

Sea Cucumbers & Structure Plots

Eve198


Week 7

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ORIGINAL ARTICLEWILEY **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	RBV	-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

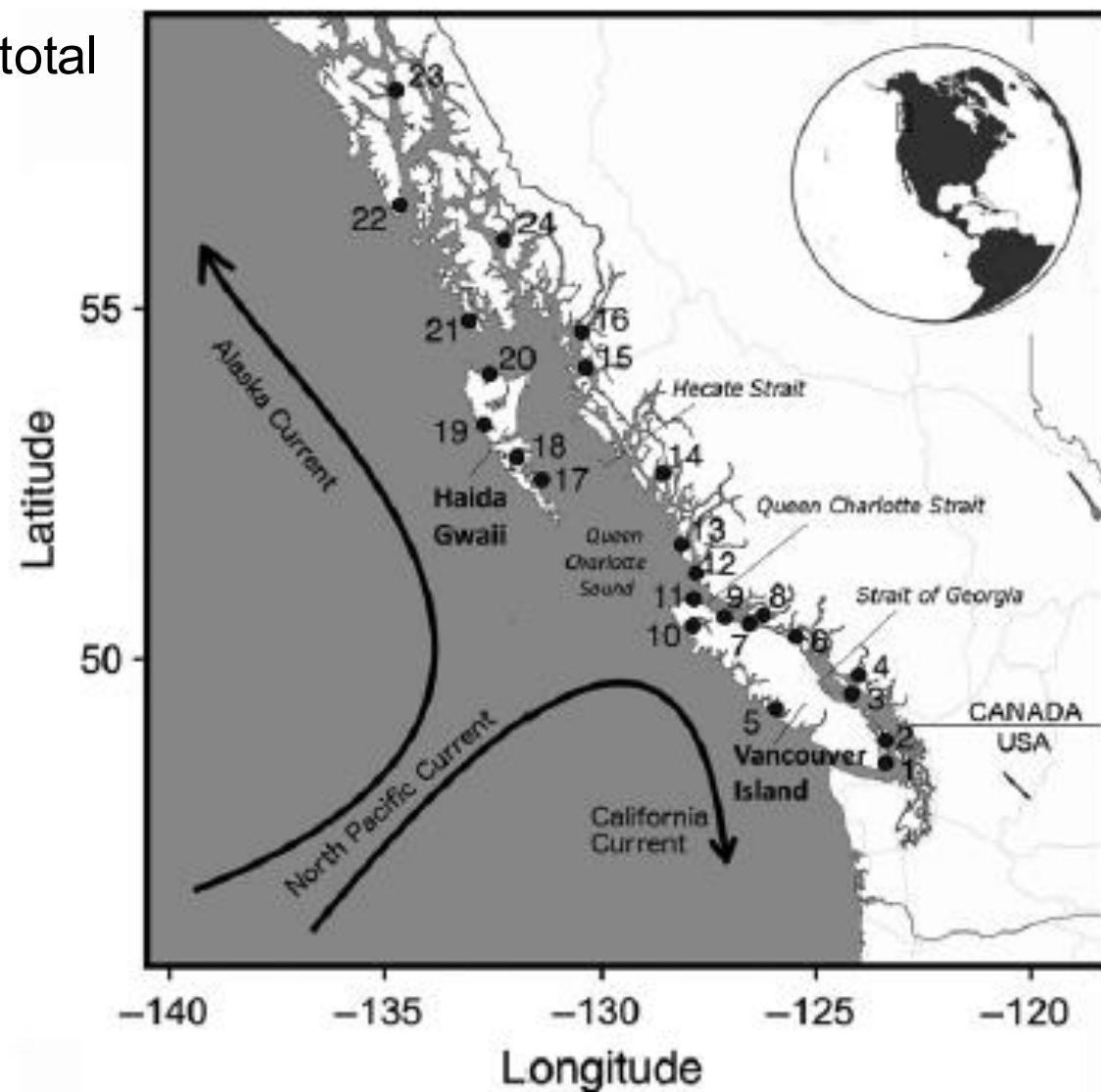


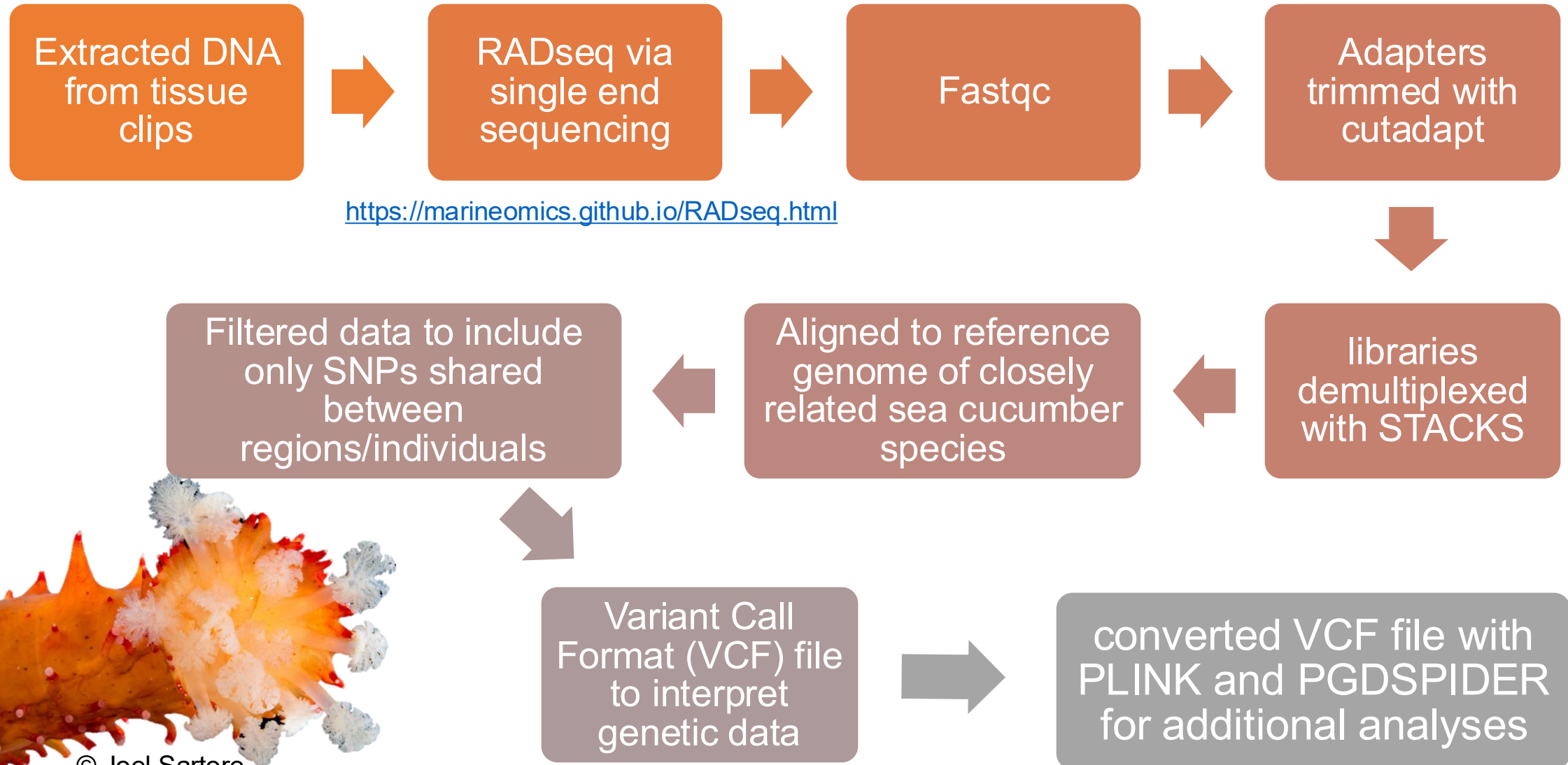
FIGURE 1 Map of sampling locations in coastal British Columbia (1–20) and southeastern Alaska (21–24). Site labels correspond with numbers in Table 1

Tested two hypotheses for spatial structure:

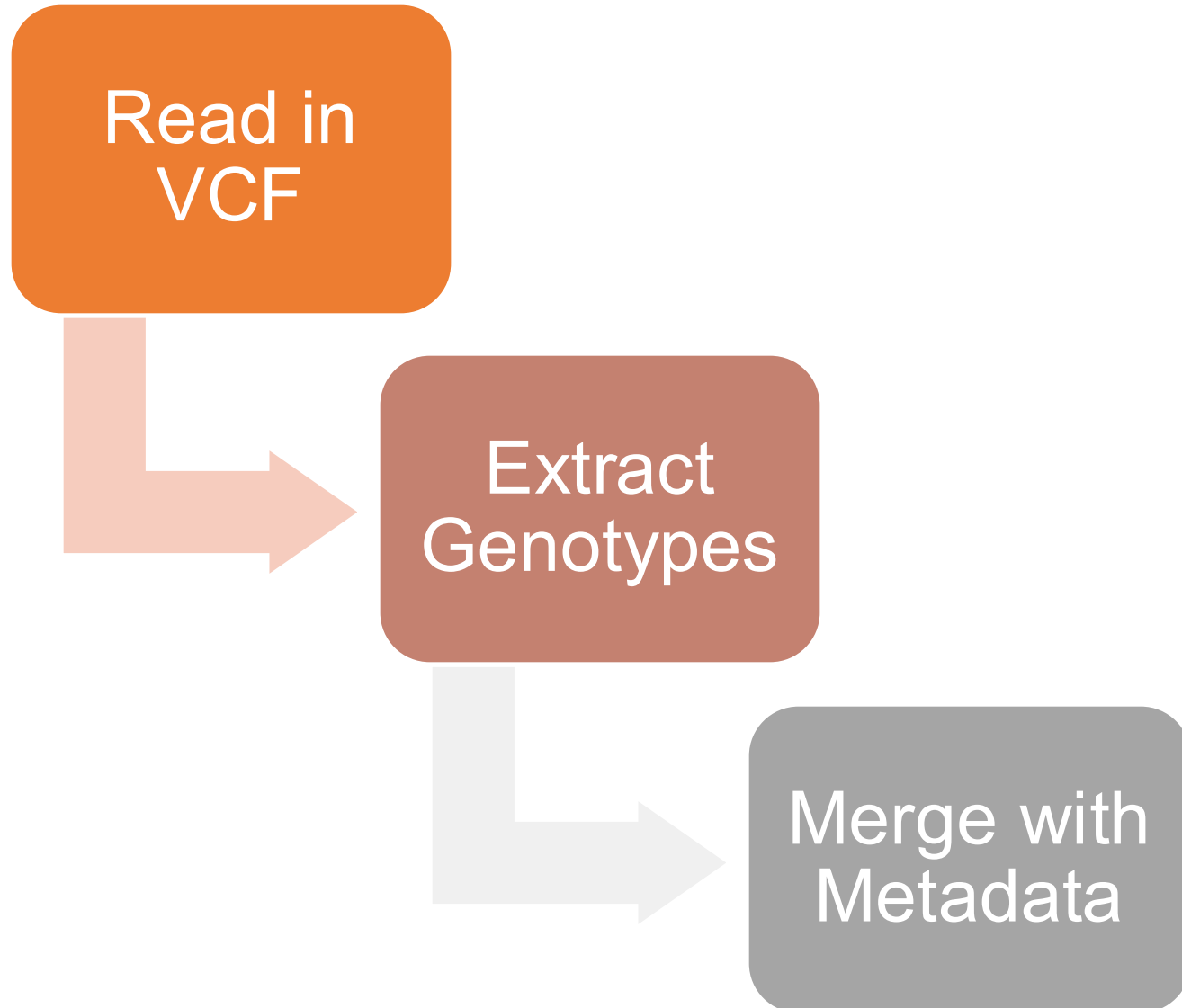
- Isolation by Distance (IBD) aka structure driven by distance
- Isolation by Resistance (IBR) aka structure driven by ocean circulation



Bioinformatic Pipeline:

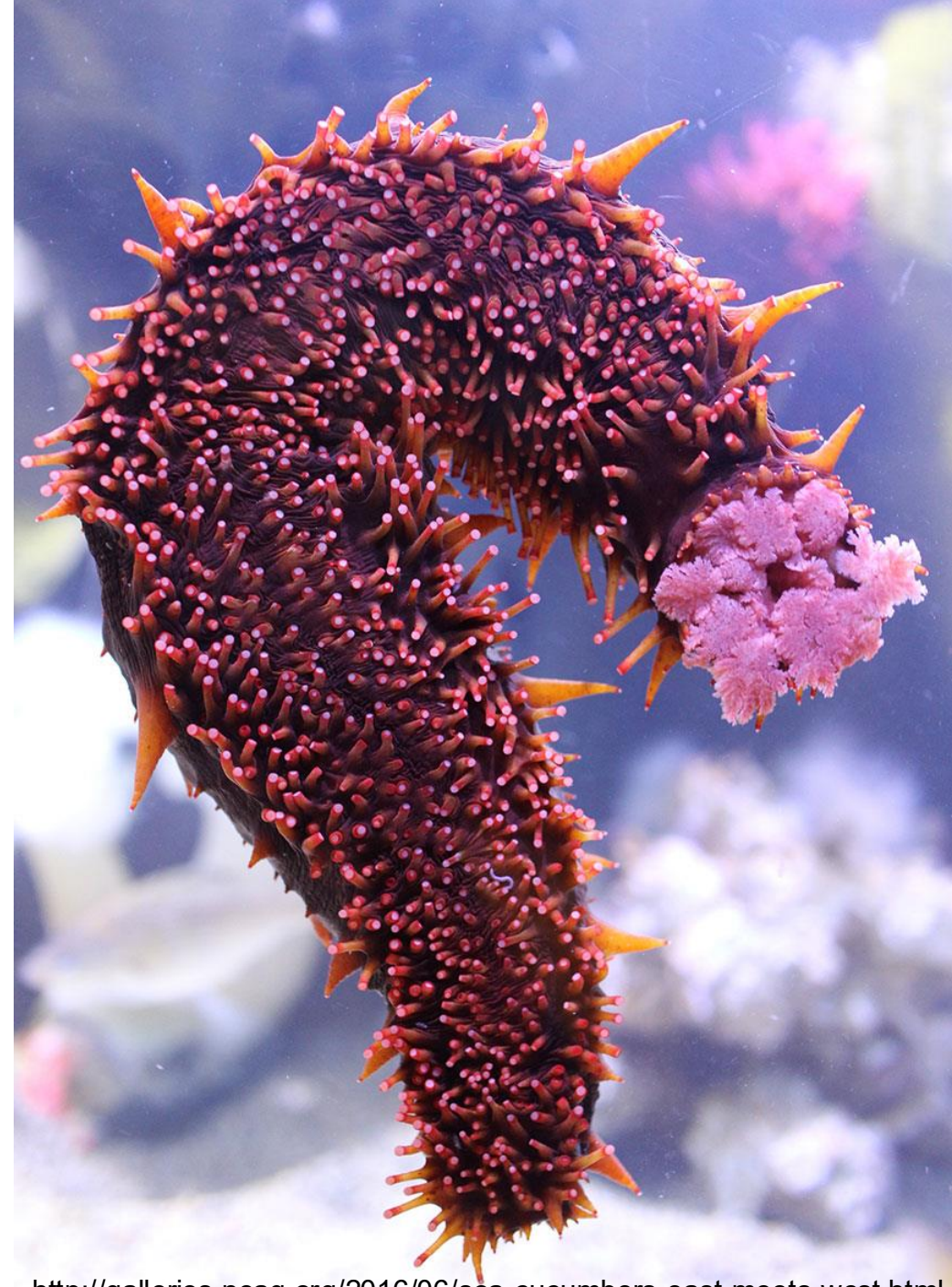


How to get the data into a friendly format for population structure analyses:



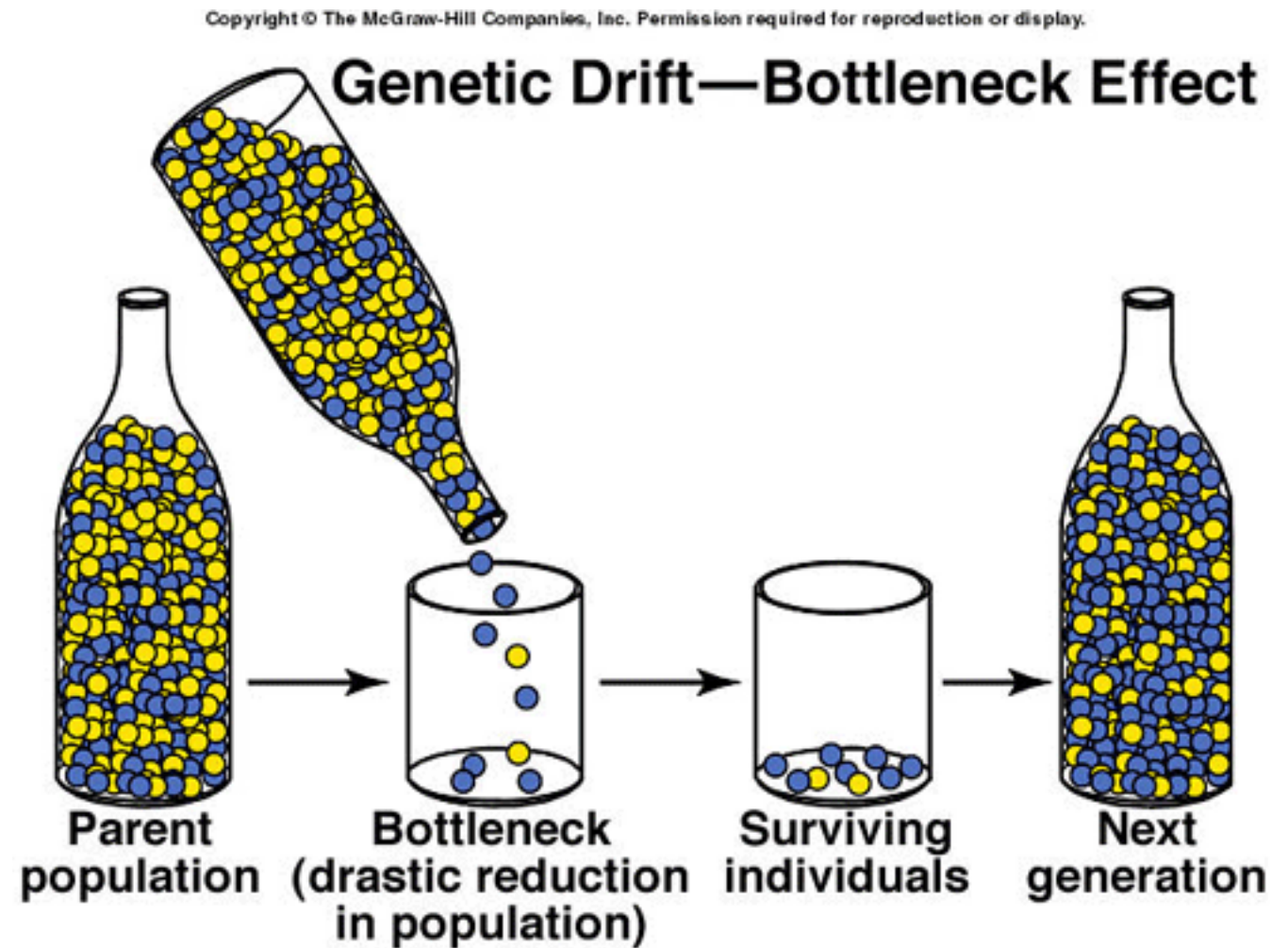
What is population structure?

- 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

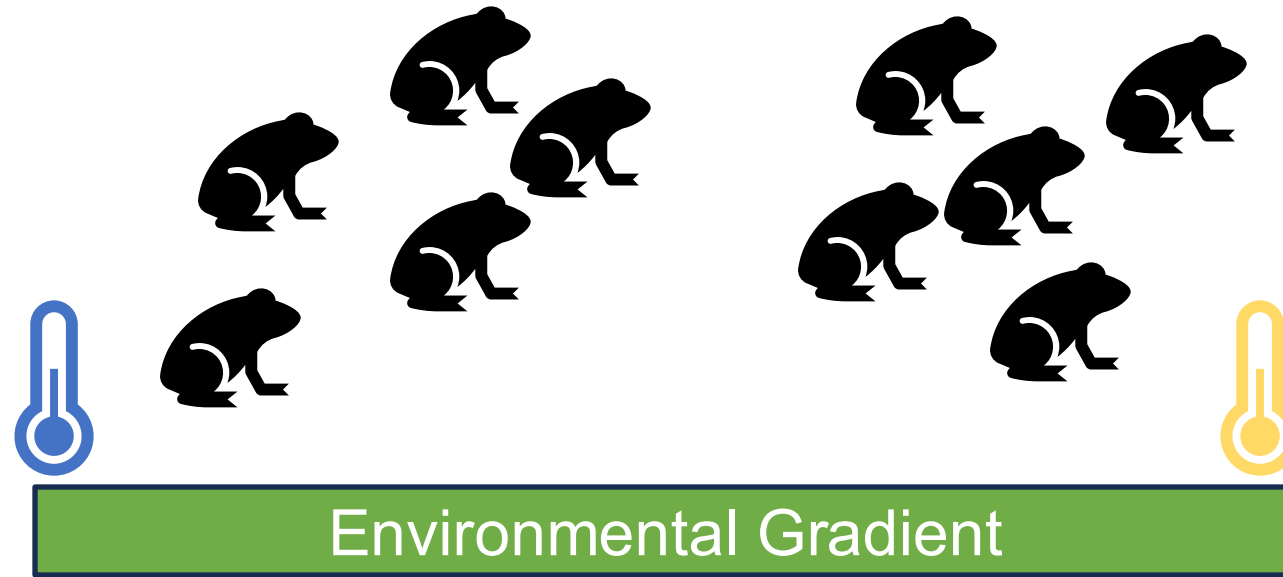


What can result in population structure?

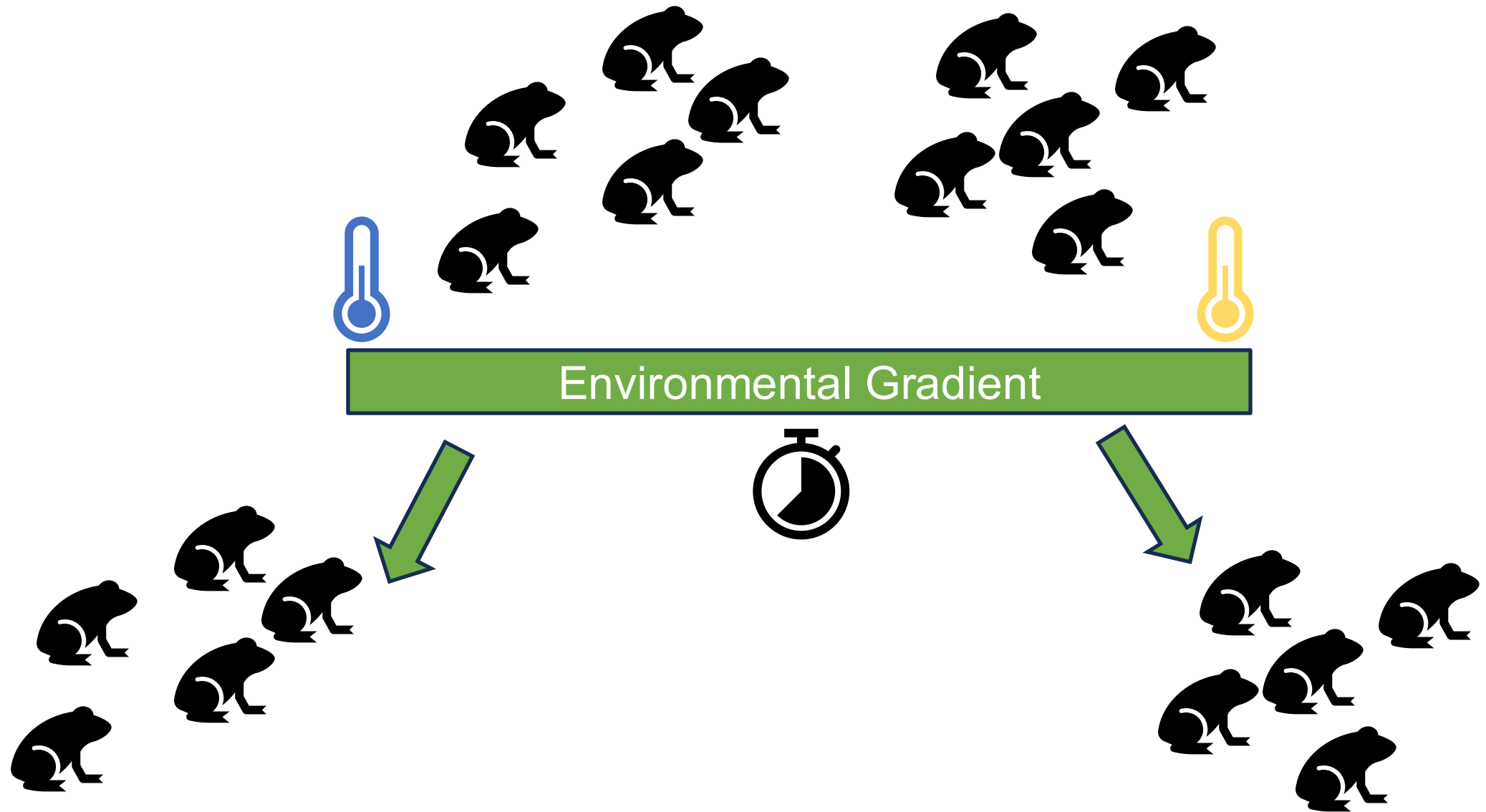
- Bottlenecks
- Founder Effects
- Selection
- Limited Gene Flow
- Nonrandom Mating



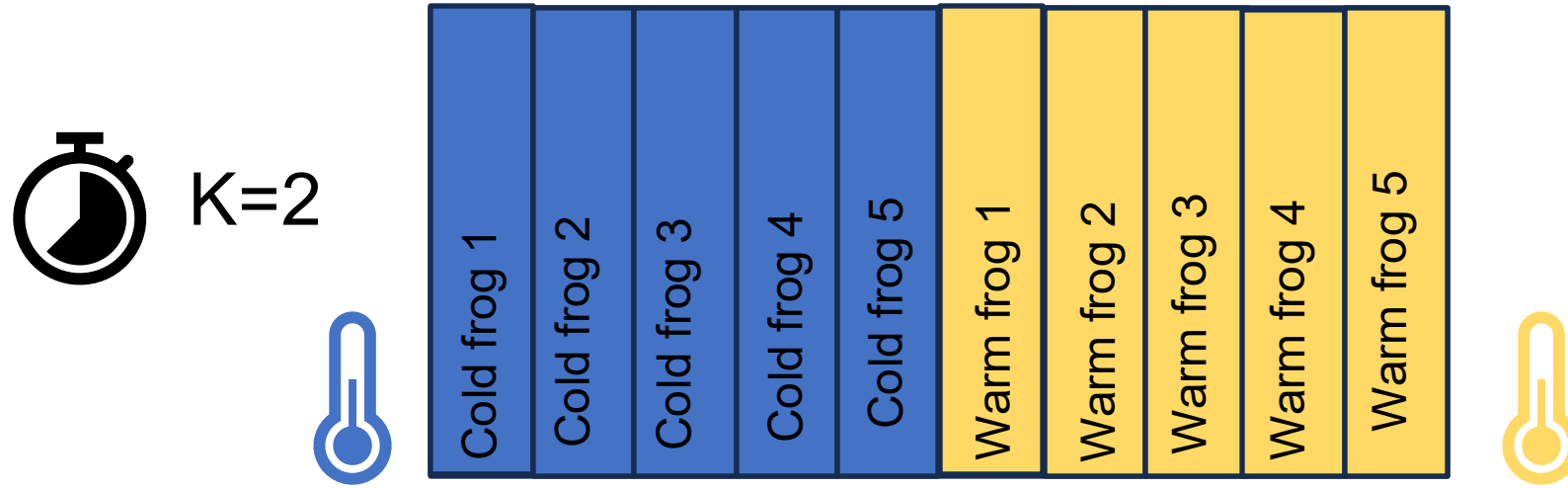
What can result in population structure: Selection



What can result in population structure: Selection



What can result in population structure: Selection



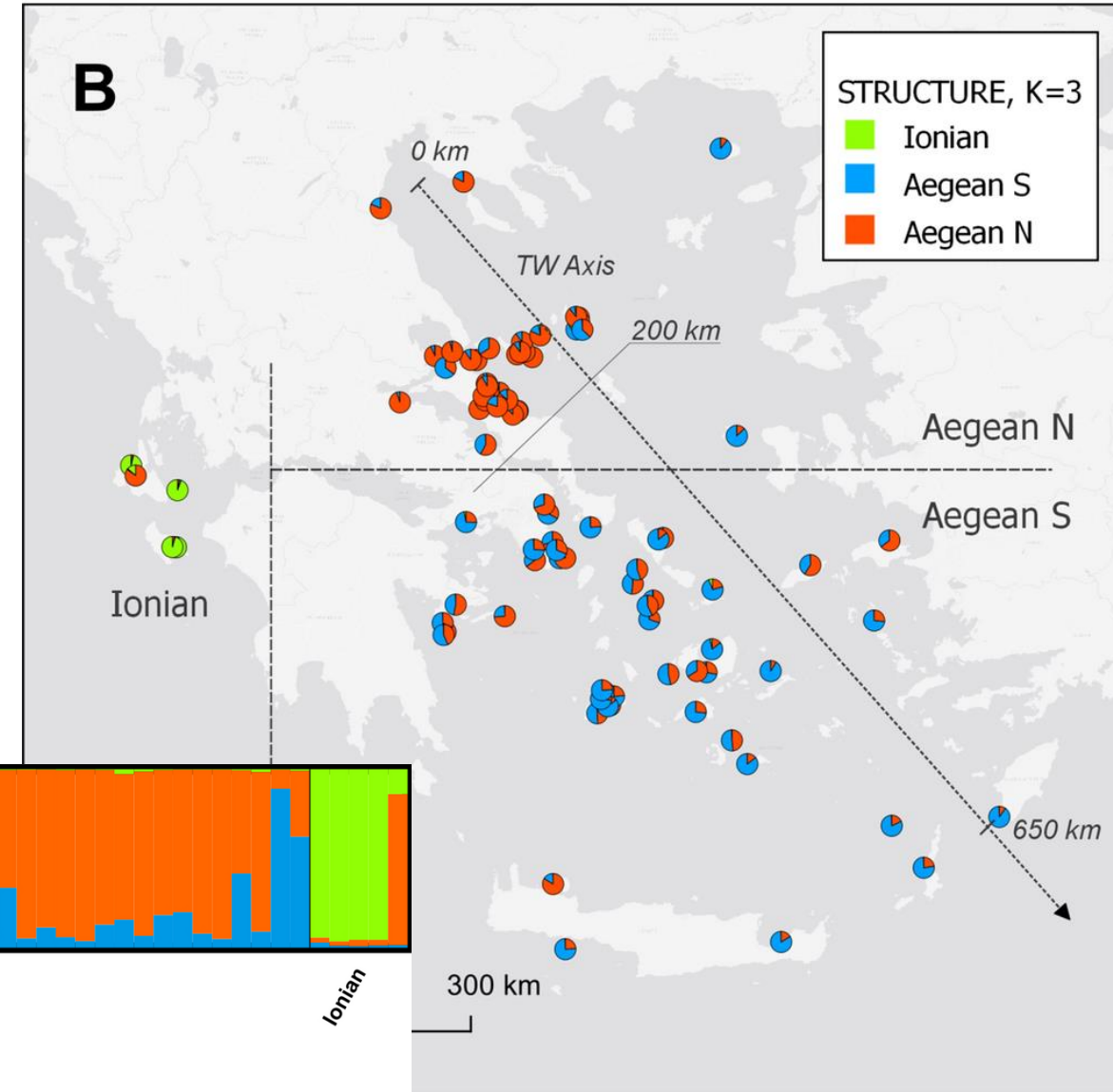
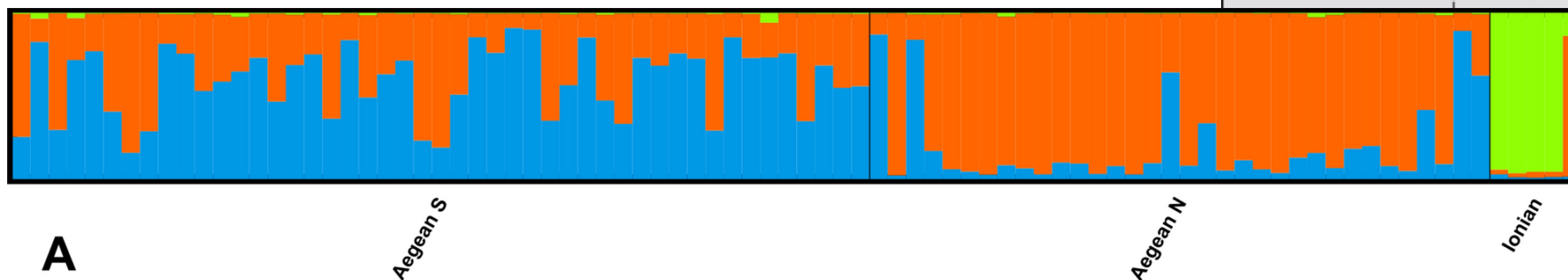
Use allele frequencies to assign likely membership for each individual to each population



What can result in population structure: Bottleneck



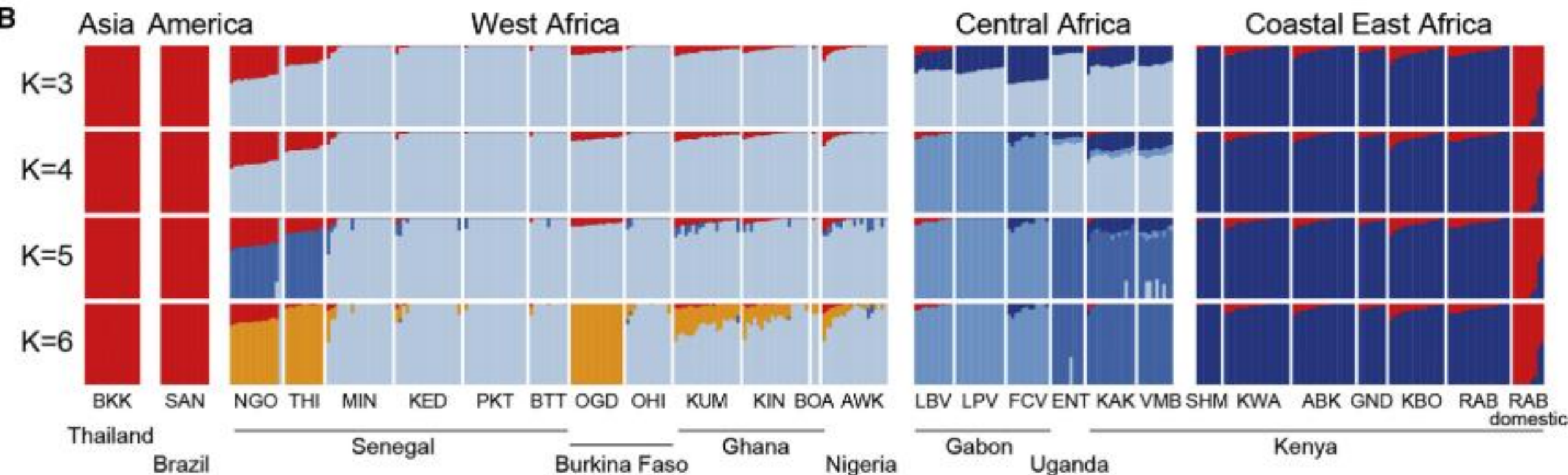
$K=3$





What can population structure tell us?

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

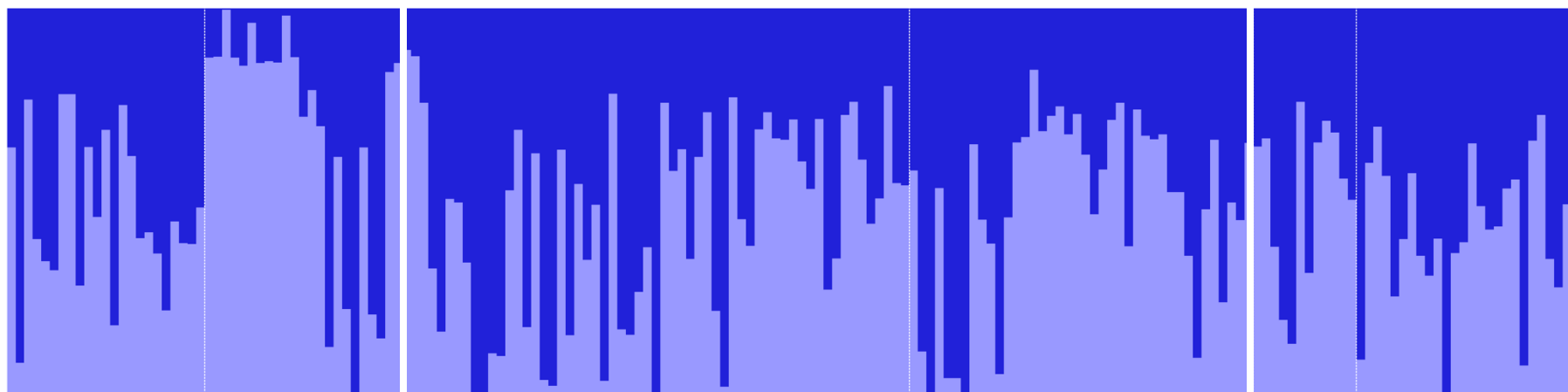




What can population structure tell us?

- 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!



Victoria, Canada

Los Angeles, CA

San Diego, CA



What can population structure tell us?

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

