

# Population Differentiation of Clam Species in British Columbia

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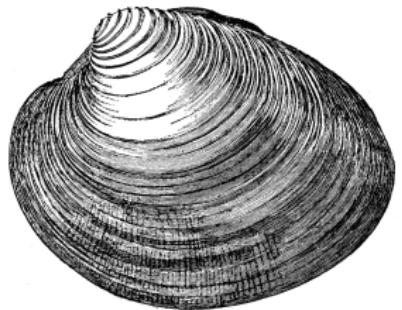
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# Background



# Summer Internship for Indigenous Peoples in Genomics (SING) Canada 2018



*Photograph by Dale Northey (2018)*

Organizers:

Kim TallBear (PhD), Jessica Bardill (PhD), Jessica Kolopenuk (PhD Candidate), Felix Breden (PhD), Jamie Scott (PhD, MD),

Pam Borghardt, Simon Wang (PhD), Deborah Bolnick (PhD), Marcia Guno, Laura Gutierrez Funderburk

# Clam Gardens



Google Earth image of clam garden EbSh-13 on Quadra Island, British Columbia by Dana Lepofsky *et al.* (2015)

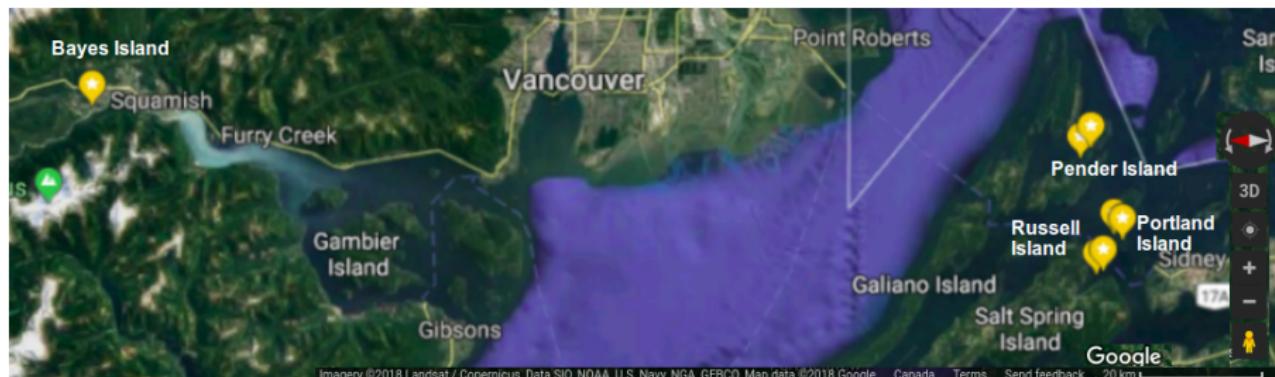
# Motivation

- To contribute knowledge towards the Gulf Islands National Park Reserve partnership with the Hul'q'umi'num and WSÁNEĆ nations to restore clam gardens
- We work, learn and play in the unceded, traditional and occupied territories of the xʷməəkwəy̓əm (Musqueam), Skwxwú7mesh (Squamish), Səl̓ílwətaʔɬ/Selilwitulh (Tsleil-Waututh) and Kwikwetlem Nations, and have a lot to learn from them

# Materials & Methods



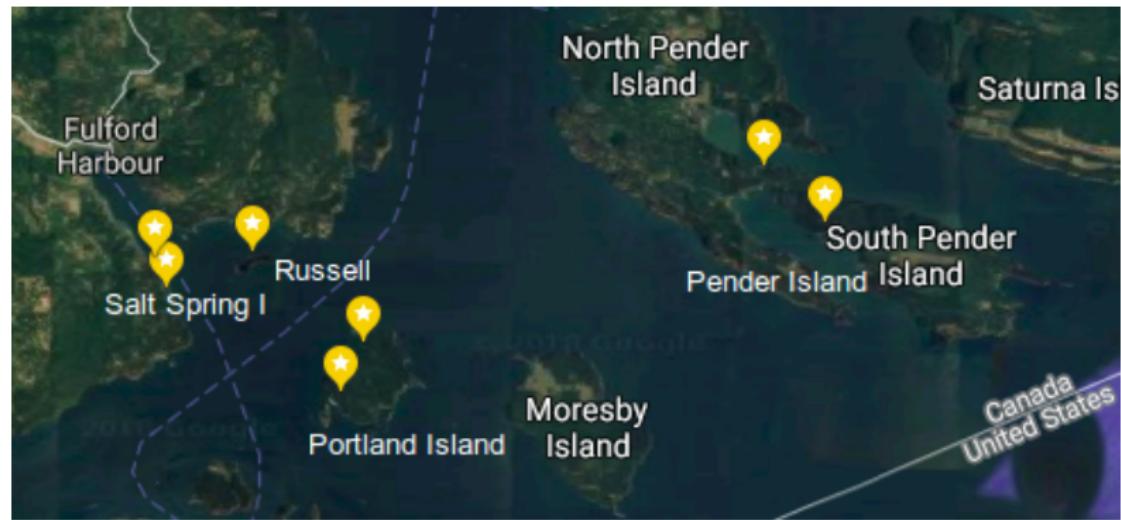
# Collected Samples



*Saxidomus gigantea* and *Leukoma staminea* samples were collected:

- Baynes Island Ecological Reserve
- two clam gardens in Salt Spring Island
- a clam garden in Russell Island
- two non-walled sites in Pender Island
- one non-walled site and one unidentified site in Portland Island

# Close up on Southern Populations



# The questions

- Are the different populations structured?
- How related are clams from these different sites?
- Are the clams on the two nearby clam gardens (Fulford Harbour and Russell Island) closely related or very distinct?
- Would restoring clam populations at select beaches help support nearby clam populations?
- And if so, which beaches, if restored, are likely to best support nearby clam populations?

# Basic (Biology) Concepts

- DNA & DNA sequence
- Gene
- Allele
- Single Nucleotide Polymorphisms (SNPs)
- Haplotype
- Sequence alignment
- Phylogeny

# The Mathematical Models

## Percent ID Matrix (PID)

Let  $n$  be the total number of sequences in a sequence alignment. Let  $0 \leq p_{ij} \leq 100$  denote the percent identity (PI) for two given sequences  $i, j$ . The PID of an alignment is an  $n \times n$  matrix such that

$$a_{ij} = \begin{cases} 100 & , \text{if } i = j \\ p_{ij} & , \text{if } i \neq j \end{cases}$$

where  $i, j$  denote, resp, the  $i$ th,  $j$ th sequences within an alignment.

# The Mathematical Models

## Unweighted Pair Group Method with Arithmetic Mean (UPGMA) (Sokal and Michener 1958)

An approach to constructing a rooted phylogenetic tree from a distance matrix (in particular a PID). Let  $d_{AB}$  denote the PI between two (different) units, say  $A, B$ .

- Identify smallest distance between units  $A, B$ . Cluster them to form unit  $AB$
- Compute new distance between  $AB$  and the remaining units  $X$

$$d_{(AB)X} = \frac{1}{2}(d_{AX} + d_{BX})$$

- Repeat this process until only two units are left

# The Statistical Models

## Analysis of Molecular Variance (AMOVA) and $\phi$ - Statistics (Excoffier (1992))

AMOVA detects population differentiation using molecular markers (haplotypes in our case).  $\phi$ -statistics estimate different levels of hierarchical subdivision between and within populations and groups within them.

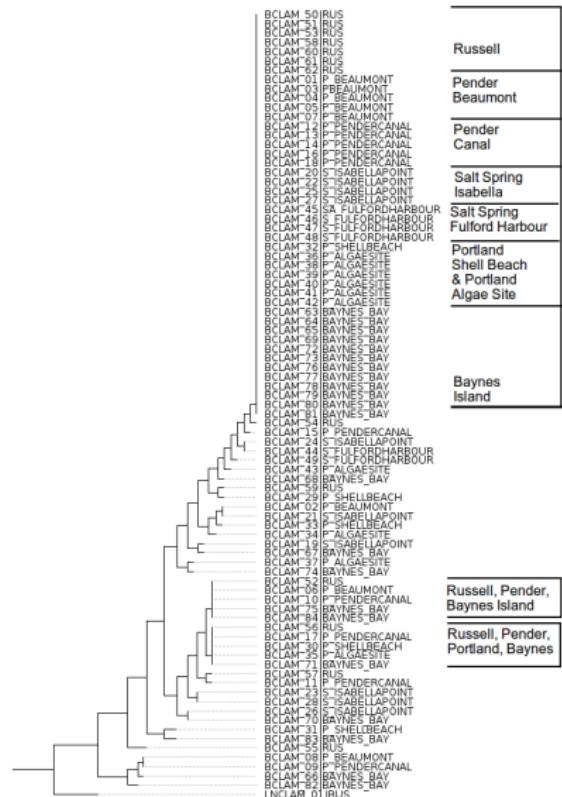
$$\phi_{ST} = \frac{\sigma_a^2 + \sigma_b^2}{\sigma^2} \quad \phi_{CT} = \frac{\sigma_a^2}{\sigma^2} \quad \phi_{SC} = \frac{\sigma_b^2}{\sigma_b^2 + \sigma_c^2}$$

where  $a$  denotes a group,  $b$  the populations and  $c$  individuals within populations. The expected square deviations are denoted by  $\sigma_a^2, \sigma_b^2, \sigma_c^2$ , respectively.

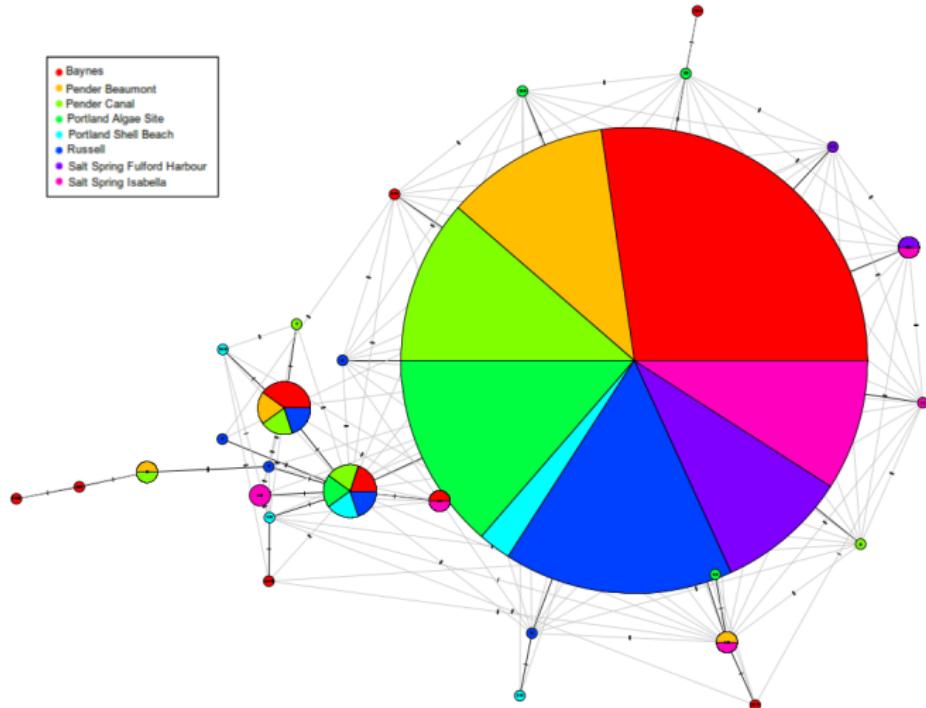
# Results



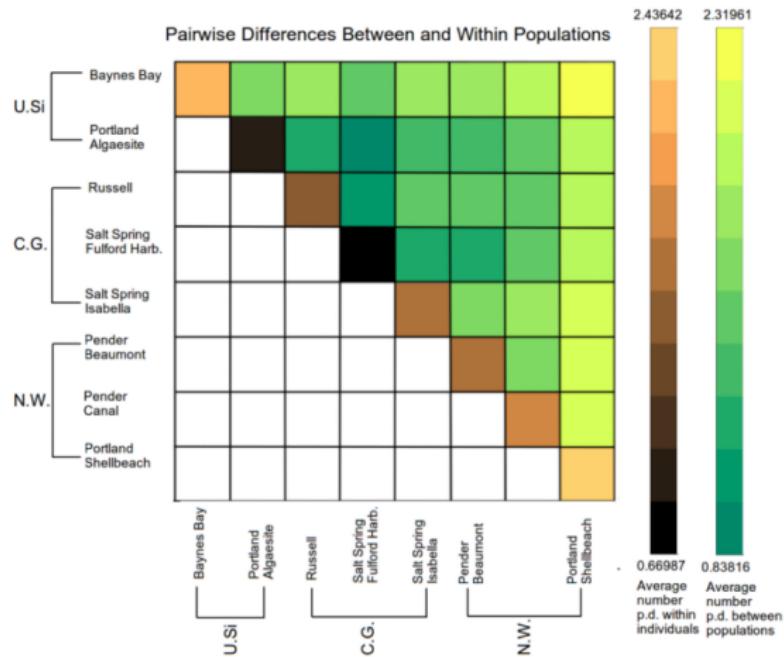
# Phylogeny: *S. gigantea* & *L. staminea*



# Haplotype Network: *S. gigantea*



# AMOVA: *S. gigantea* Clam gardens, non-walled and unidentified sites

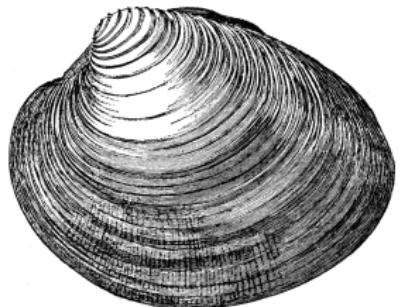


Source of variation	d.f.	Sum of squares	Variance components	Percentage of variation
Among groups	2	1.789	0.00626 $V_a$	0.75
Among populations	5	3.734	-0.00972 $V_b$	-1.16
Within populations	76	63.700	0.83815 $V_c$	100.41
Total	83	69.222	0.83469	
Fixation Index				
$\phi_{SC}$		-0.01174		
$\phi_{ST}$		-0.00415		
$\phi_{CT}$		0.00750		

# Two Potential Candidates



# Discussion



# What Does This Mean for Clam Garden Restoration?

- We learned that there is little to no structure between the populations
- Clams from different sites shared one common haplotype
- Clams the two nearby clam gardens (Fulford Harbour and Russell Island) were closely related
- Fulford Harbour clam gardens are good candidates for further exploration, however we must be careful before introducing new taxa into sites
- This means that clam gardeners from different sites within the area we covered can collaborate with one another

# Open Questions

- Can we identify source or sink populations?
- Is there some sort of “signal” on a sequence level that would help us identify clams from clam gardens vs clams from non-walled sites?
- Revisit candidate sites for uniform, larger data sets

# Acknowledgements



Vice President, Academic  
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Department of Mathematics



Indigenous Student Centre at SFU



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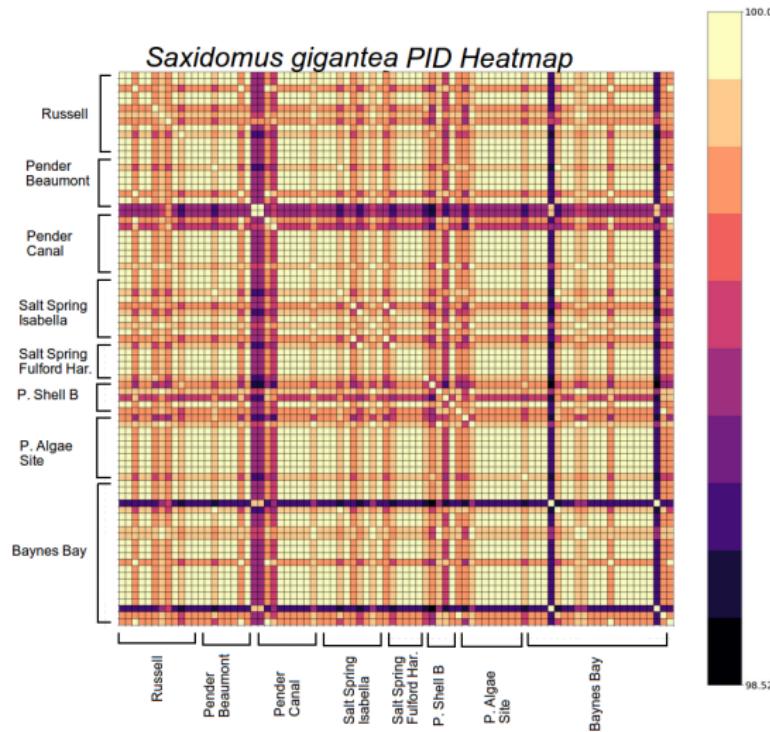


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# PID *S. gigantea*



# PID *S. gigantea* & *L. staminea*

