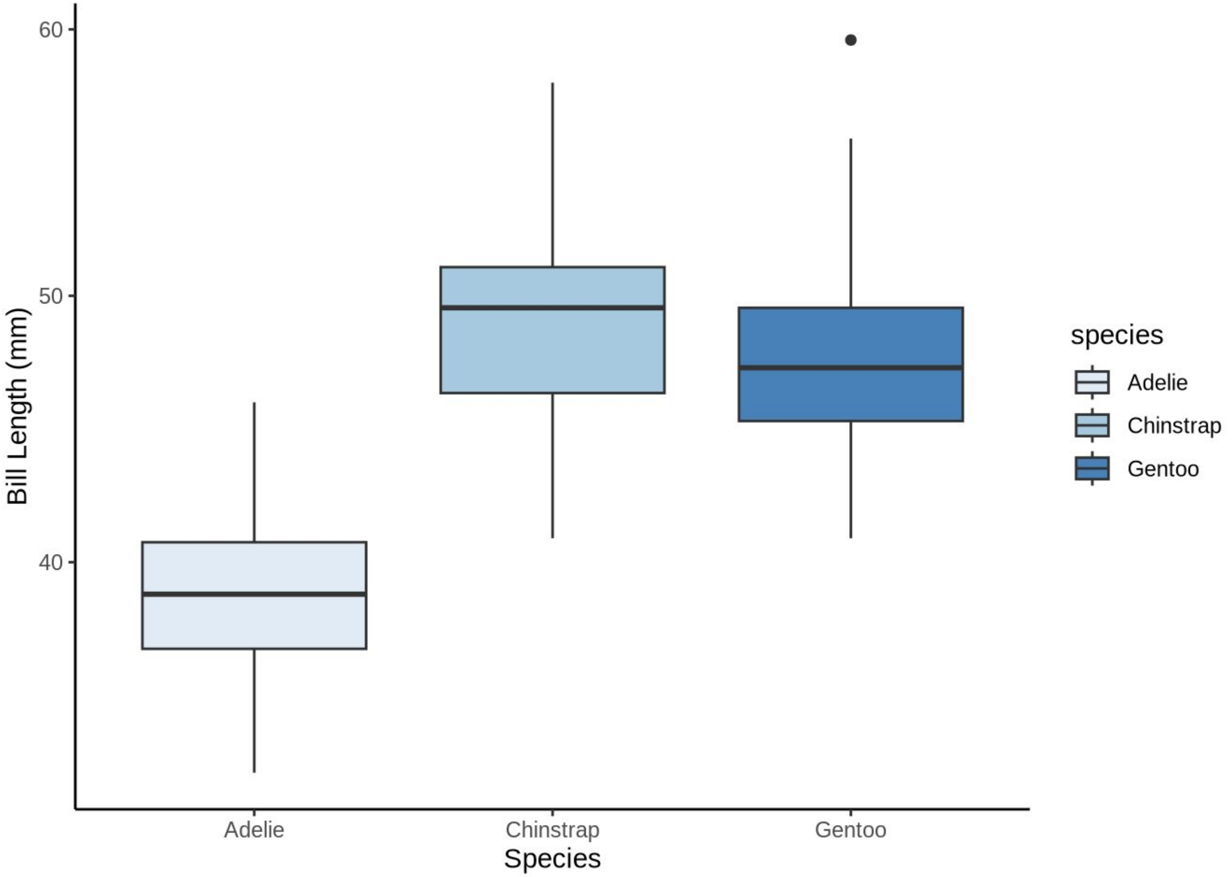
Sea Cucumbers & Structure Plots

Eve198

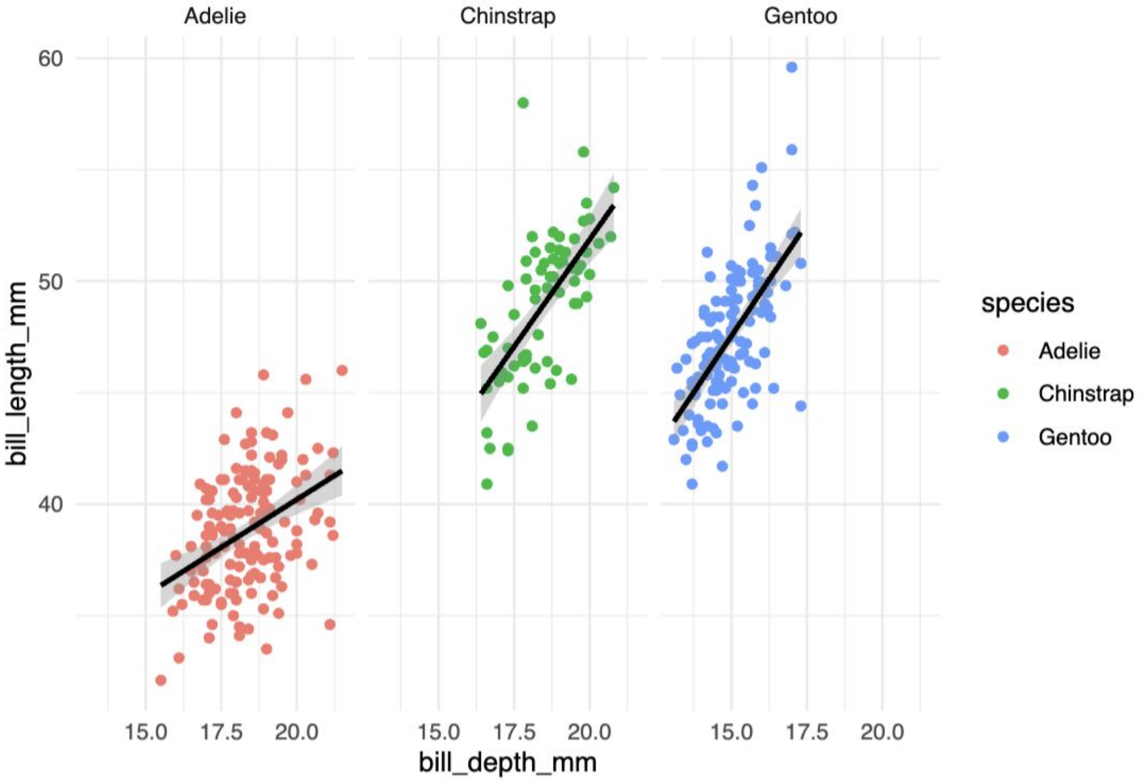
Week 7

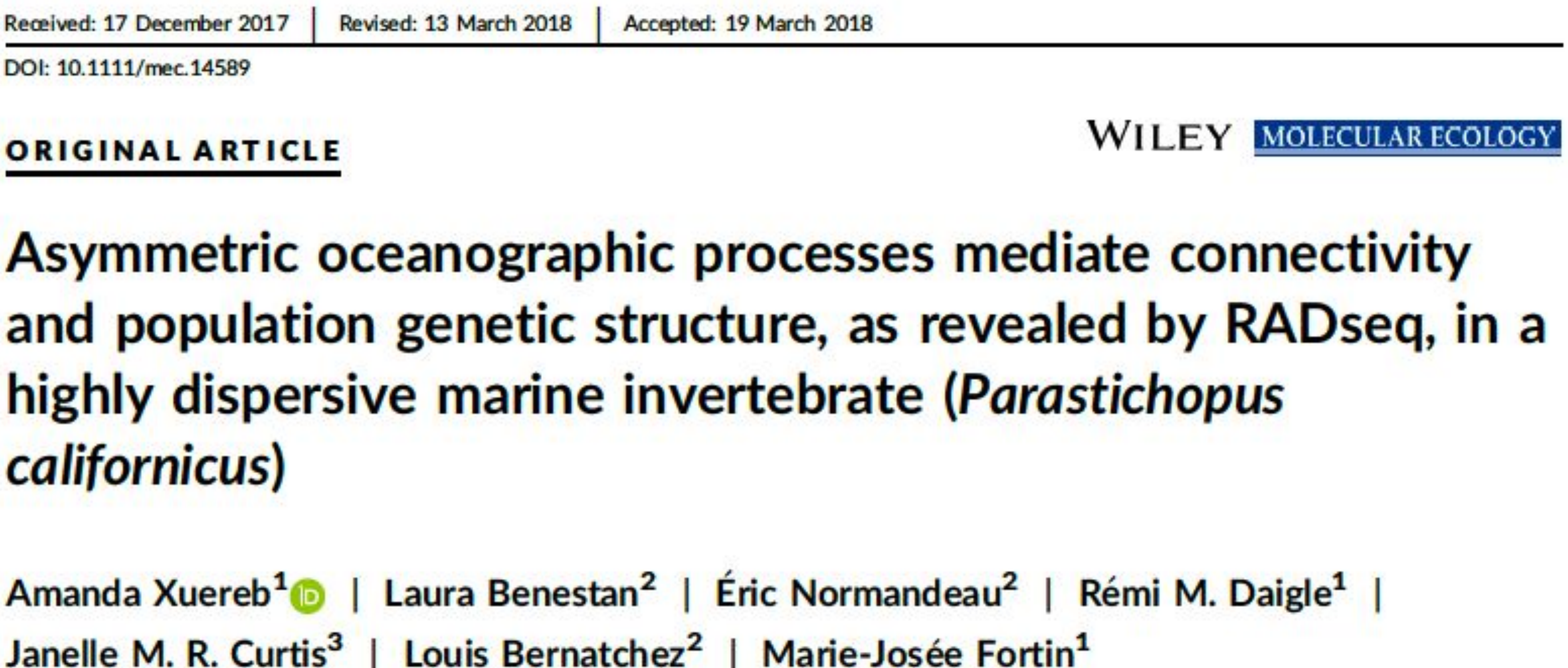
Last Week's HW

Q2:



Q3:





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ORIGINAL ARTICLE

WILEY MOLECULAR ECOLOGY

Asymmetric oceanographic processes mediate connectivity and population genetic structure, as revealed by RADseq, in a highly dispersive marine invertebrate (*Parastichopus californicus*)

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N=30-41 individuals per site, 24 sites total
N=717 individuals total

TABLE 1 Geographic coordinates, number of samples collected (N_s) and successfully genotyped (N_g), observed and expected heterozygosity (H_o and H_e, respectively), the measured inbreeding coefficient (G_{IS}), and the betweenness centrality calculated from the Population Graph of genetic covariance across sampling locations

No.	Site	Site code	Longitude	Latitude	N_s	N_g	H_o	H_e	G_{IS}	Betweenness centrality
South region										
1	Ogden Point	OGD	−123.387	48.408	33	31	0.114	0.117	0.021	11
2	Southern Gulf Islands	SGI	−123.380	48.757	41	31	0.105	0.111	0.053	9
3	Lasqueti	LAS	−124.183	49.475	40	28	0.111	0.115	0.038	11
4	Jervis Inlet	JER	−124.001	49.753	41	32	0.110	0.115	0.041	4
5	Tofino	TOF	−125.938	49.248	30	20	0.105	0.110	0.049	12
6	Rock Bay	RBY	−125.467	50.330	41	32	0.108	0.113	0.044	2
7	Cracroft Island	CRA	−126.565	50.521	31	28	0.103	0.111	0.067	23
8	Shewell Island	SHE	−126.238	50.659	41	32	0.106	0.113	0.059	8
9	Malcolm Island	MAL	−127.128	50.627	41	33	0.11	0.115	0.043	5
10	Quatsino	QUA	−127.872	50.500	41	32	0.105	0.112	0.061	75
11	Hope Island	HOP	−127.851	50.899	41	34	0.11	0.115	0.044	13
12	Table Island	TBL	−127.804	51.272	41	32	0.108	0.114	0.051	6
North region										
13	Calvert Island	CAL	−128.143	51.690	30	30	0.112	0.114	0.013	96
14	Tolmie	TOL	−128.578	52.713	30	29	0.111	0.114	0.021	16
15	Prince Rupert	PRI	−130.366	54.197	31	30	0.114	0.115	0.012	0
16	Legace Bay	LEG	−130.464	54.682	31	28	0.115	0.116	0.01	3
17	Juan Perez	JUA	−131.396	52.632	34	30	0.111	0.113	0.017	3
18	Selwyn	SEL	−131.905	52.939	34	32	0.112	0.114	0.017	1
19	Rennell Sound	REN	−132.66	53.399	33	30	0.115	0.116	0.014	24
20	Mazarredo	MAZ	−132.553	54.100	35	30	0.113	0.114	0.011	11
21	Alaska 1	AK1	−133.019	54.835	30	28	0.111	0.112	0.013	35
22	Alaska 2	AK2	−134.633	56.364	30	27	0.113	0.114	0.006	3
23	Alaska 3	AK3	−134.715	57.828	30	28	0.112	0.115	0.022	16
24	Alaska 4	AK4	−132.217	55.914	30	30	0.112	0.115	0.022	10

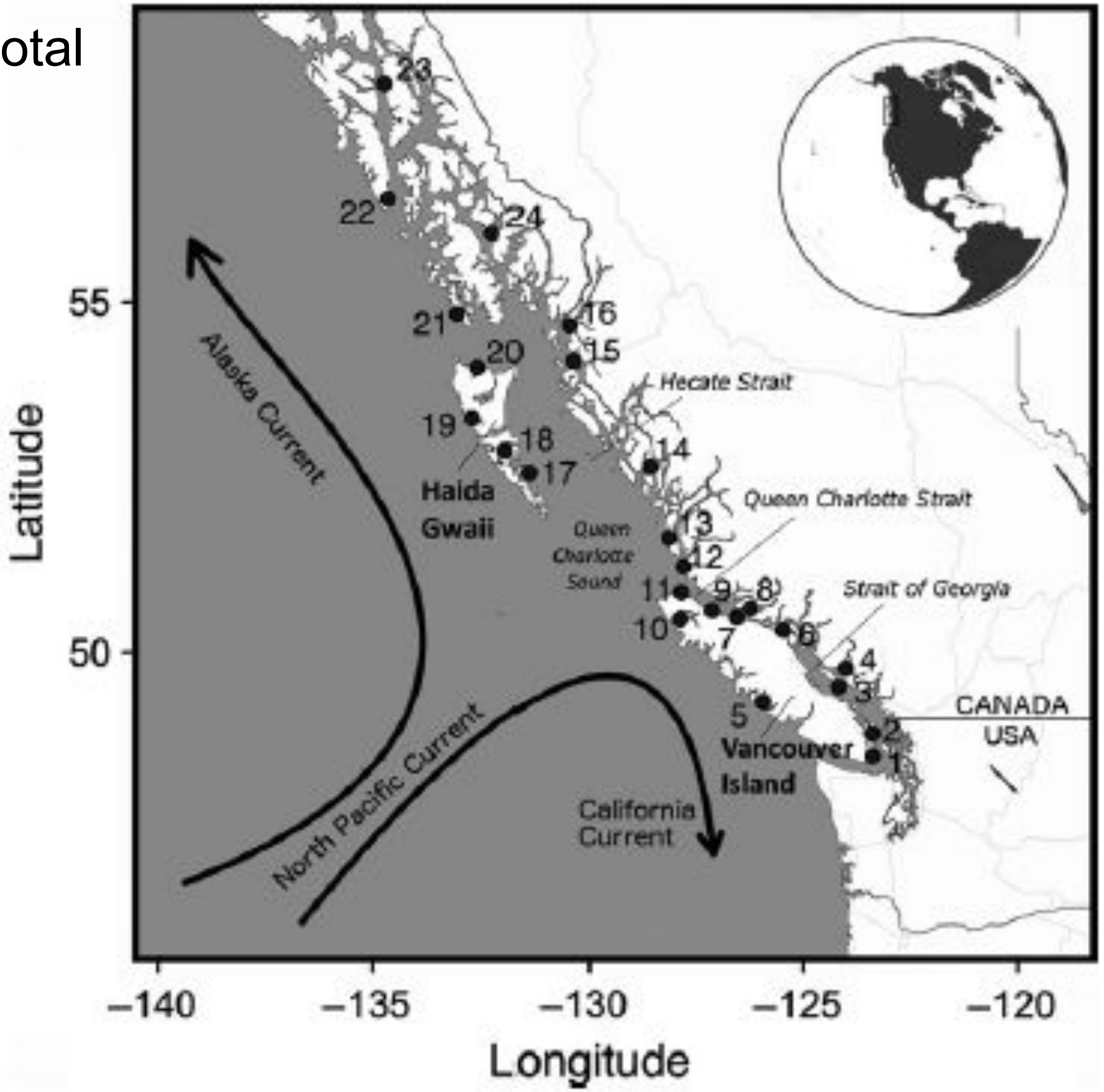

FIGURE 1 Map of sampling locations in coastal British Columbia (1–20) and southeastern Alaska (21–24). Site labels correspond with numbers in Table 1

Tested two hypotheses for spatial structure:

- Isolation by Distance (IBD) aka structure driven by distance
- Isolation by Resistance (IBR) aka structure driven by ocean circulation

Bioinformatic Pipeline:

Extracted DNA from tissue clips

RADseq via single end sequencing

Fastqc

Adapters trimmed with cutadapt

libraries demultiplexed with STACKS

Aligned to reference genome of closely related sea cucumber species

Filtered data to include only SNPs shared between regions/individuals

Variant Call Format (VCF) file to interpret genetic data

converted VCF file with PLINK and PGDSPIDER for additional analyses

https://marineomics.github.io/RADseq.html

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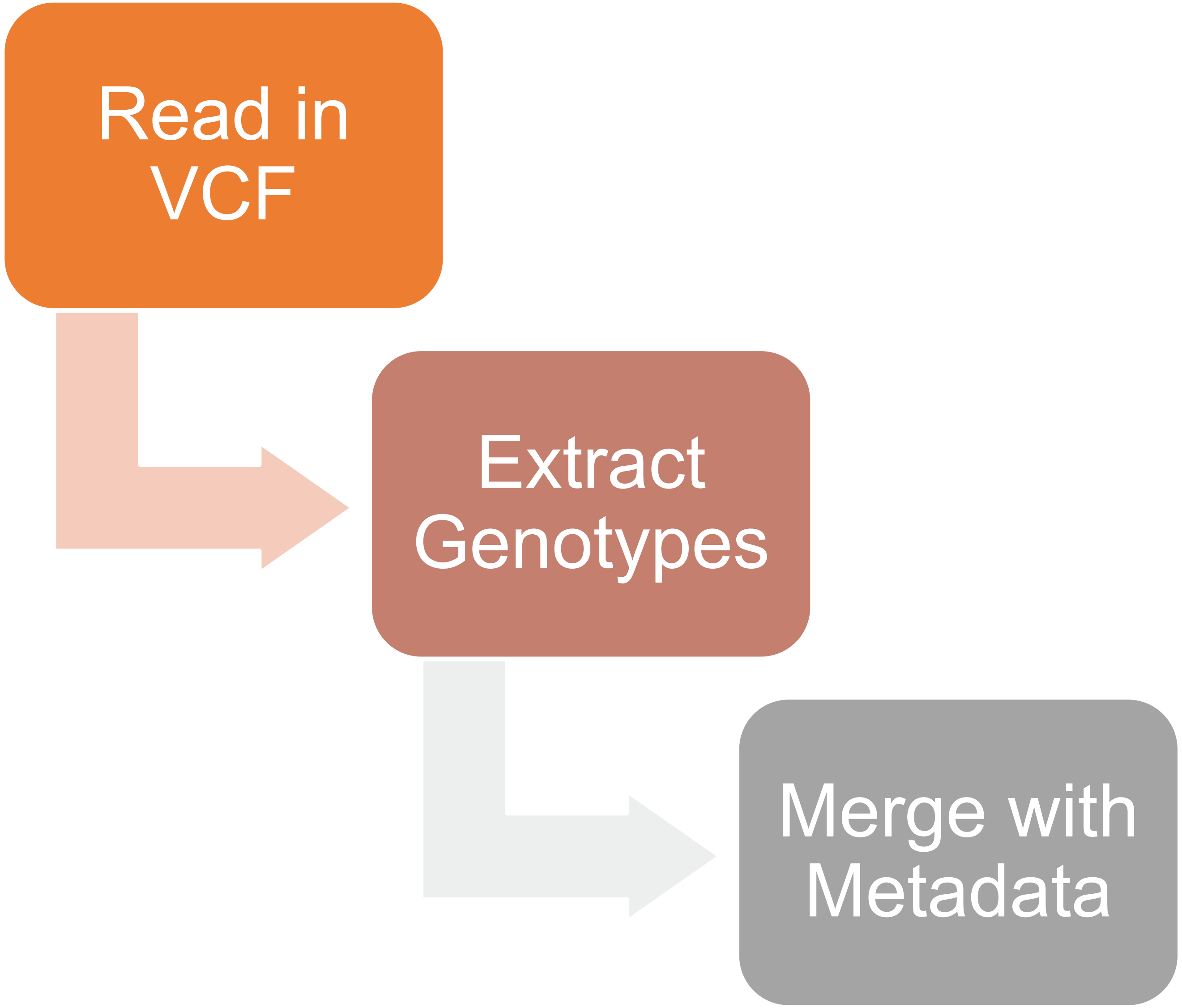
How to get the data into a friendly format for population structure analyses:



Read in VCF

Extract Genotypes

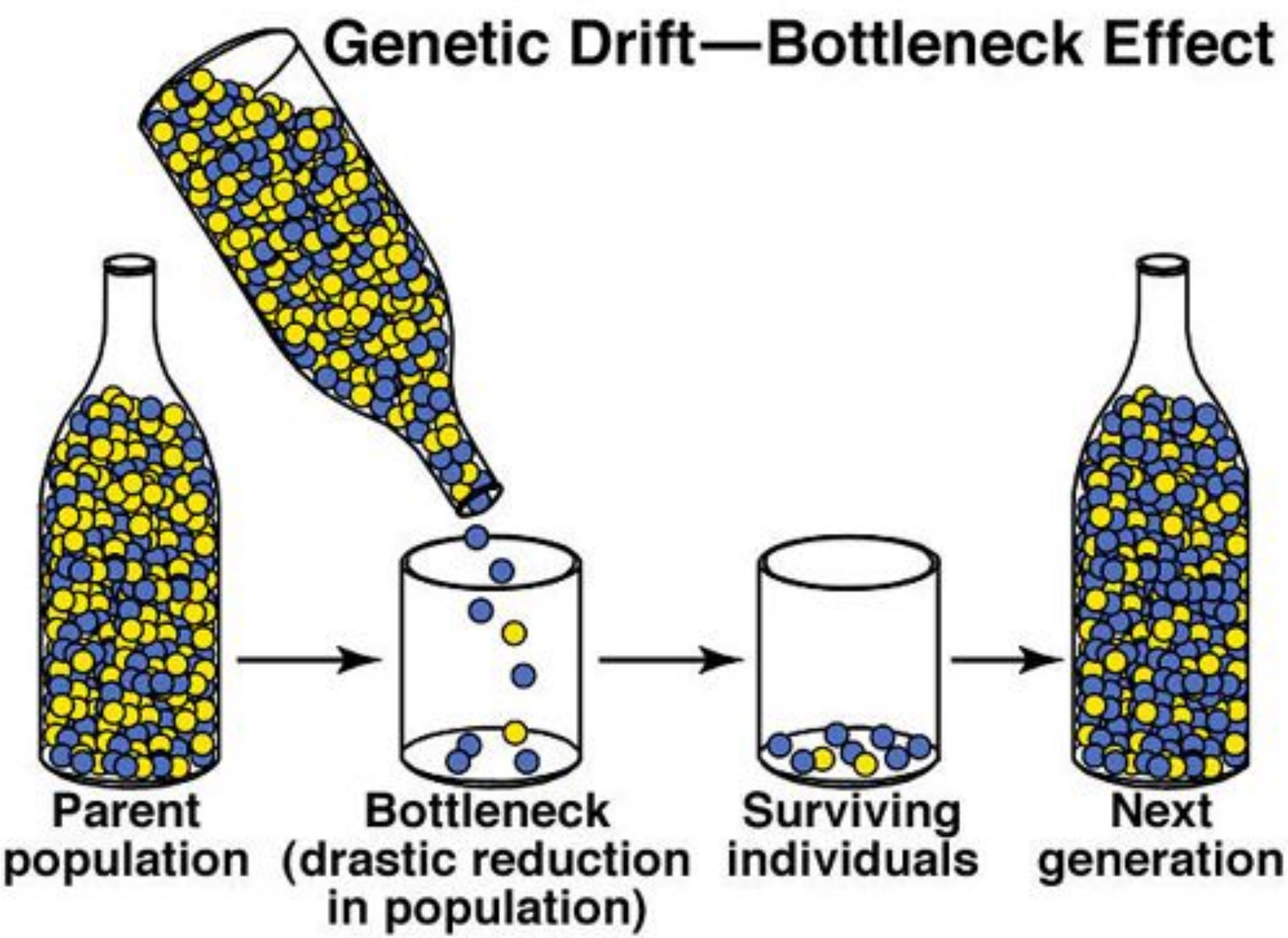
Merge with Metadata

What is population structure?

- Differences in allele/genotype frequencies between populations
- Genotypes share ancestry from some number (K) of ancestral populations
- No structure=little or no variation between populations
- What group are you= q-matrix
- Useful in identifying differences in ancestry between populations

http://galleries.neaq.org/2016/06/sea-cucumbers-east-meets-west.html

What can result in population structure?



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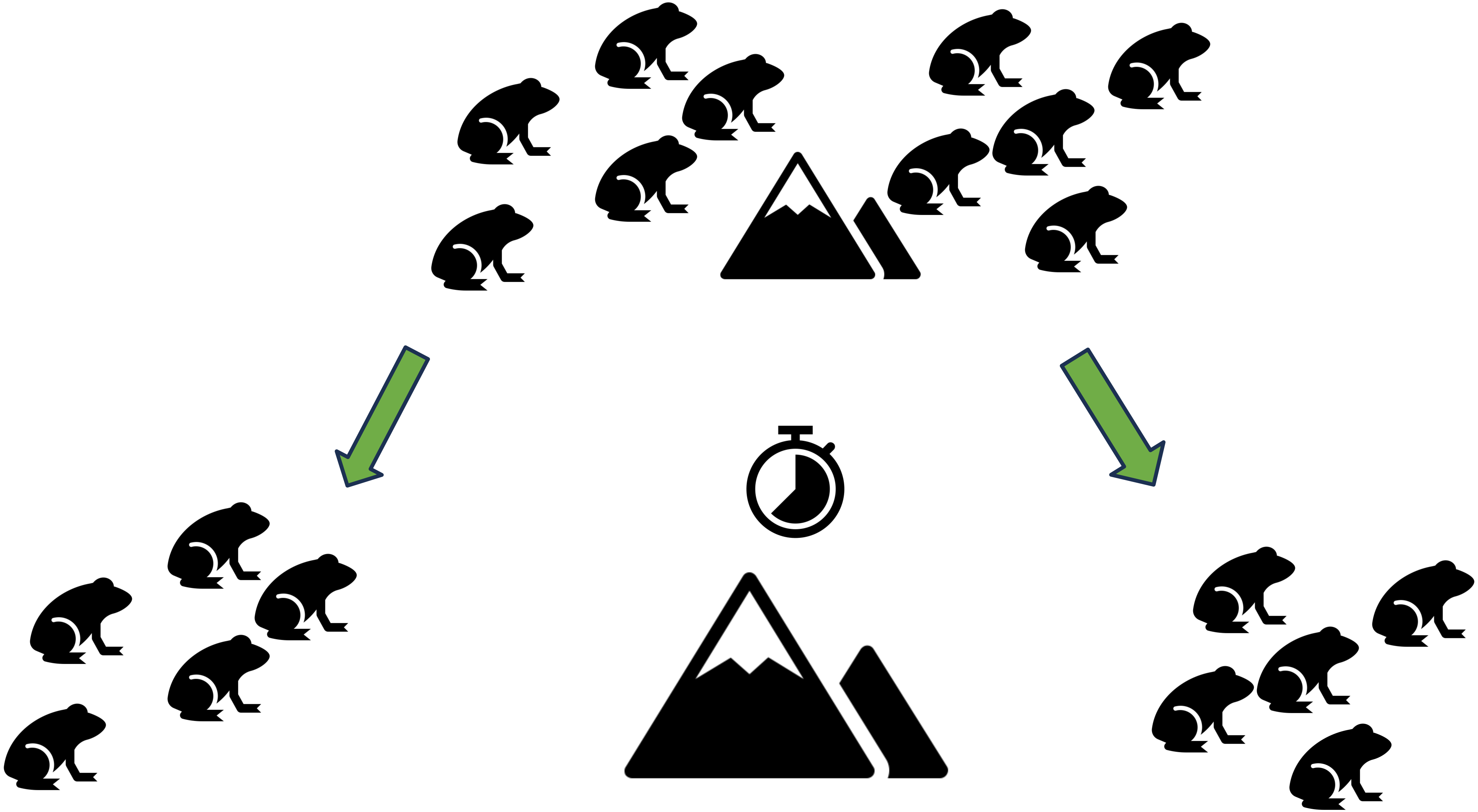
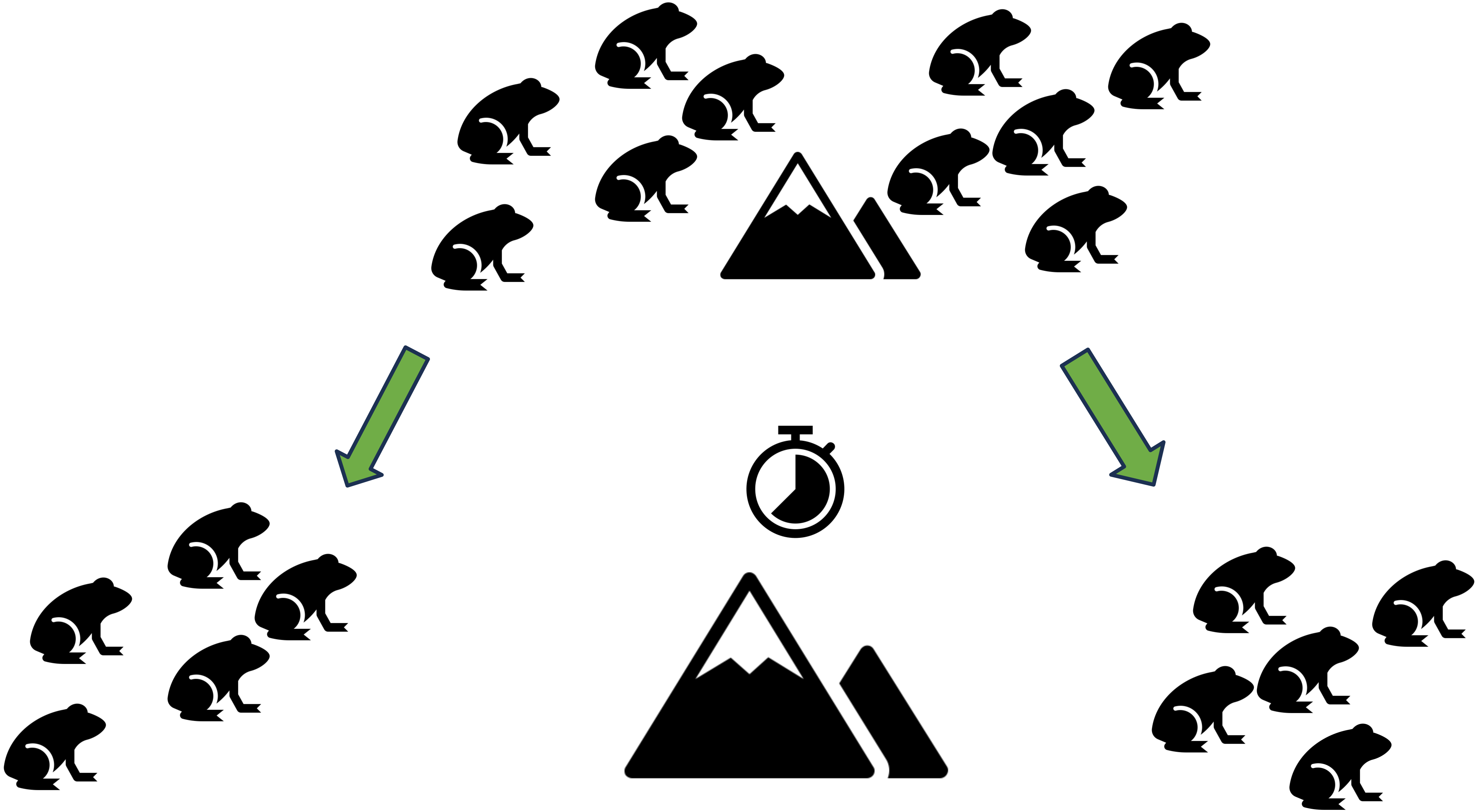
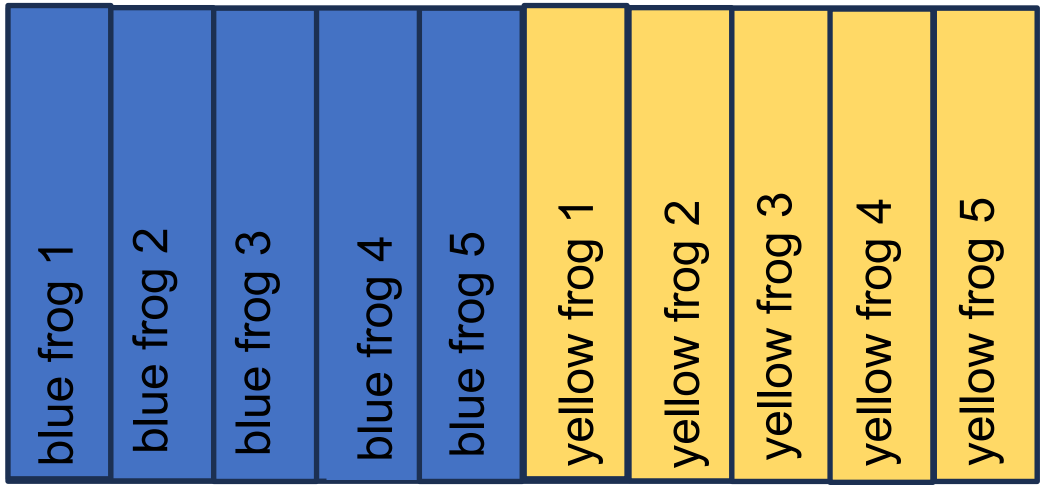


What can result in population structure:



What can result in population structure:

K=2



Use allele frequencies to assign likely membership for each individual to each population

Examples of population structure

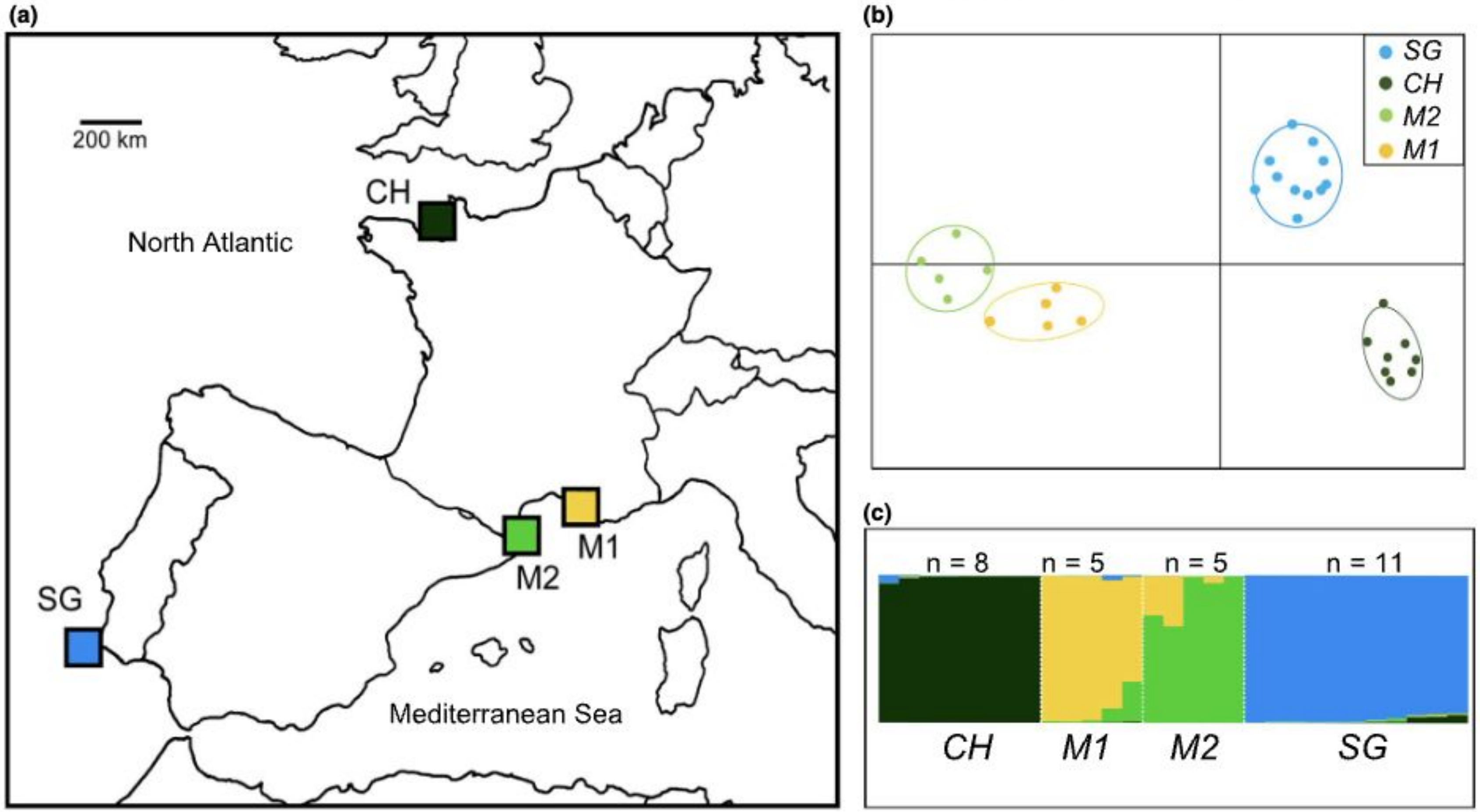


FIGURE 3 (a) Map of collection locations for *Alcyonium coralloides*, (b) Discriminant Analysis of Principal Components (DAPC) plot, and (c) probability of membership graph from structure analysis for *A. coralloides* (152 SNPs, $K = 4$) populations (M1: Marseille, France, M2: Banyuls-sur-Mer, France, CH: Iles Chausey, France, SG: Sagres, Portugal) [Colour figure can be viewed at wileyonlinelibrary.com]

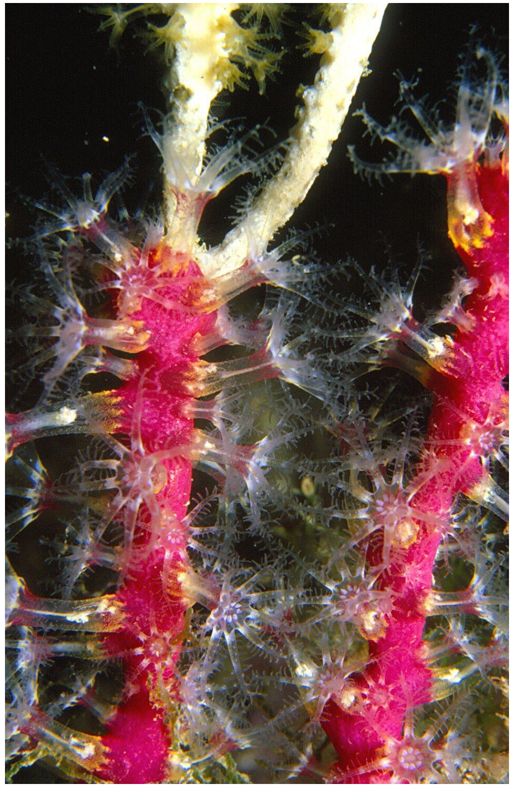
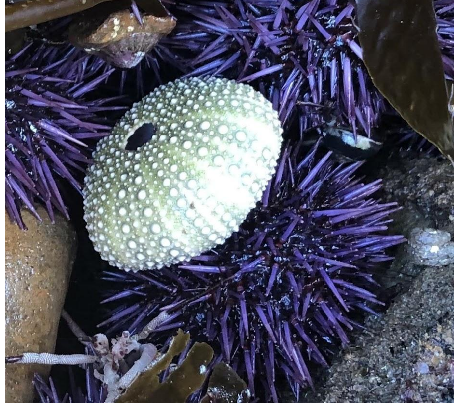


Image from Wikimedia Commons

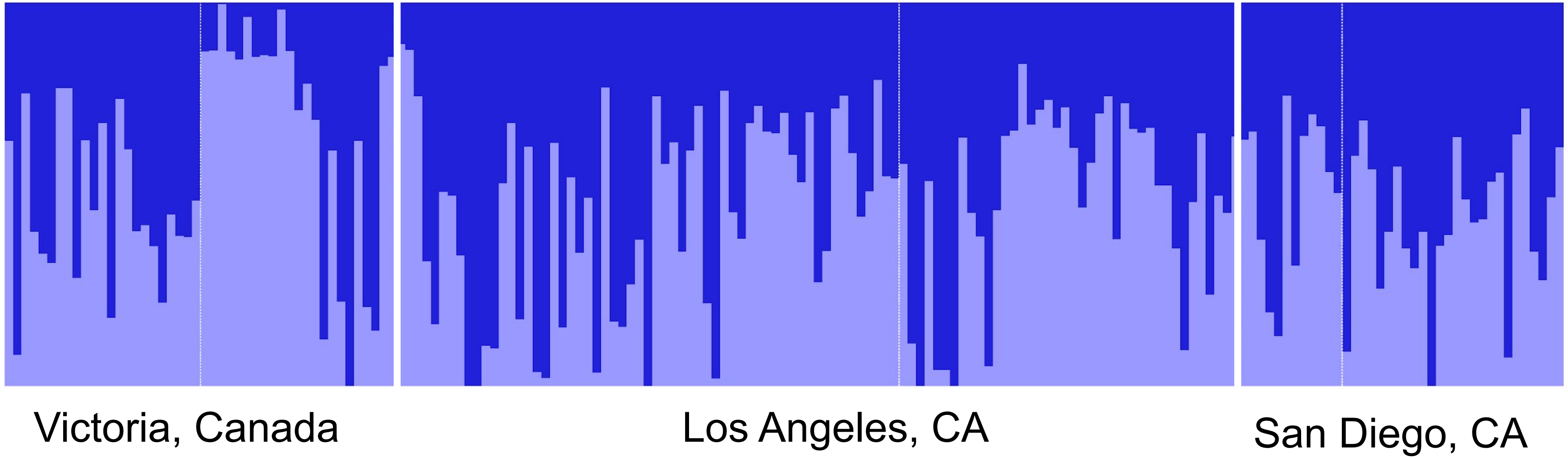
Erickson et al. (2021): New approaches to species delimitation and population structure of anthozoans: Two case studies of octocorals using ultraconserved elements and exons

Examples of population structure



- Modeling genetic clusters/variation in samples by frequency of genotypes
- K= the number of clusters/groups within our dataset

K=2 shown, but no structure between groups!



Armstrong *et al.*, 2025 (preprint): [Parallel polygenic urban adaptation despite high gene flow in a coastal marine invertebrate]

Examples of population structure


© Wikipedia

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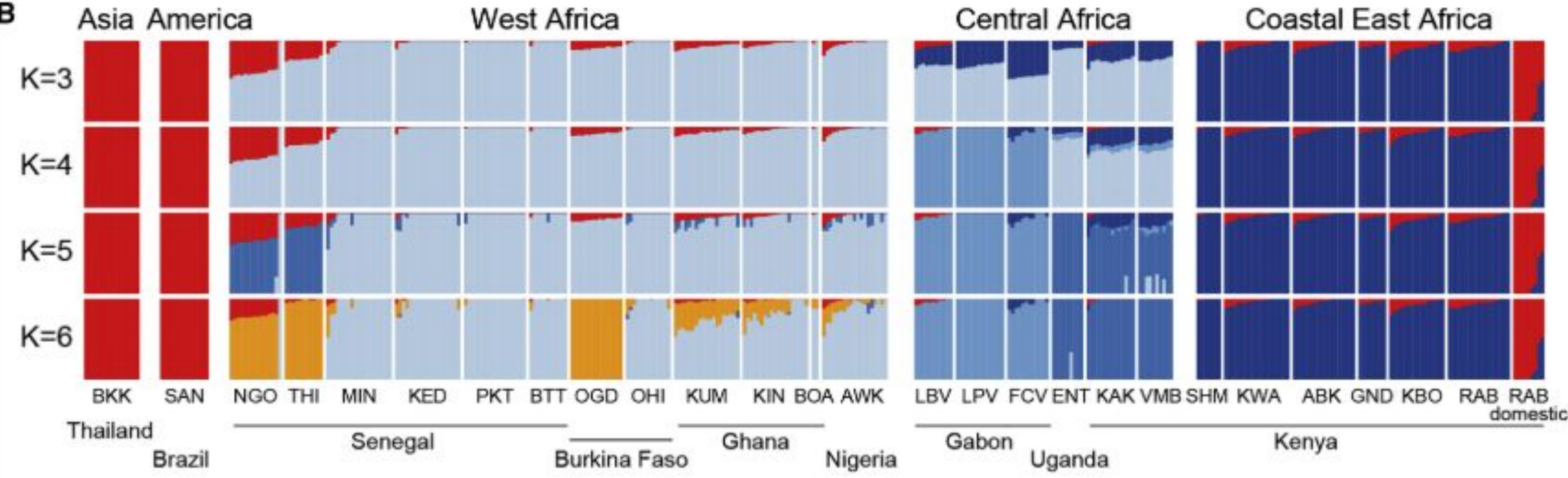

Rose *et al.*, 2020: [Climate and Urbanization Drive Mosquito Preference for Humans]