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Genetic risk assessment model for native shellfish aquaculture

Natalie Lowell
WA Sea Grant

Genetic risk assessment of native shellfish aquaculture

Natalie Lowell[1], Eric Ward[2], Brent Vadopalas[1], Bobbi Hudson[3], Benoit Eudeline[4], Christopher Eardley[5], and Lorenz Hauser[1]

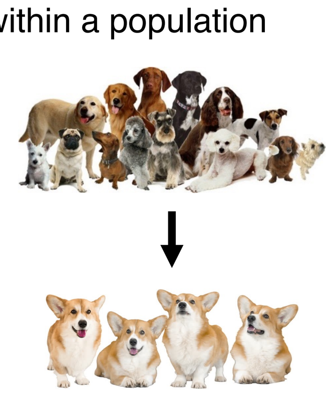
1 – School of Aquatic and Fishery Sciences, University of Washington, Seattle, Washington, USA.
2 – Northwest Fisheries Science Center, NOAA, Seattle, Washington, USA.
3 – Pacific Shellfish Institute, Olympia, Washington, USA
4 - Taylor Shellfish Farms Inc, Quilcene, Washington, USA.
5 – Washington Department of Fish and Wildlife, Port Townsend, Washington, USA

Introduction

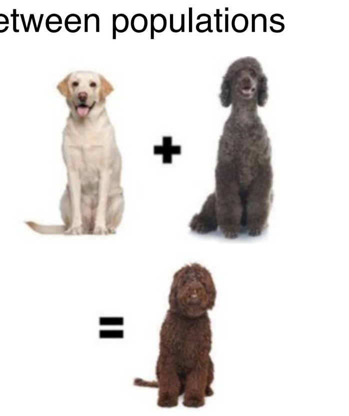
- Aquaculture is rapidly developing worldwide[1]
- Shellfish growers are expanding cultivation of native shellfish species because introduction of non-native species for aquaculture is severely restricted
- Aquaculture of native species may pose **genetic risks** to wild populations if farmed and wild individuals interbreed[2]
- Genetic risks may increase the population extinction risk[2]; we value shellfish stocks for their own sake, for their fisheries, and for their role as broodstock in the aquaculture industry

Explanation of Genetic Risks

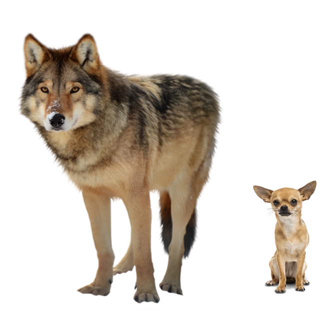
Genetic Risk 1: Loss of genetic diversity within a population



Genetic Risk 2: Loss of genetic diversity between populations



Genetic Risk 3: Loss of fitness due to domestication selection



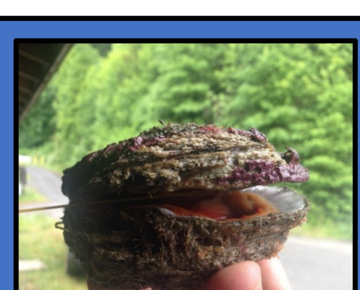
Research questions

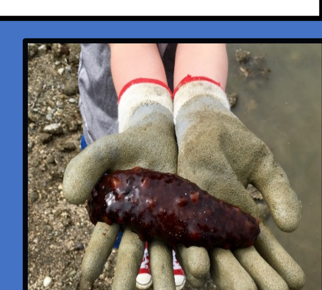
- **Proof of concept**: Can we build a model for assessing the genetic risks of native shellfish aquaculture?
- **Olympia oyster case study**: How do the genetic risk outcomes differ based on production scenario (restoration, commercial, or worst-case-scenario), scale of escape rate, and strength of selection?

Significance

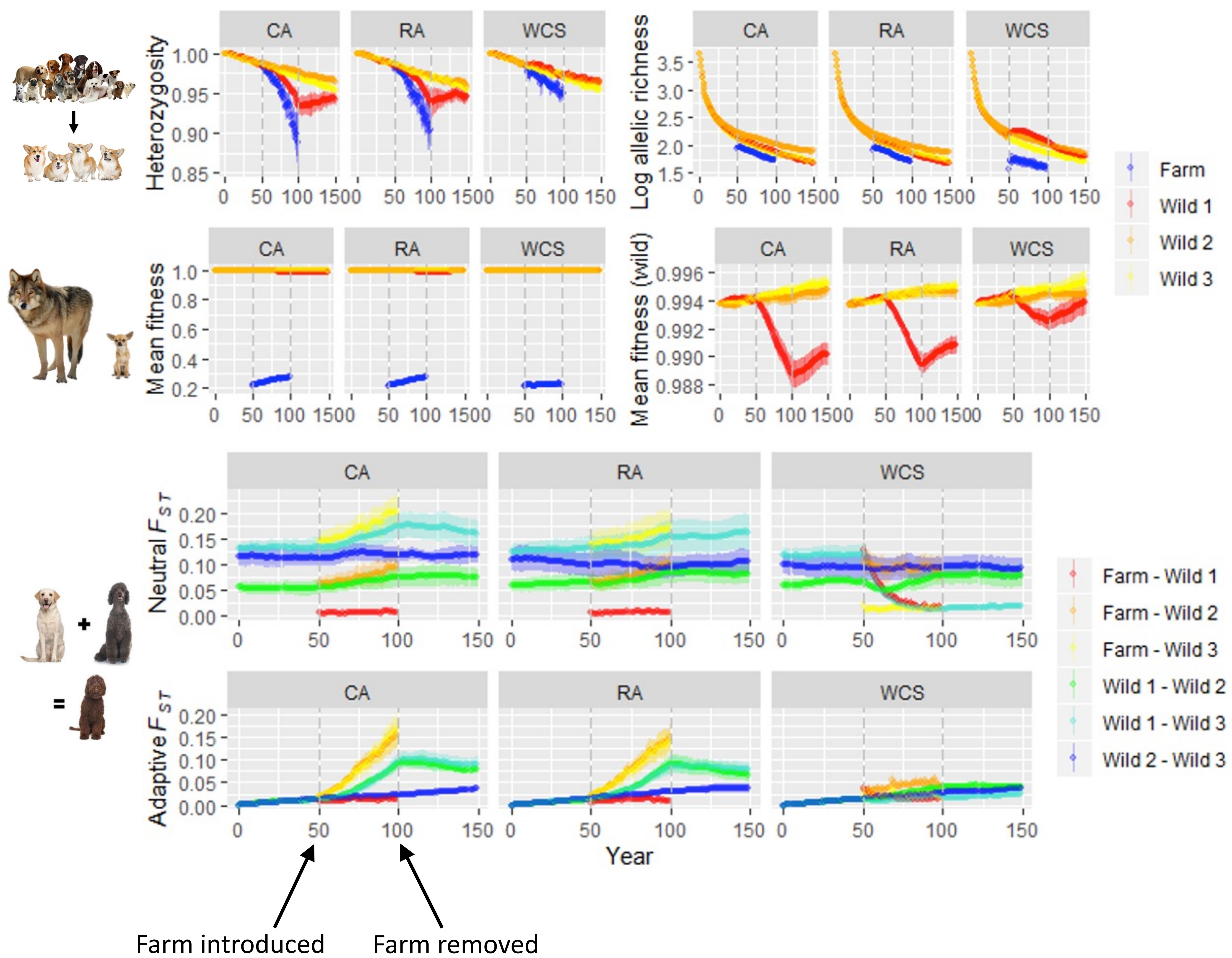
- The literature on genetic risks of aquaculture is limited almost entirely to finfish, largely Pacific salmon
- Although learning lessons can be inferred from the genetic risks of finfish aquaculture literature, life history parameters differ between finfish and shellfish in ways that could impact genetic risks

	Pacific salmon	(Most) Shellfish
Relative fecundity	Low	High
Reproductive strategy	Semelparity	Iteroparity
Larval development	Benthic	Pelagic
Harvest time	Before reproduction	After reproduction
Location of reproduction	Freshwater	Marine



Results under high selection and high escape conditions

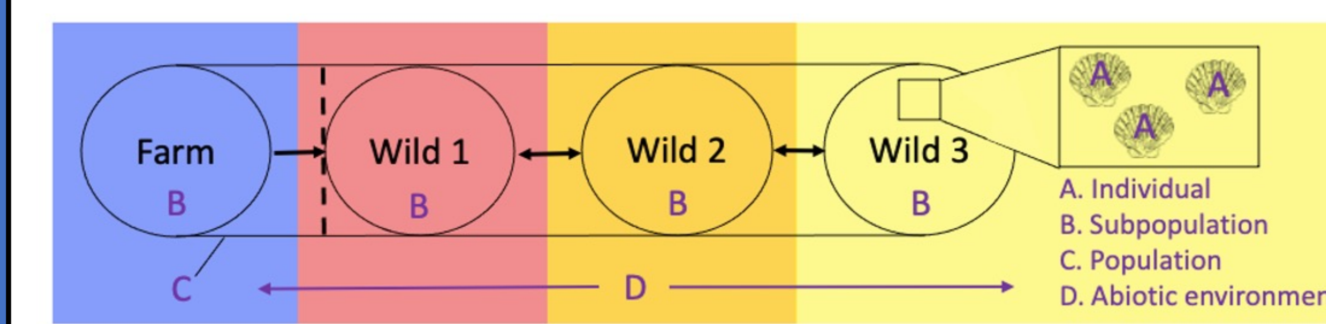


CA = commercial aquaculture, **RA** = restoration aquaculture, **WCS** = worst case scenario

Takeaways

1. **Localized effects in Olympia oyster due to limited migration.** Expect impacts to be smaller but more widespread in species with higher connectivity.
2. **Rapid reduction in neutral differentiation when using foreign broodstock**. Furthermore, neutral differentiation among wild subpopulations did not restore over timescales relevant to aquaculture enterprises (50 years or about 15 generations).
3. **Greater reduction in neutral heterozygosity in scenarios with more broodstock under high selection conditions**. Larger broodstock sizes allow for selection to be more efficient, which can reduce the effective number of breeders and result in loss of neutral genetic diversity.

Methods



1. We constructed an open-source, forward-time simulation genetic model using the simuPOP[3] toolkit and parameterized the model using parameters from the literature and grower survey data.

	Allele	
	0	1
Wild 1	1	1-s
Wild 2	1	1-2s
Wild 3	1	1-3s
Farm	1-z	1

2. We simulated local adaptation and domestication selection dynamics
3. We compared 3 production scenarios under each set of conditions: high or low escape rate and selection

	Source	Number	Returned	Harvest
Conservation aquaculture (CA)	Local (Wild 1)	100 / year	No	Yes
Restoration aquaculture (RA)	Local (Wild 1)	100 / year	Yes	No
Worst case scenario (WCS)	Foreign (Wild 3)	100 / 3 years	No	Yes

4. We measured

- **Diversity within populations**: heterozygosity & log allelic richness
- **Diversity among populations**: neutral and adaptive F_{ST}
- **Changes in fitness**: Mean fitness

Literature cited

1. Merino, G. *et al.* Can marine fisheries and aquaculture meet fish demand from a growing human population in a changing climate? *Global Environmental Change* **22,** 795–806 (2012).
2. Waples, R. S., Hindar, K. & Hard, J. J. *Genetic Risks Associated with Marine Aquaculture.* (2012).
3. Peng, B. & Kimmel, M. simuPOP: a forward-time population genetics simulation environment. *Bioinformatics* **21,** 3686–3687 (2005).

Further information

Dr. Natalie Lowell
nclowell@uw.edu
760.420.2281

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