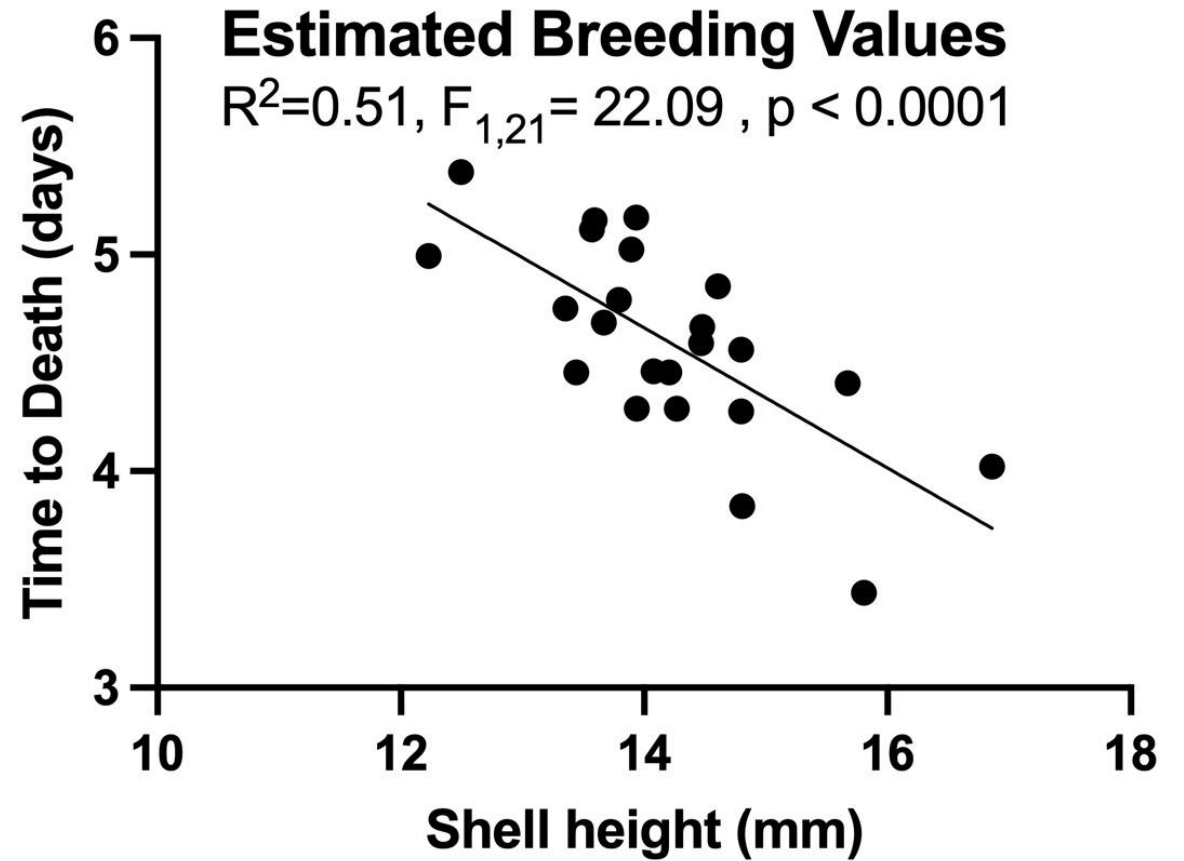
Estimated Breeding Values



Growth rate is negatively correlated with survival



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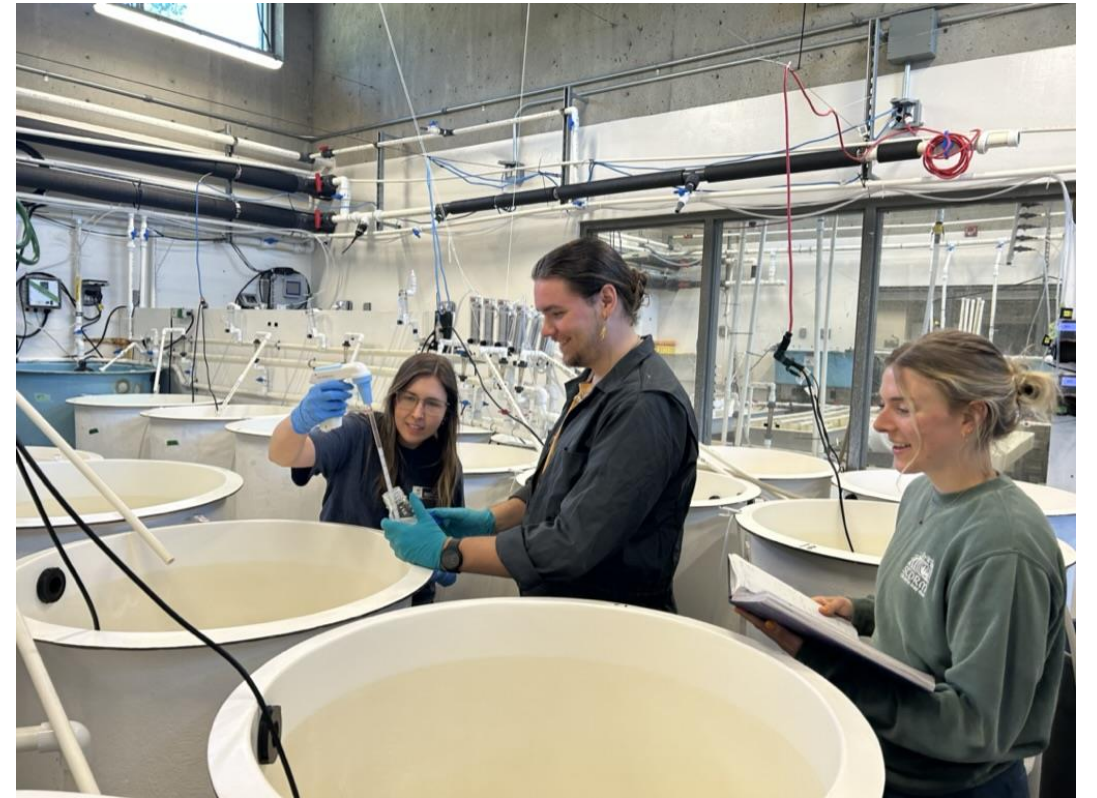


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*Something Old
Something New,
Something Borrowed,
Something Blue.*





Something Old: Physical Based Tagging (PBT)



Shellfish Tag Pros

- Cheap (\$0.35).
- Common garden/mixed families.
- Can easily track individual through time.

Shellfish Tag Cons

- Time consuming.
- Lost tags – missing data (human error, high energy environments, biofouling)
- Difficult to read.

Something New: Amplicon Genotyping Panel



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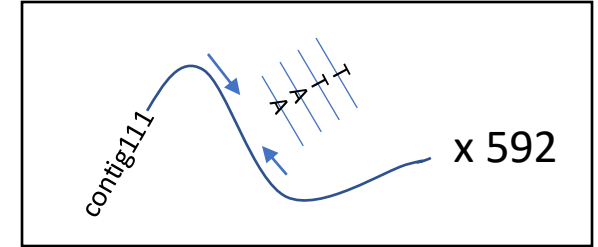
G3, 2024, 14(9), jkae125
<https://doi.org/10.1093/g3journal/jkae125>
Advance Access Publication Date: 13 June 2024
Investigation

An amplicon panel for high-throughput and low-cost genotyping of Pacific oyster

Ben J.G. Sutherland^{1,2*}, Neil F. Thompson,³ Liam B. Surry,² Krishna Reddy Gujjula,⁴ Claudio D. Carrasco,⁴ Srinivas Chadaram,⁴ Spencer L. Lunda,⁵ Christopher J. Langdon,⁶ Amy M. Chan,⁷ Curtis A. Suttle,^{7,8,9,10} Timothy J. Green²

¹Sutherland Bioinformatics, Lantzville, BC V0R 2H0, Canada
²Faculty of Science and Technology, Vancouver Island University, Nanaimo, BC V9R 5S5, Canada
³United States Department of Agriculture, Hatfield Marine Science Center, Pacific Shellfish Research Unit, Agricultural Research Service, Newport, OR 97365, USA
⁴ThermoFisher Scientific, 2130 Woodward Street, Austin, TX 78744, USA
⁵Department of Microbiology, Oregon State University, 226 Nash Hall, Corvallis, OR 97331, USA
⁶Hatfield Marine Science Center, 2030 SE Marine Science Dr., Oregon State University, Coastal Oregon Marine Experiment Station, Newport, OR 97365, USA
⁷Department of Earth, Ocean and Atmospheric Sciences, The University of British Columbia, Vancouver, BC V6T 1Z4, Canada
⁸Department of Microbiology and Immunology, The University of British Columbia, Vancouver, BC V6T 1Z3, Canada
⁹Department of Botany, The University of British Columbia, Vancouver, BC V6T 1Z4, Canada
¹⁰Institute for the Oceans and Fisheries, The University of British Columbia, Vancouver, BC V6T 1Z4, Canada

*Corresponding author: Sutherland Bioinformatics, Lantzville, BC V0R 2H0, Canada. Email: Sutherland.Bioinformatics@protonmail.com



Parentage
Genomic Selection
Marker-Assisted Selection



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Something Borrowed: Bioinformatic tools

Aquaculture 612 (2020) 743096



Pedigree-based genome-wide imputation using a low-density amplicon panel for the highly polymorphic Pacific oyster *Crassostrea gigas*

Ben J.G. Sutherland^{a,b,*}, Konstantin Divilov^c, Neil F. Thompson^d, Thomas A. Delomas^e, Spencer I. Landa^f, Christopher J. Langdon^g, Timothy J. Green^h

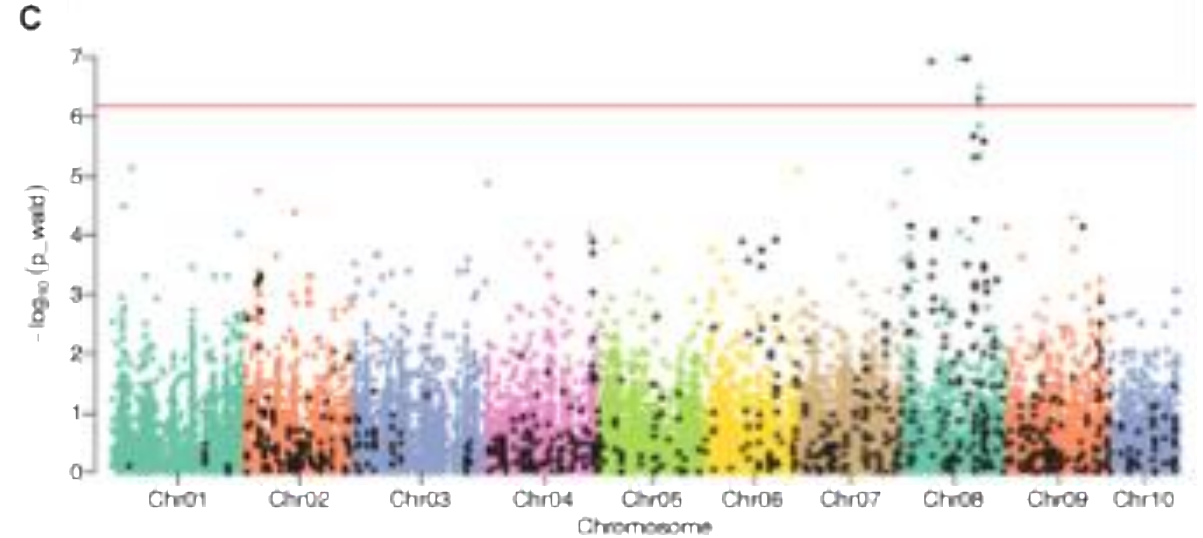
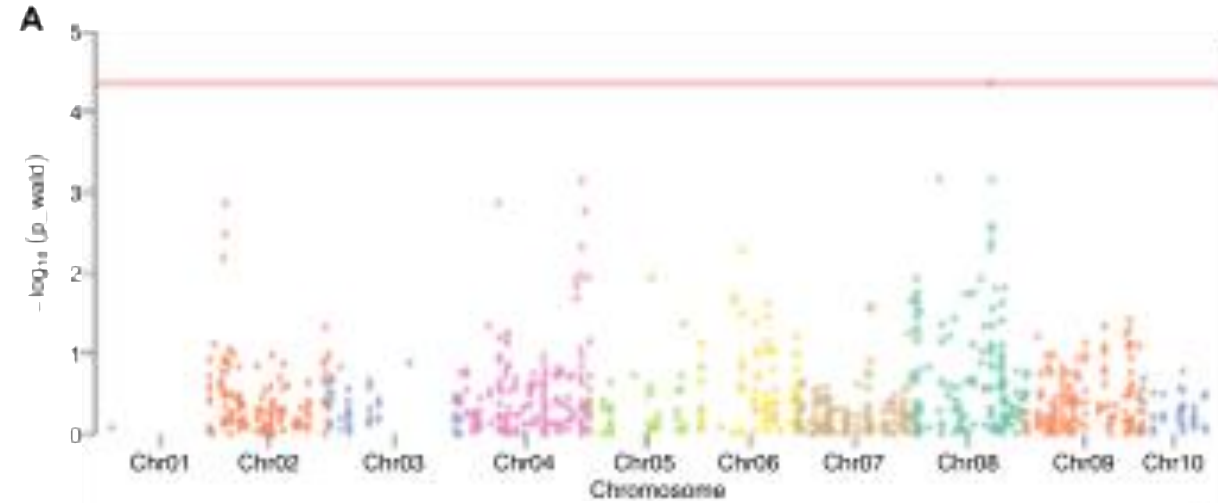
^a Faculty of Science and Technology, Vancouver Island University, Nanaimo, BC V9B 5S5, Canada
^b Sustainable Aquaculture, Lunenburg, NS V9B 2Y9, Canada
^c Center for Quantitative Life Sciences, Oregon State University, Corvallis, OR 97331, USA
^d Pacific Shellfish Research Unit, USDA Agricultural Research Service, 2030 SW Marine Science Drive, Newport, Oregon 97156, USA
^e Agricultural Research Service, United States Department of Agriculture, National Cold Water Marine Aquaculture Center, 603 CRA, 130 Flagg Road, Kingman, AZ 86401, USA
^f Oregon State University, Department of Microbiology, 226 Nash Hall, Corvallis, OR 97331, USA
^g Oregon State University, Coastal Oregon Marine Experiment Station, Hatfield Marine Science Center, 3000 SE Marine Science Dr., Newport, OR 97156, USA

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Whole-genome resequencing

ABSTRACT

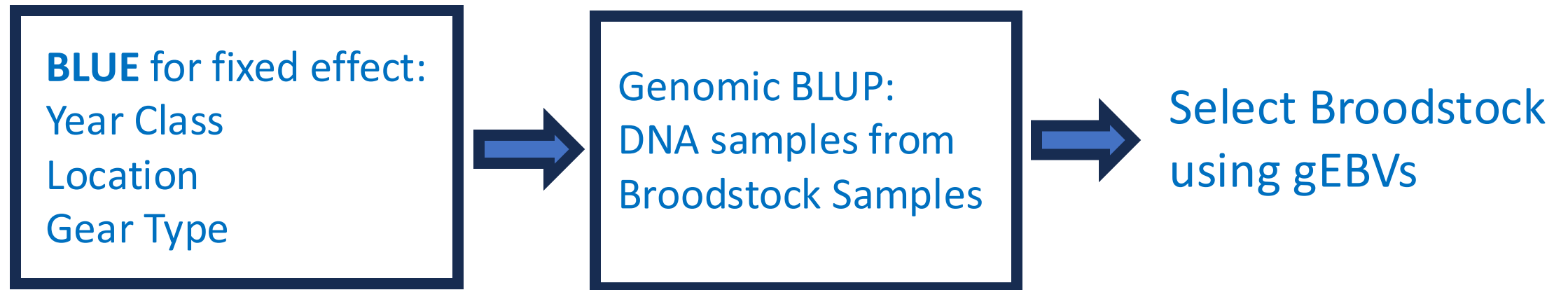
High-density genomic data are instrumental for selective breeding, but the costs associated with these approaches can hinder progress, as is the case for most aquaculture species. A strategy to reduce genotyping costs is to genotype a few select individuals at high density (e.g., parents, grandparents), and many others at low density (e.g., offspring), then impute genotypes. This has been demonstrated in silico for the Pacific oyster *Crassostrea gigas* but was particularly challenging relative to other species and has never been empirically tested. Here, four families of Pacific oysters, bred via marker-assisted selection for variation at a locus for field survival in an oyster herpesvirus (OHV-1)-positive estuary, were exposed to OHV-1 then genotyped using a low-density amplicon panel ($n = 240$ individuals). Parents were genotyped with the amplicon panel and by whole-genome resequencing. Offspring genotypes were imputed, and accuracy was determined by comparing against high-density genomic data for offspring. Imputation resulted in reduced minor allele frequencies and enriched homozygosity relative to empirical data. An in silico three-generation analysis was used to investigate the effect of deepening the pedigree, resulting in superior concordance in genotypes ($CC = 84.5\%$) and allelic dropout ($r = 0.73$) compared to two-generation imputation ($CC = 75.3\%$, $r = 0.63$). Genome-wide associations to OHV-1 survivorship with imputed data identified significantly associated regions on the expected chromosome 5, but not at the expected position based on previous work, pointing to a potentially more complex genetic architecture for the trait. Our results empirically demonstrate the utility of amplicon panel-based genome-wide imputation in shellfish, and thus enable low-cost selective breeding techniques.





Something Blue: Best Linear Unbiased Estimation

Two –stage analysis to consider fixed effects of year on mortality, followed by gBLUP on broodstock and selection candidates.





Genomic Selection



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2025 Evaluating Genomic Selection for VIU BEP:

- Complex Trait: Genomic selection to Vibrio and heatwave (Denman Moody)
- Simple Trait: Marker-Assisted Selection (MAS) for growth rate and Ocean Acidification (James Dennis-Orr)