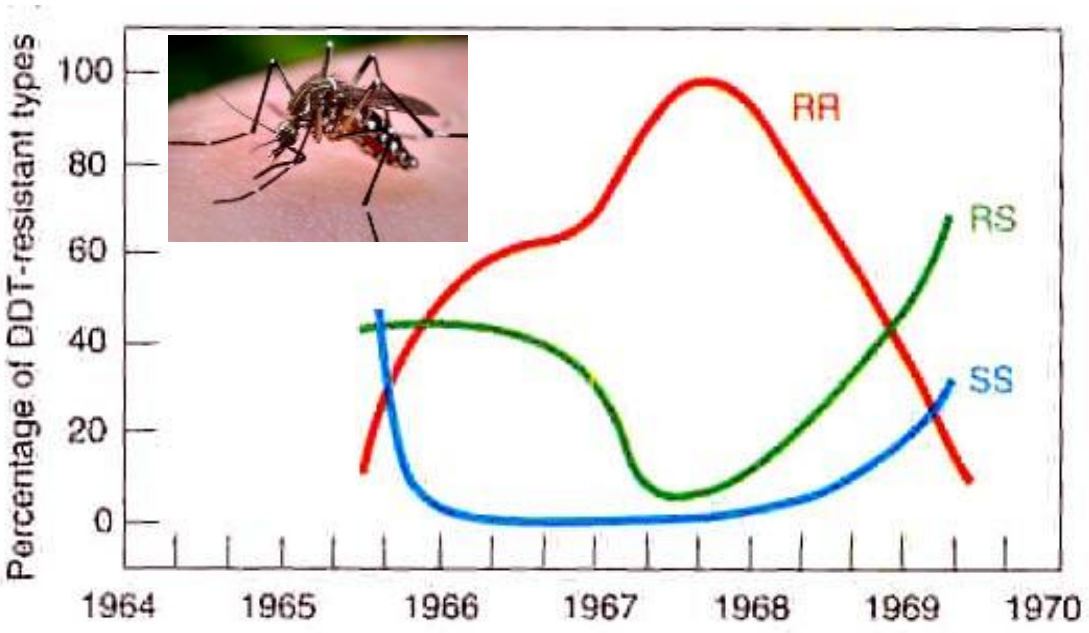
Selection and Adaptive Potential

Adam Stow

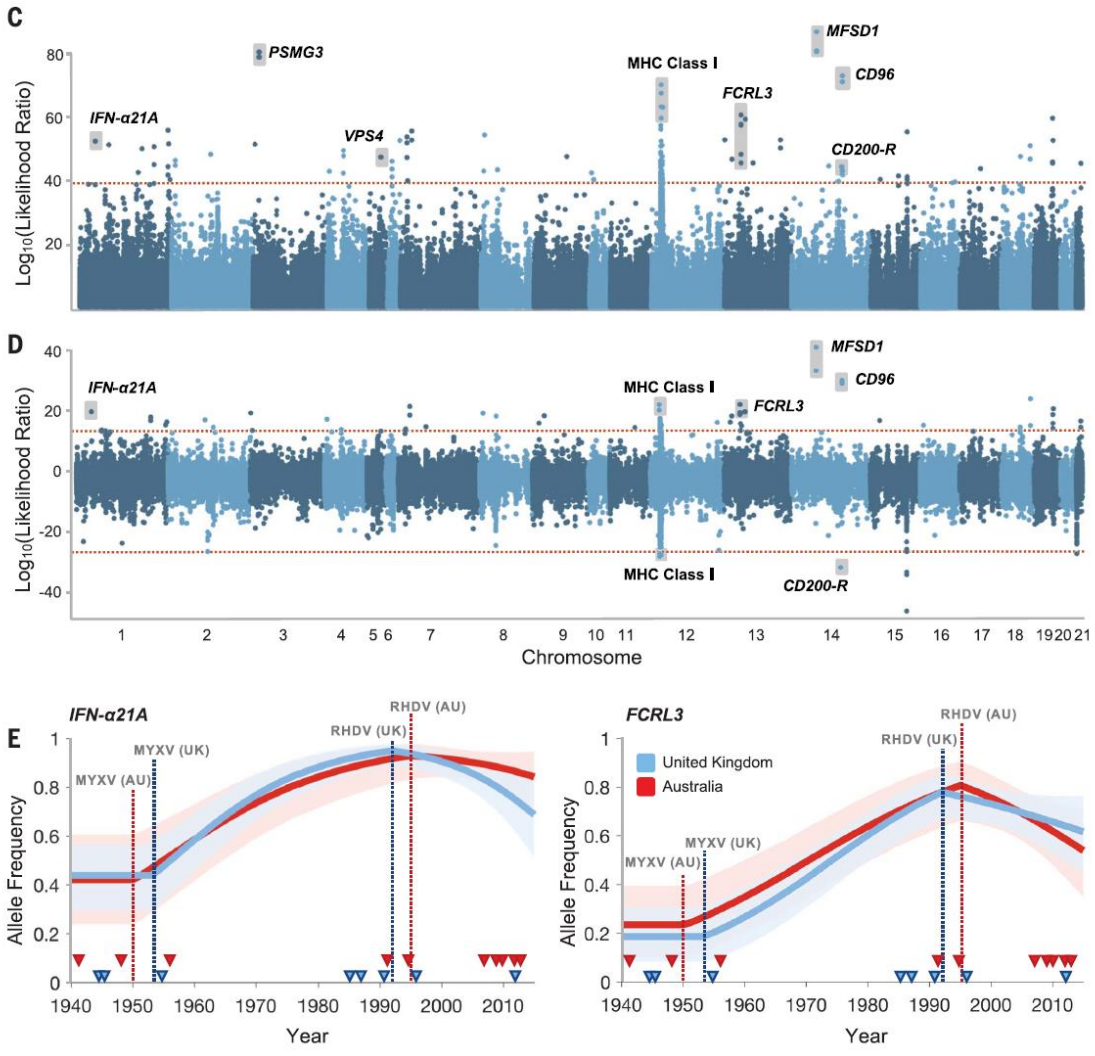
What is adaptive potential?

The ability of a population to respond adaptively to a new selective pressure



How genotype frequencies among populations of *A. aegypti* mosquito larvae change in response to insecticide. (a) Mosquitoes and larvae. (b) Changing proportions of resistance genotypes of *A. aegypti* (larvae) under selection with DDT, and after selection was relaxed, in a suburb of Bangkok, Thailand.

Enough standing genetic variation for evolution



Alleles selected for by myxoma virus

Decrease in Myxoma virulence

Alves et al. Science 2019

Can we use genomics to estimate adaptive potential?

Using genomics to characterize evolutionary potential for conservation of wild populations

Katherine A. Harrisson, Alexandra Pavlova, Marina Telonis-Scott and Paul Sunnucks

Evolutionary Applications

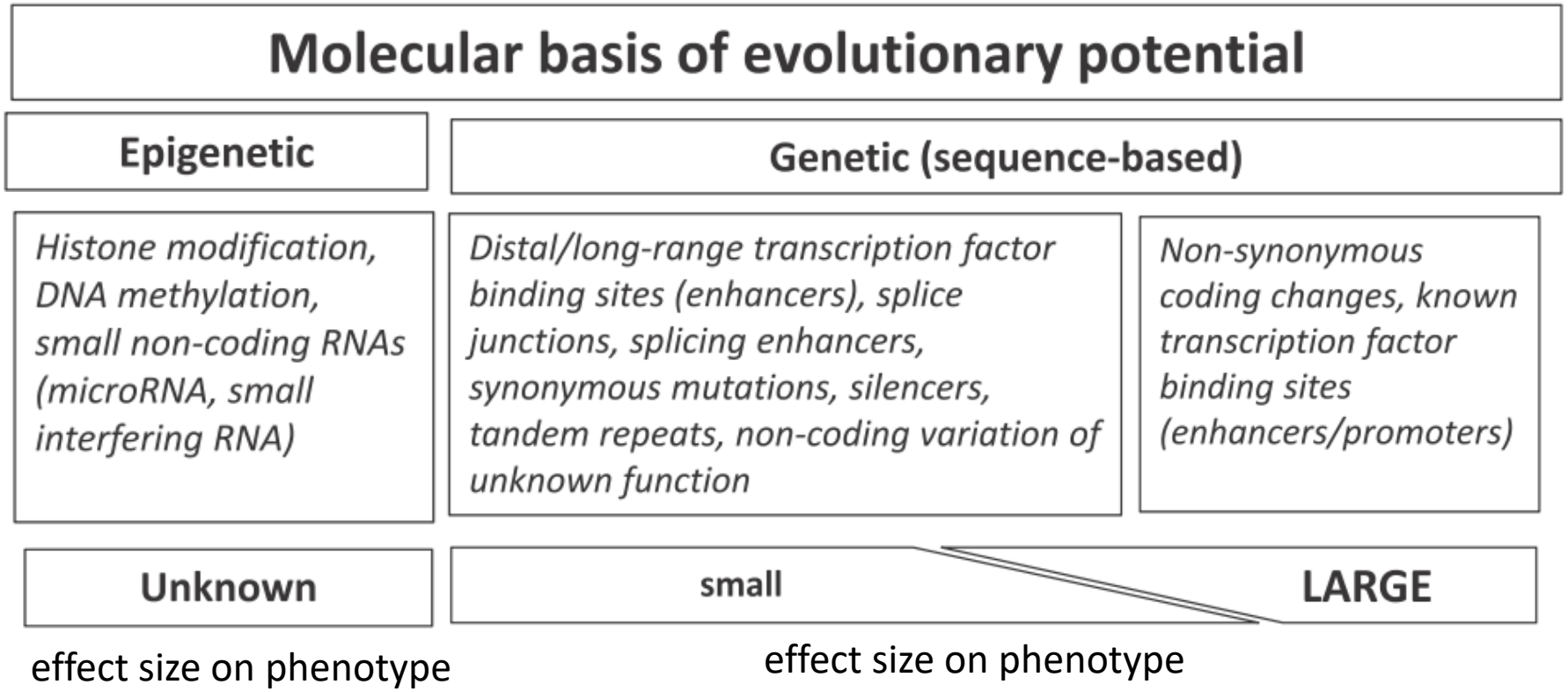
doi:10.1111/eva.12149

We could try and get estimates from genes of known function….but,

Given the current levels of understanding of how genomes work in non-model organisms screening genome wide diversity will usually give a better estimate of evolutionary potential.

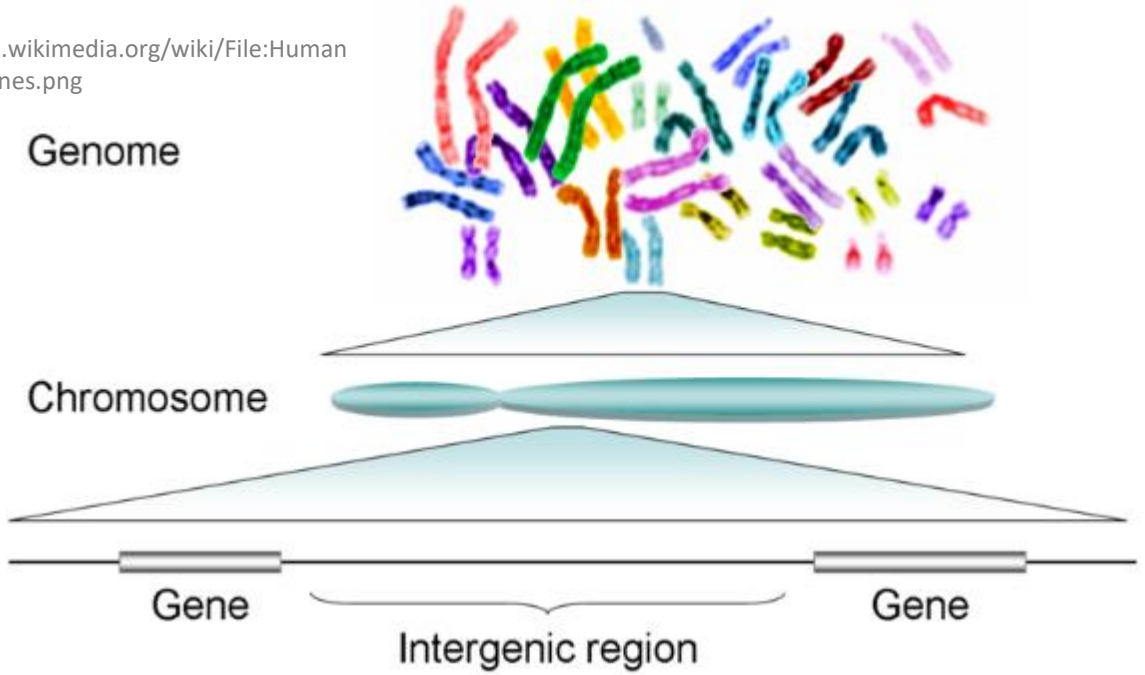
Two distinct components of evolutionary potential

- **Genetic** (DNA-sequence-based)
- **Epigenetic** (non-DNA-sequence-based)



Adaptive variation has been found in parts of the genome previously thought non-functional

Figure: http://commons.wikimedia.org/wiki/File:Human_genome_to_genes.png



Comparing rat and mouse genomes, a great number of evolutionarily conserved sequences (i.e probably have a function) were intergenic, far from known genes

How much of the genome has a function?

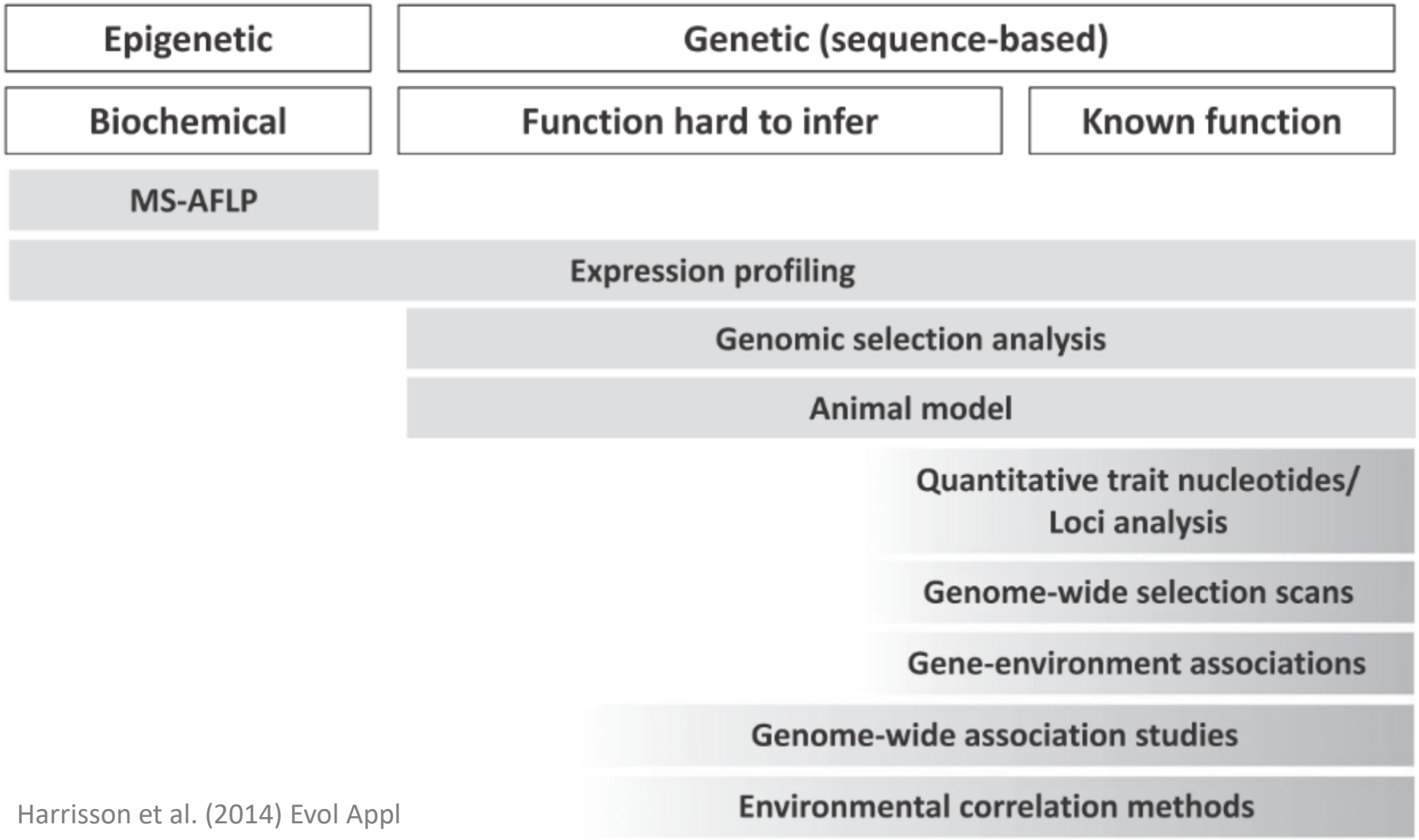
- In humans only ~ 1.5% of sequence codes for amino acids

- at least ~ 10–15% of sequence is evolutionarily conserved in a way that suggests it is potentially under selection and has a function

To better understand evolutionary potential and what drives localised adaptation it's useful to find parts of the genome influenced by selection.

How is it done, and how effective is it?

Methods to infer selection are complex, numerous, emerging



Harrisson et al. (2014) Evol Appl

Three main recent insights into evolutionary potential

summarized by Harrisson et al. 2014:

(1) Rapid adaptive evolution is driven predominantly by changes in gene expression

(2) Most traits are polygenic (controlled by lots of genes of small effect)

(3) Most recent adaptation is due to subtle shifts of allele frequencies

Detecting environmental selection using genomic data

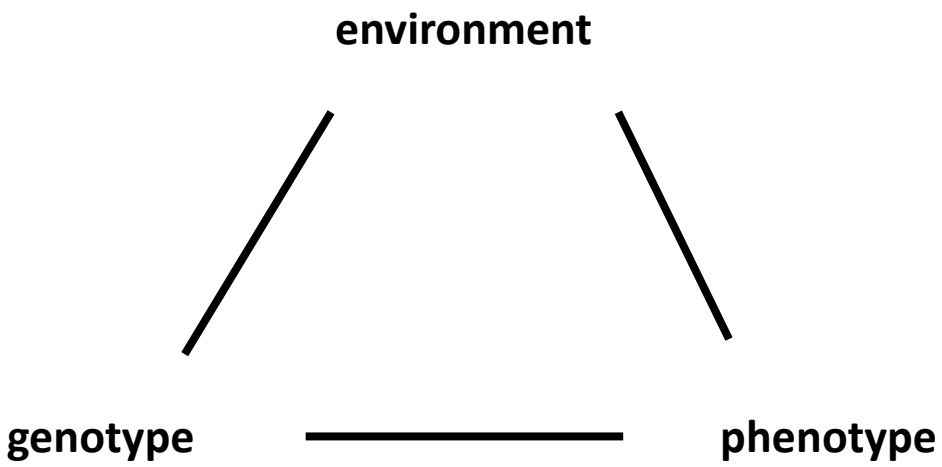
Goals

environmental variables that shape adaptive variation

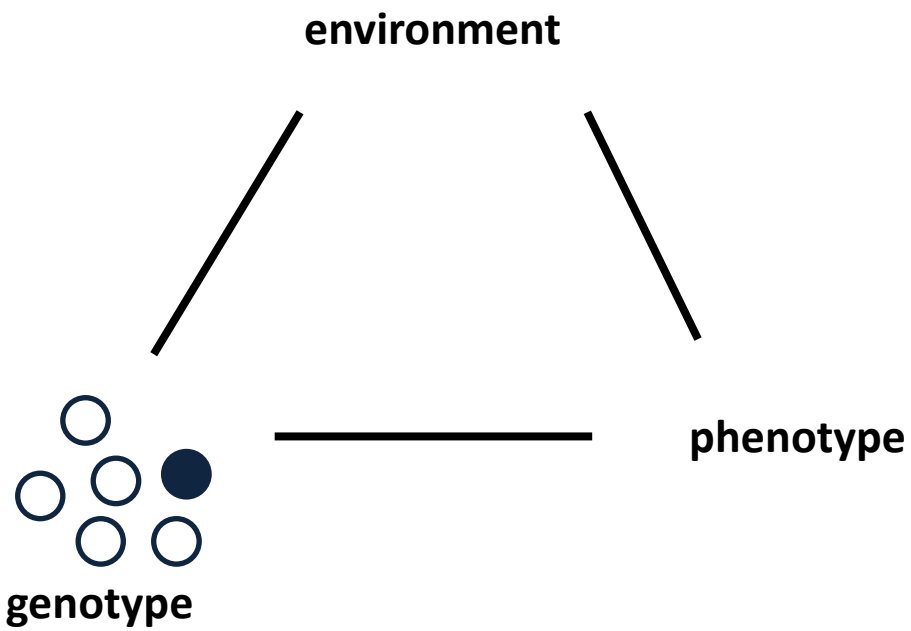
gene variants that drive local adaptation

Rellstab et al. 2015

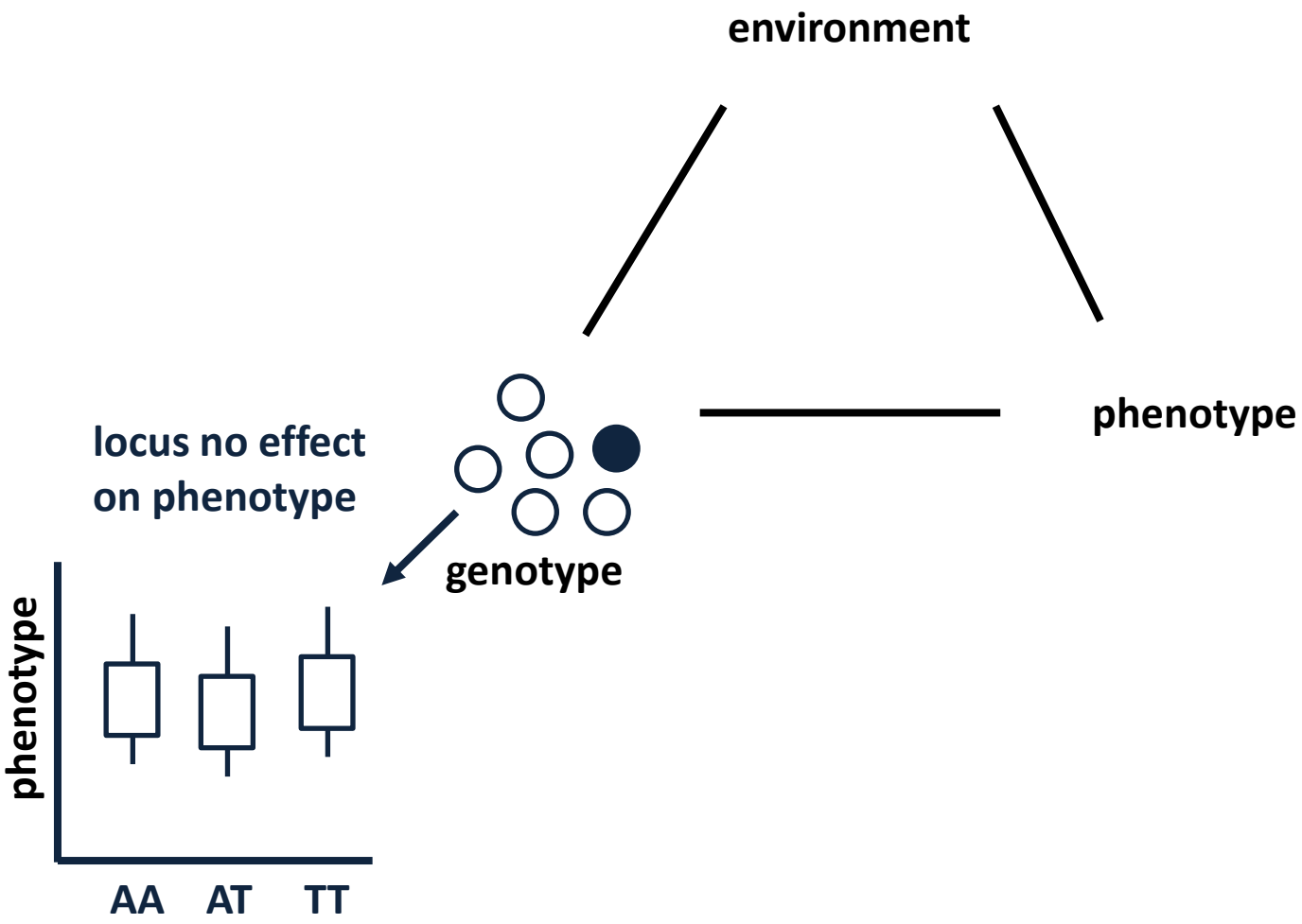
Adaptation: process and patterns



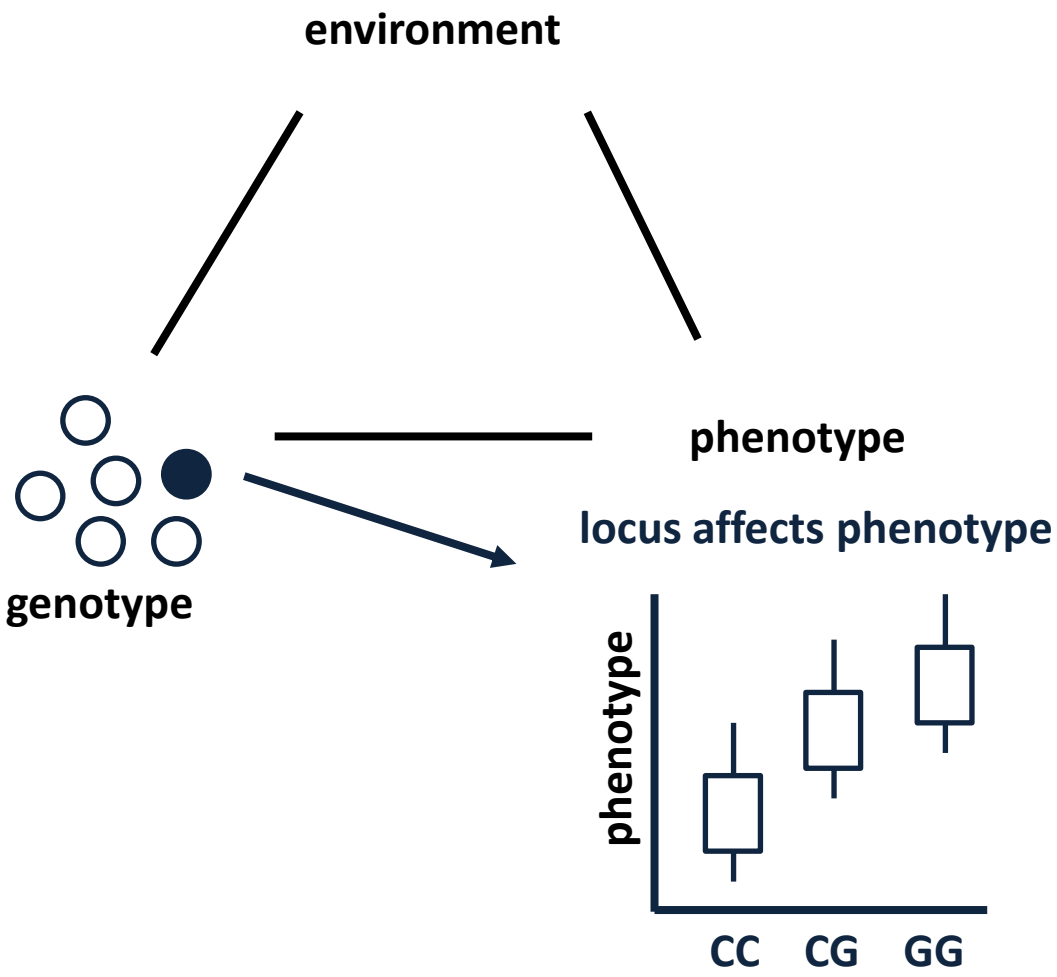
Adaptation: process and patterns



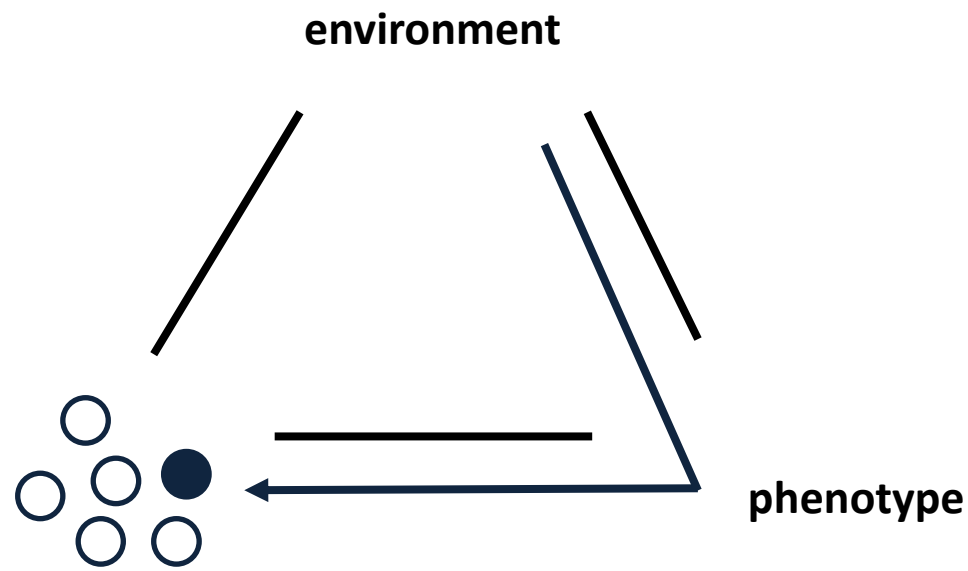
Adaptation: process and patterns



Adaptation: process and patterns



Adaptation: process and patterns



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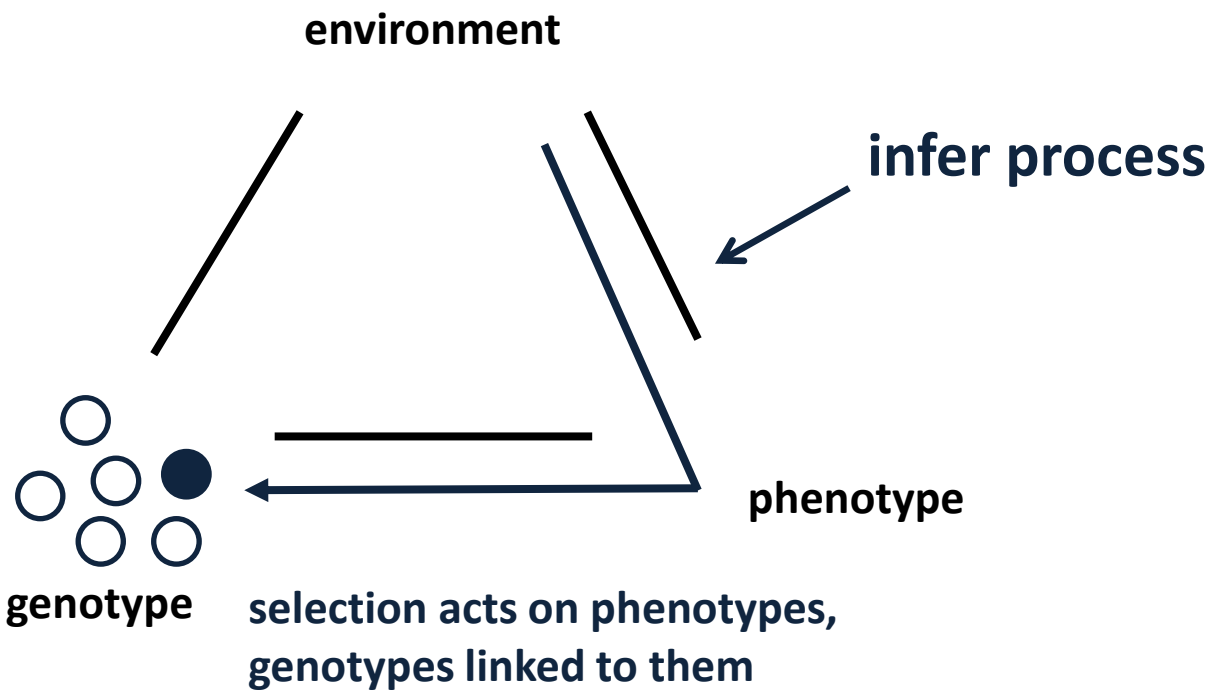
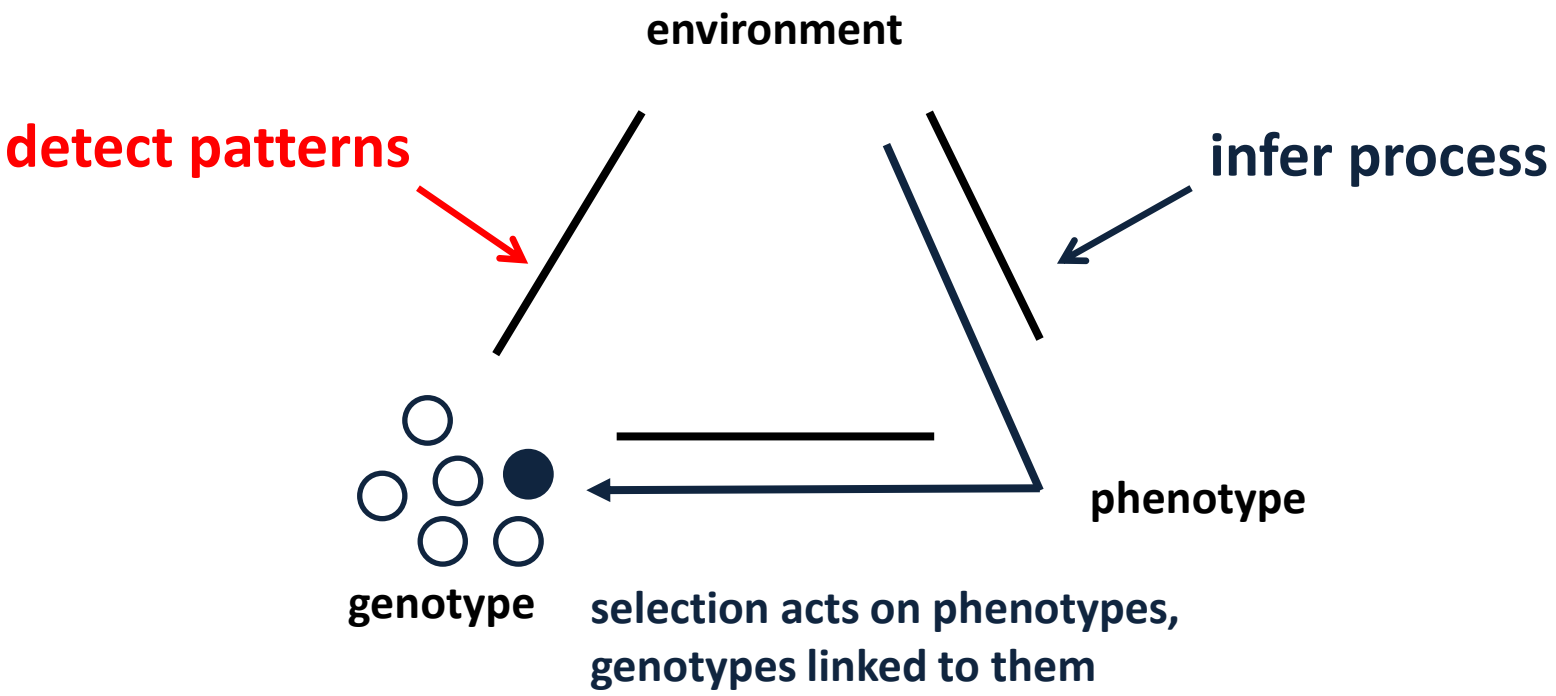


Adaptation: process and patterns



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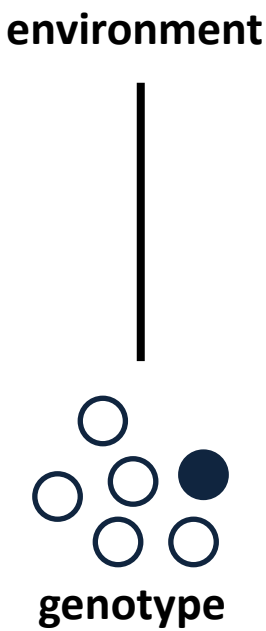
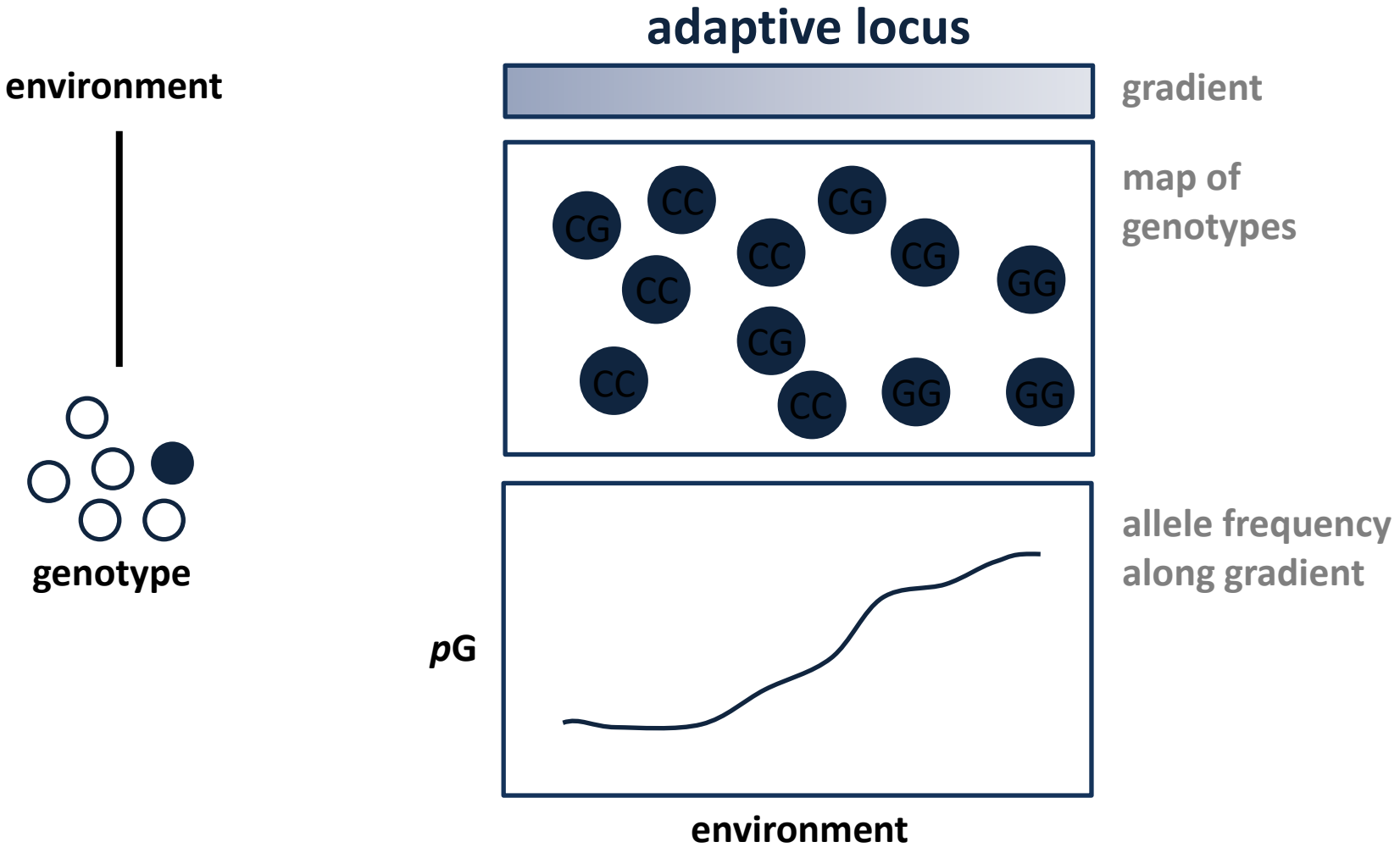
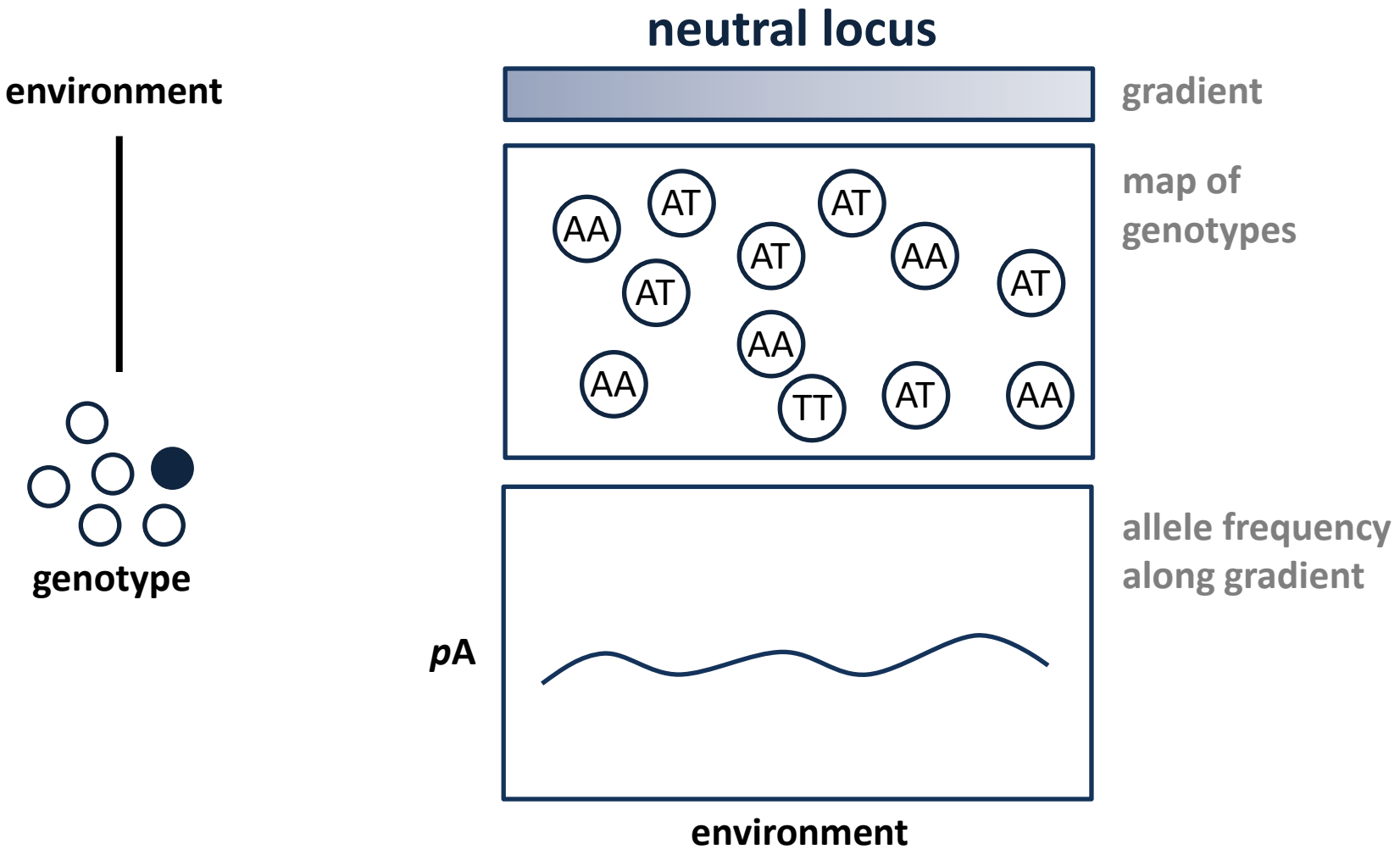


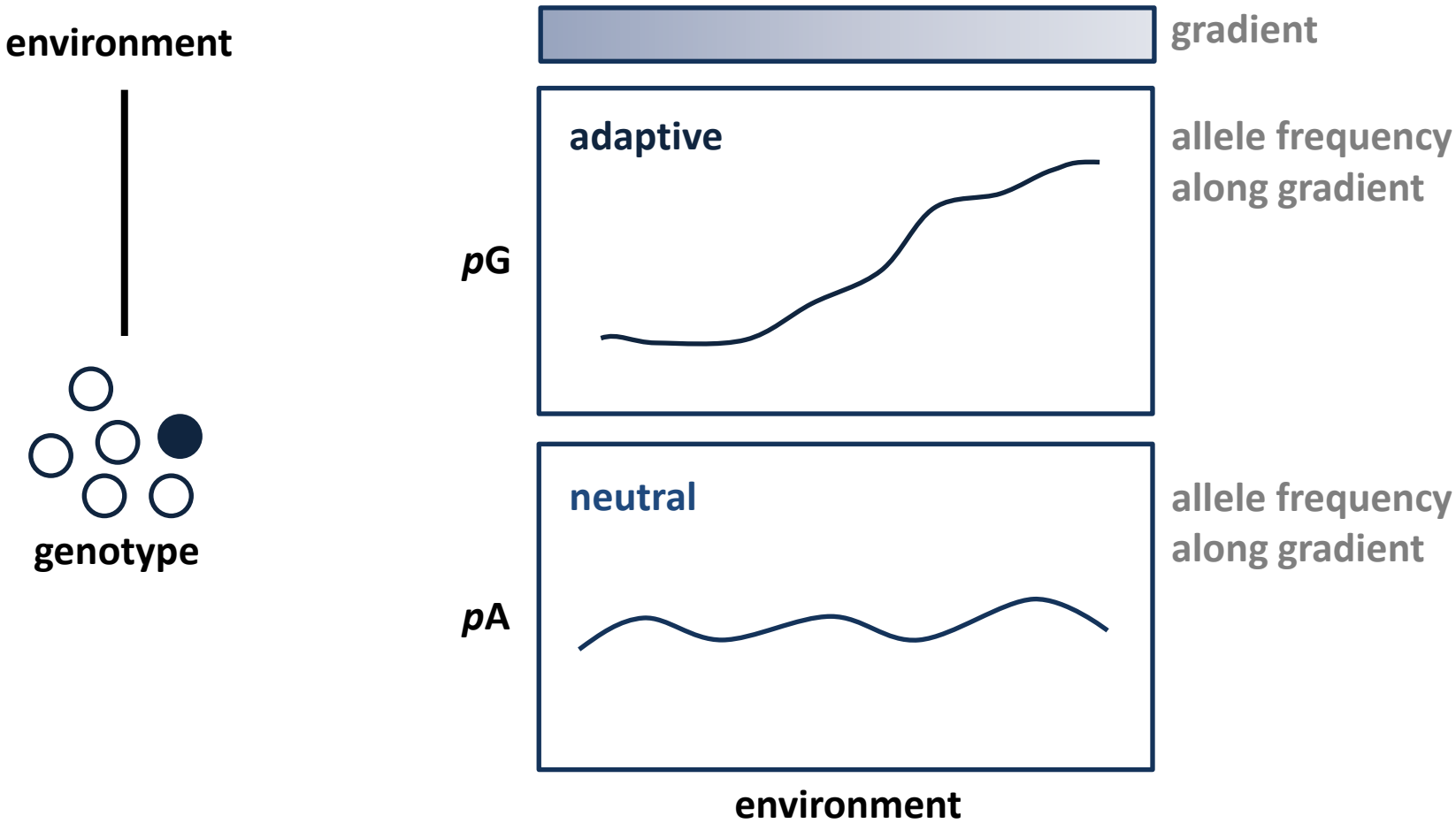
Adaptation: process and patterns



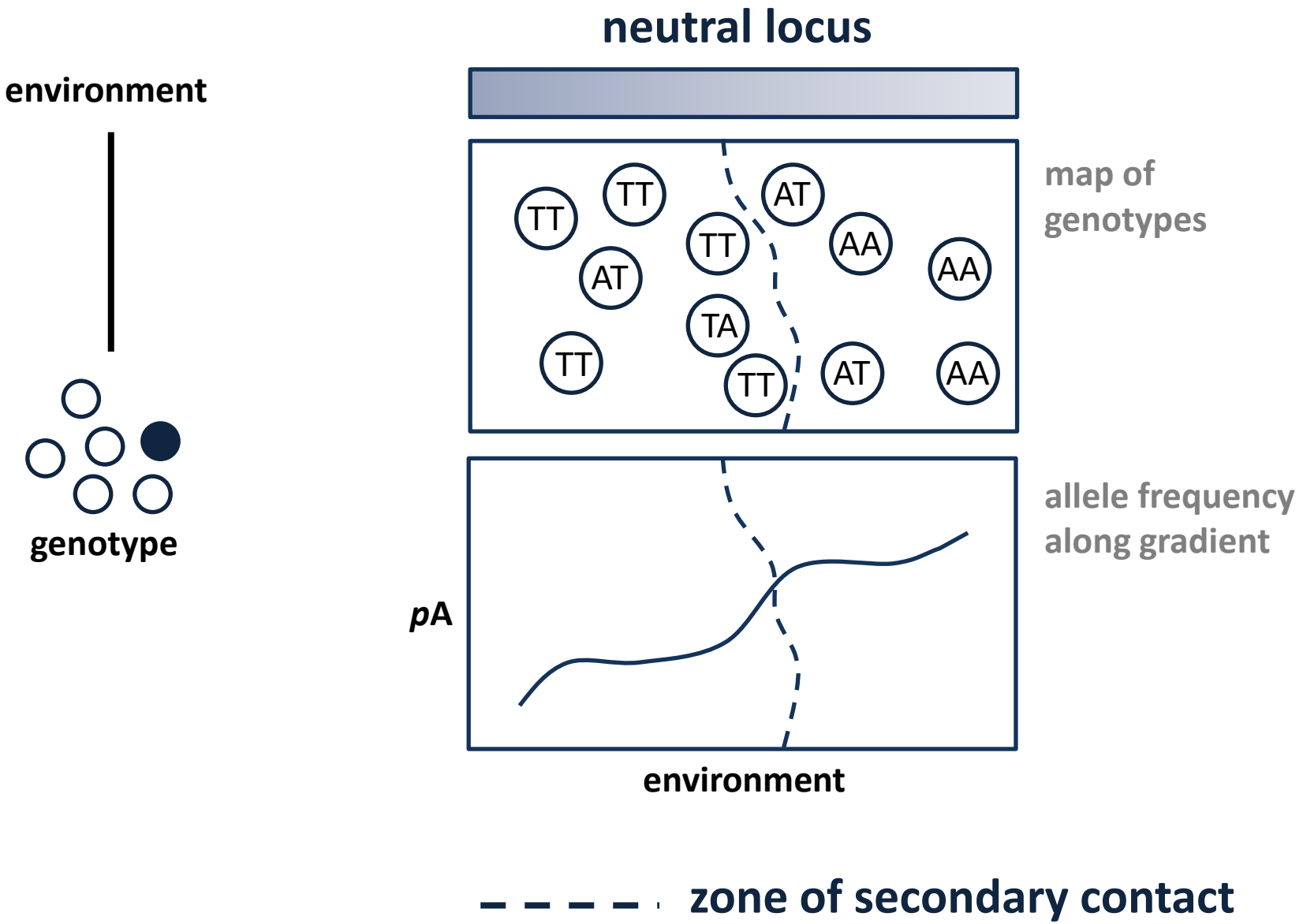
Adaptation: process and patterns



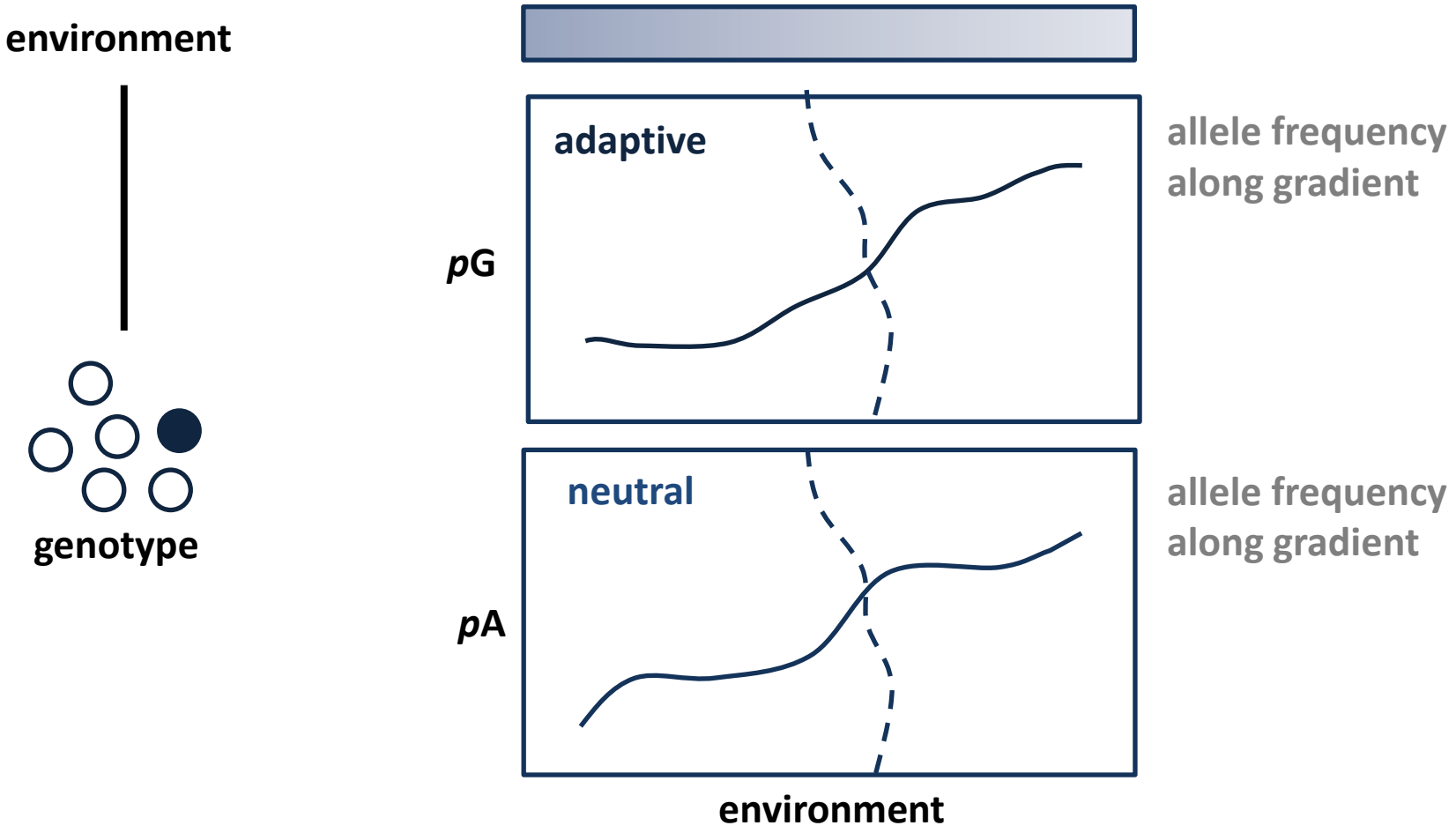
Adaptation: process and patterns



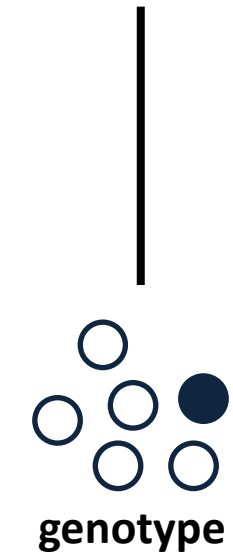
Adaptation: process and patterns



Key challenge: distinguishing from neutral variation

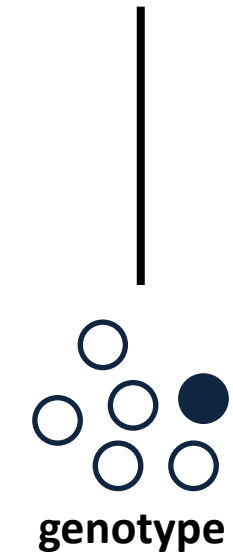


Data



Sample	Pop	Lat	Lon	RF	Temp
S1	P1	-15.1	132.3	328.4	23.6
S2	P1	-15.1	132.3	328.4	23.6
S3	P1	-15.1	132.3	328.4	23.6
S4	P1	-15.1	132.3	328.4	23.6
S5	P2	-15.7	135.4	312.8	21.2
S6	P2	-15.7	135.4	312.8	21.2
S7	P2	-15.7	135.4	312.8	21.2

Data



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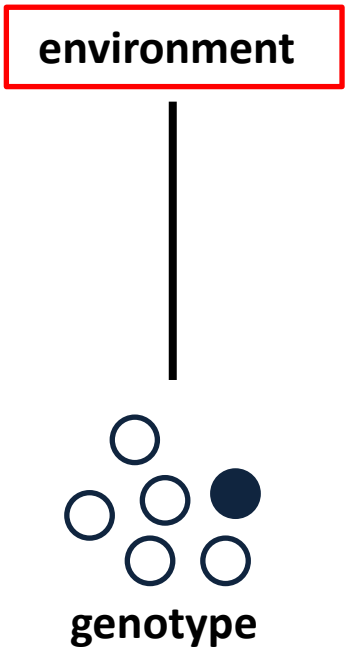
S7	P2	-15.7	135.4	312.8	21.2

sampling

Data

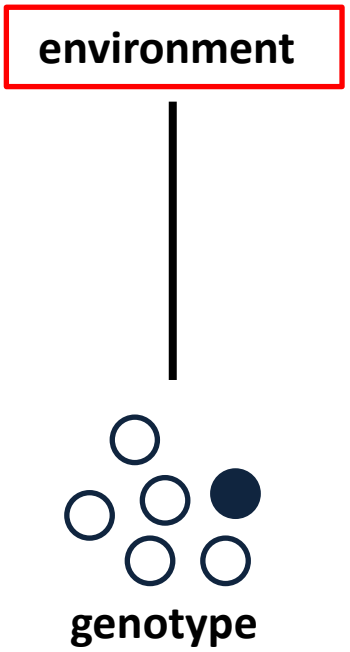


Sample	Lat	Lon	RF	Temp
S1	-15.1	132.3	328.4	23.6
S2	-15.2	132.5	329.2	23.3
S3	-15.4	132.1	326.3	24.0
S4	-15.4	132.7	324.4	22.4
S5	-15.5	133.6	318.6	22.6
S6	-15.7	134.2	314.8	21.8
S7	-15.7	135.4	312.8	21.2

measure these (map datum)

how to get these?

Data



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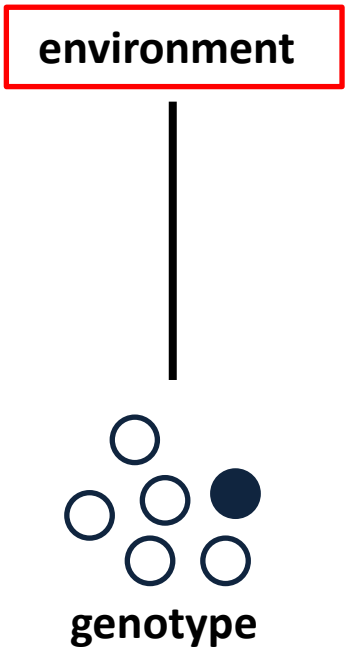
S6	-15.7	134.2	314.8	21.8
S7	-15.7	135.4	312.8	21.2

measure these (map datum)

how to get these?

WorldClim (consider local measurements…)

Data



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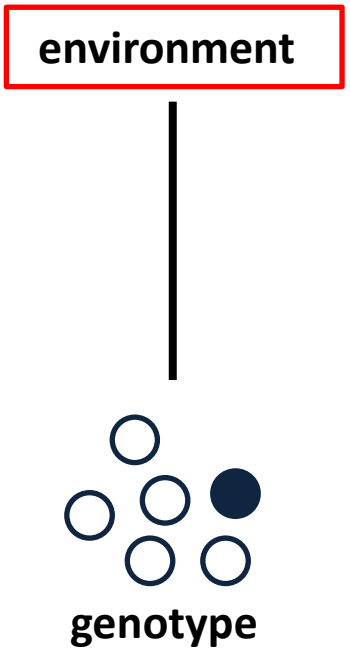
Data



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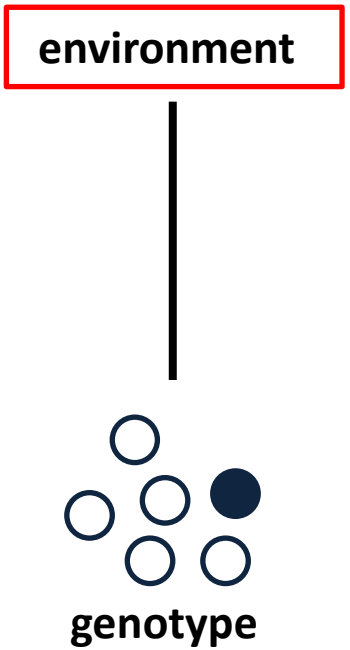
many choices

what matters to your species?

Data



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S6	-15.7	134.2	314.8	21.8
S7	-15.7	135.4	312.8	21.2

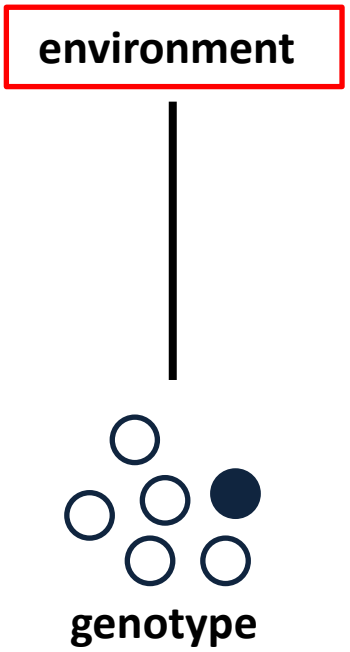
many choices

all available vs. hypothesis-driven → what matters to your species?

kinds of variables (e.g. aquatic life-stages)

thresholds (e.g. frost intolerance)

Data



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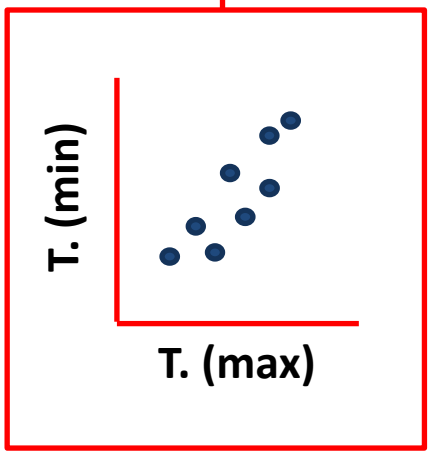
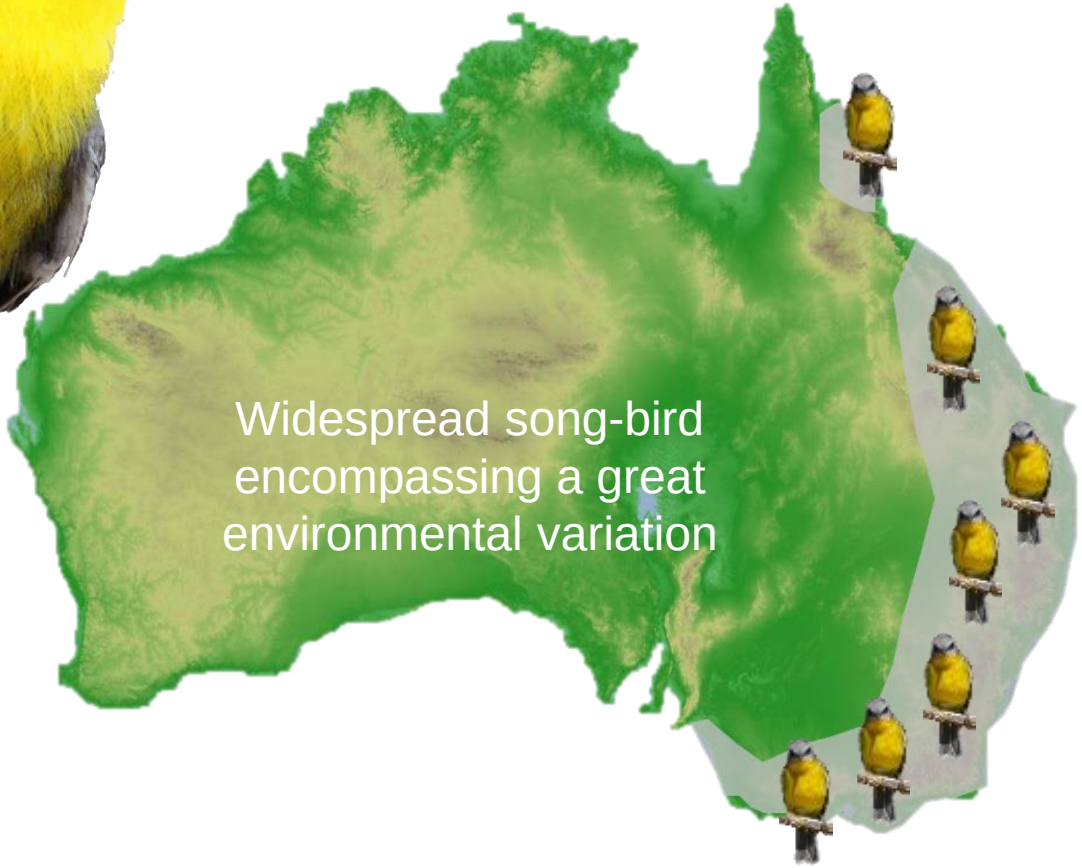
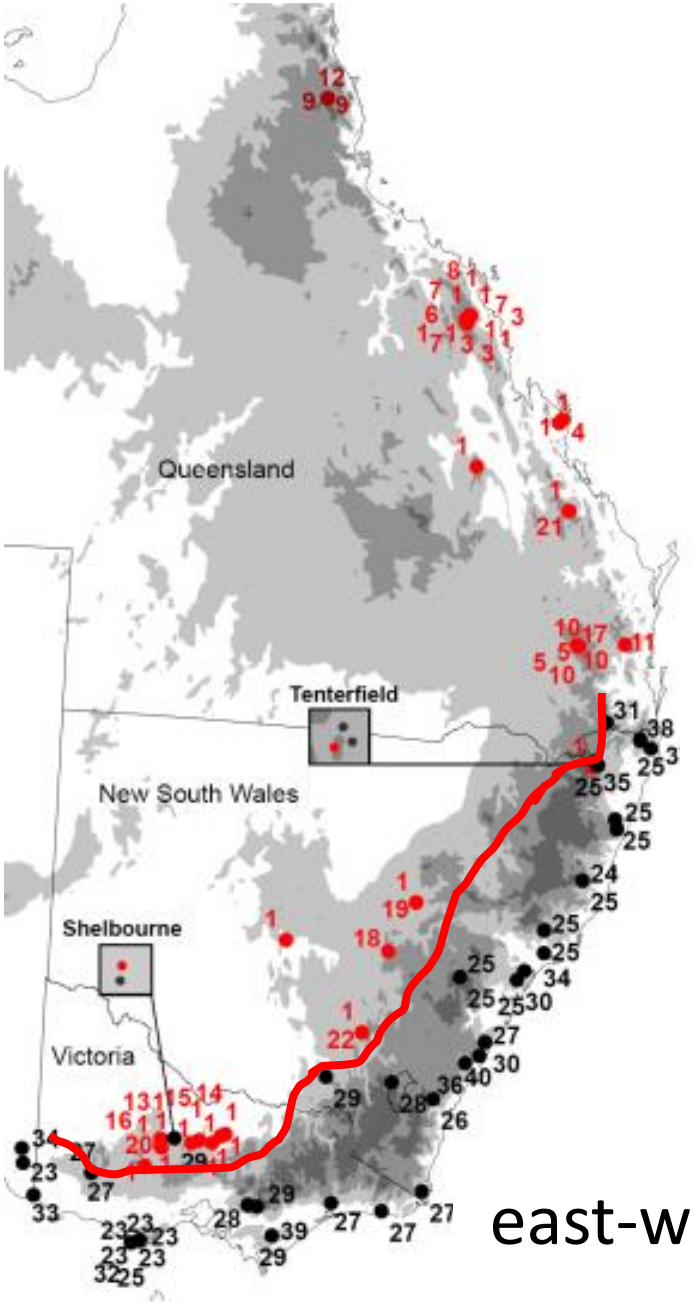
S2	-15.2	132.5	329.2	29.3	23.4
S3	-15.4	132.1	326.3	30.0	25.5
S4	-15.4	132.7	324.4	28.4	22.4
S5	-15.5	133.6	318.6	28.6	24.1
S6	-15.7	134.2	314.8	27.8	20.6
S7	-15.7	135.4	312.8	27.2	22.1

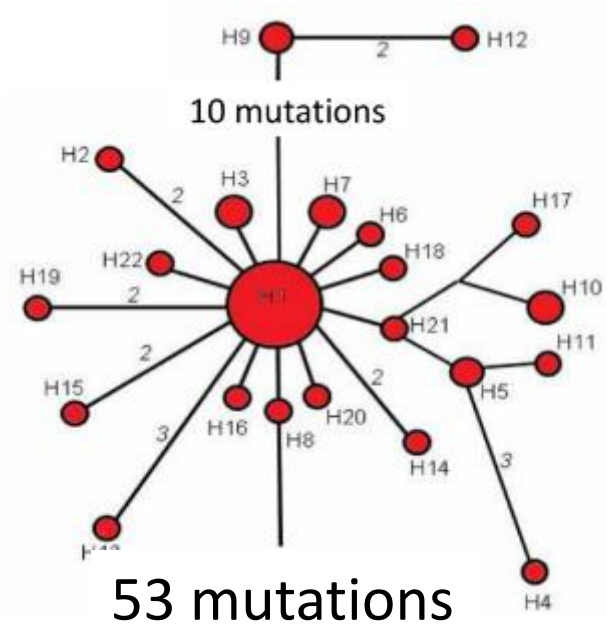


Eastern Yellow Robin

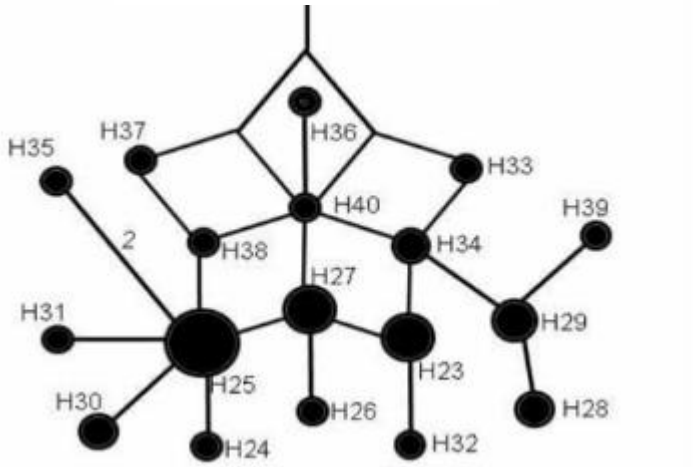


Pattern: Mitochondrial DNA sequences





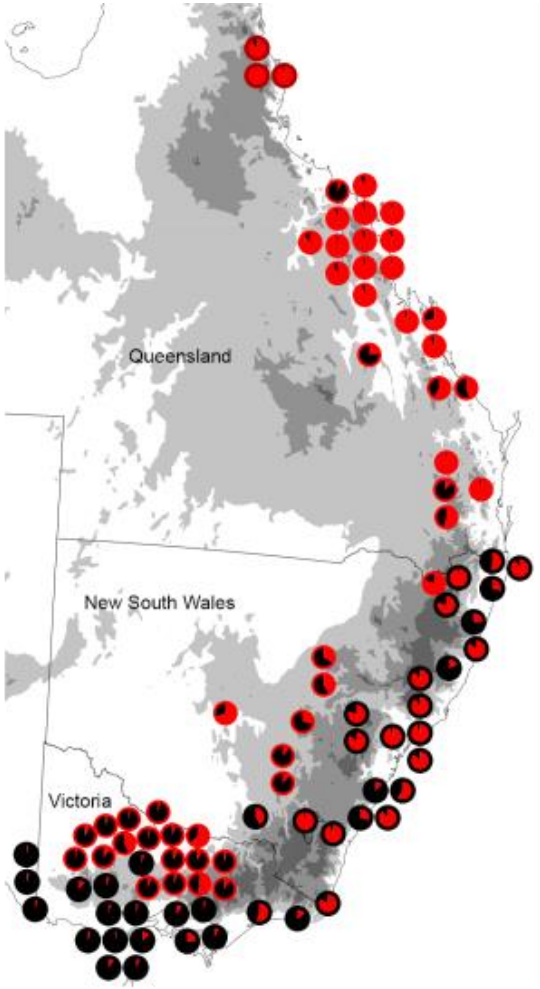
53 mutations



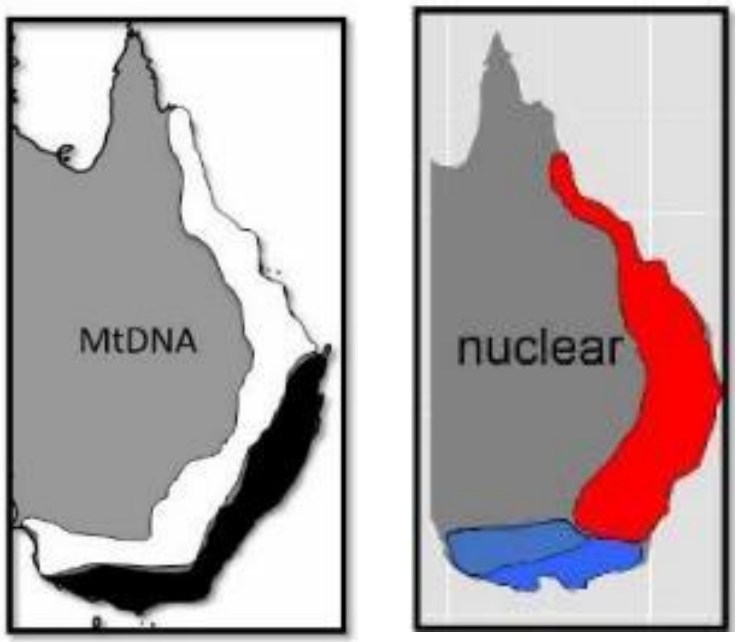
east-west split across Gt. Dividing Range

Pattern: Nuclear microsatellites

north-south pattern



Summary 2 genomes, completely different patterns



Having ruled out the boring alternatives, we inferred interesting female-associated selection:

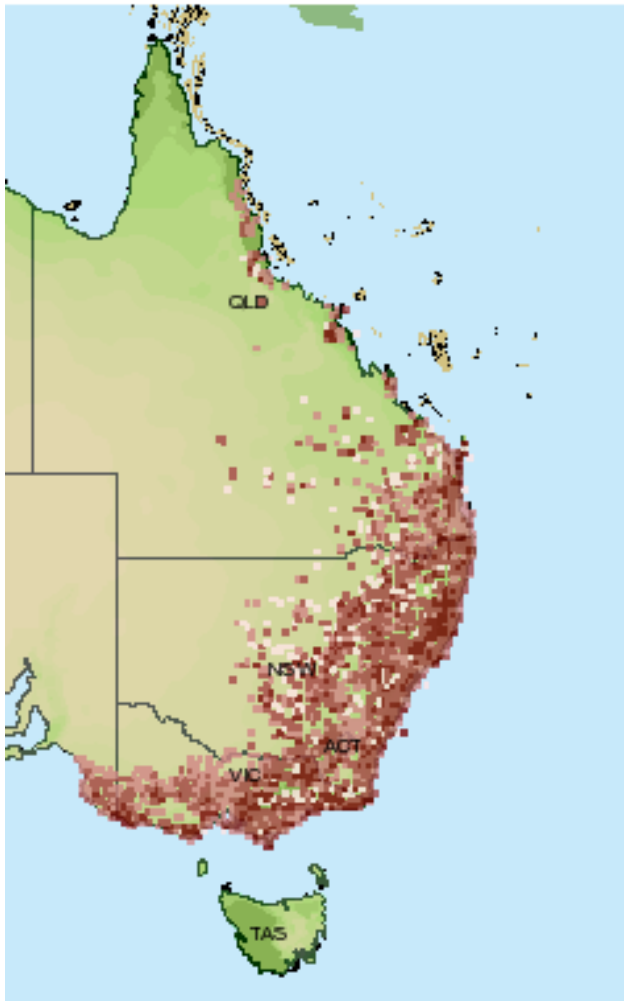
Reasons in Pavlova *et al*. 2013 Perched at the mito-nuclear crossroads: divergent mitochondrial lineages correlate with environment in the face of ongoing nuclear gene flow in an Australian bird. *Evolution* 67, 3412–3428

Sasha Pavlova

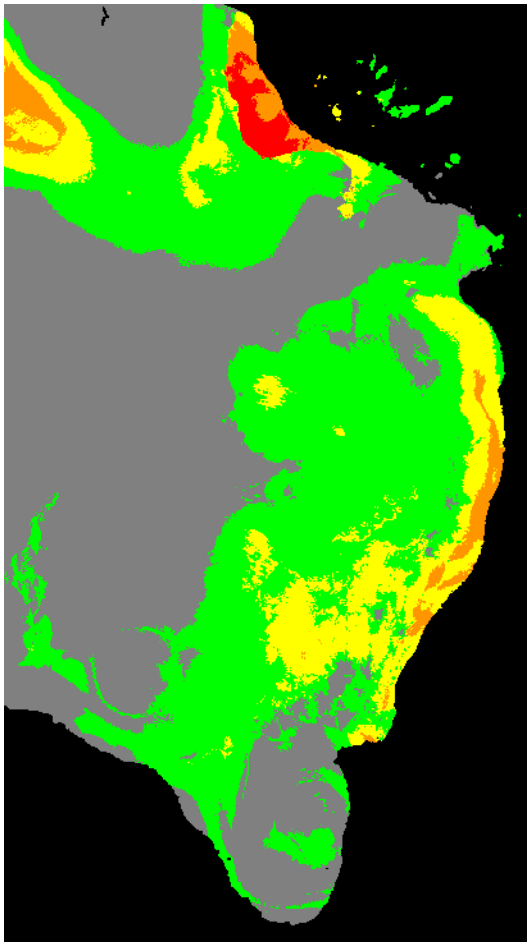
1. Vicariance: Is/was the Great Dividing Range a barrier?

No

Current distribution is continuous

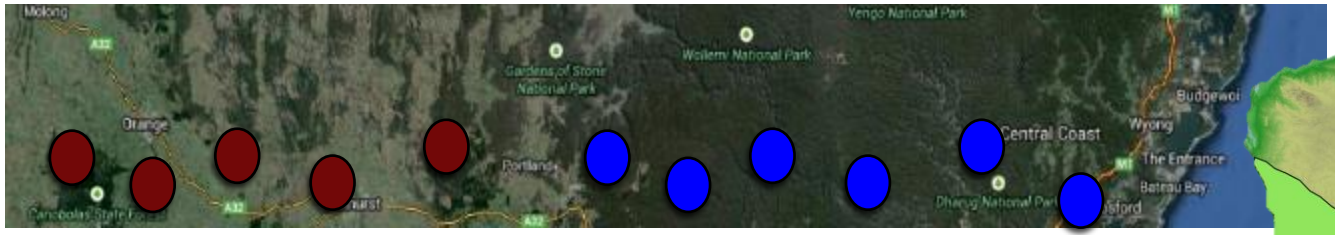


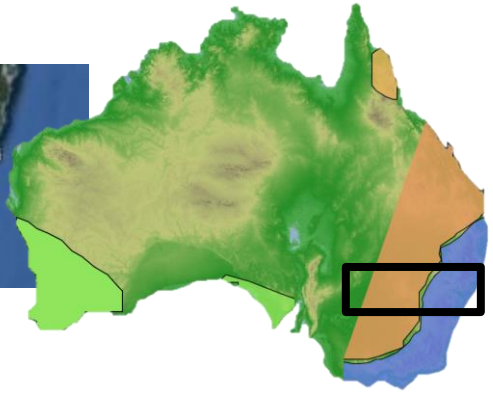
Last glacial maximum – no split over the GDR



2. Chance mtDNA split? No

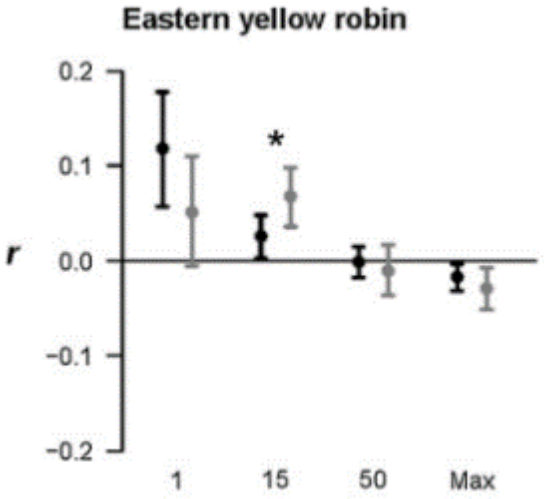
mtDNA lineages remain geographically distinct for >1500 km, even though they are well within the dispersal distance of a robin





3. Females immobile(philopatric)?

No Dispersal is **female-biased**



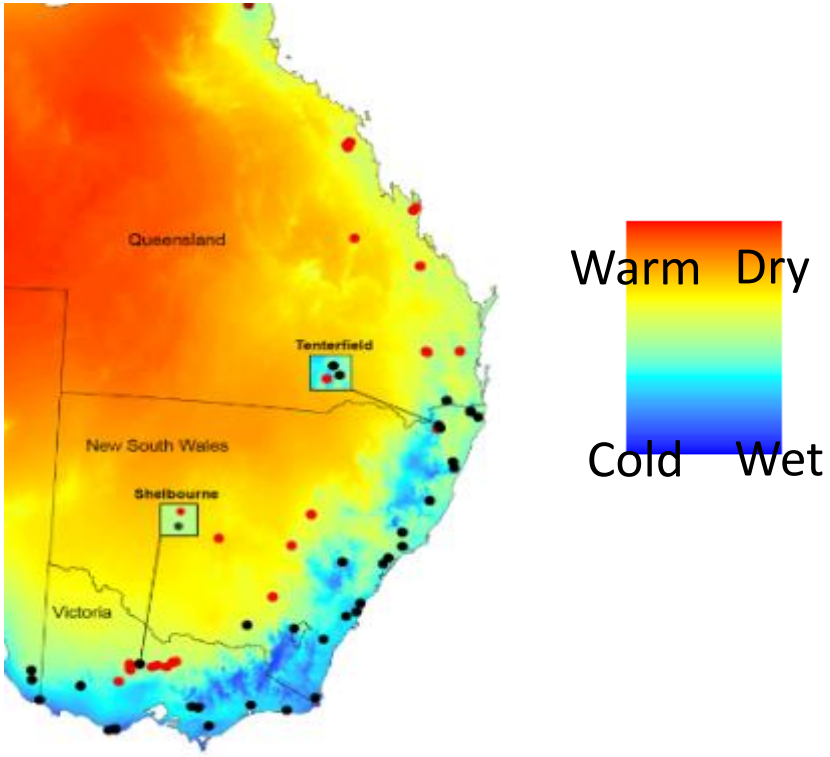
Harrisson et al. (2012) spatial autocorrelation

Female in grey, **male in black**

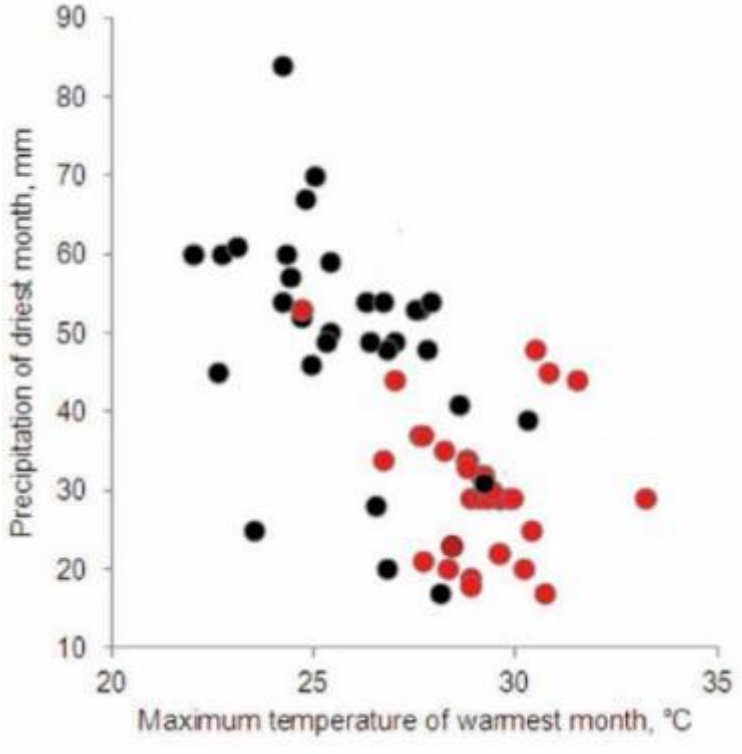
4. Female-associated selection – looks like it

Significant correlation of mtDNA with climate variables

Max. temp of the warmest month



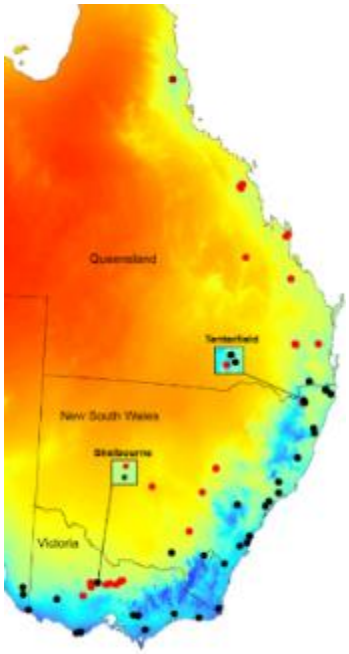
Environmental Association Analysis (EAA)
(also called Genetic–environment associations (GEA): alleles correlate with environments



...remains significant after accounting for geography (by dbRDA)

EMPHASIS …the fact that a potential driver remains significant after accounting for geography (by dbRDA)

Australia's climate is highly correlated with geography:
eg it's warmer in the north and cooler in the south

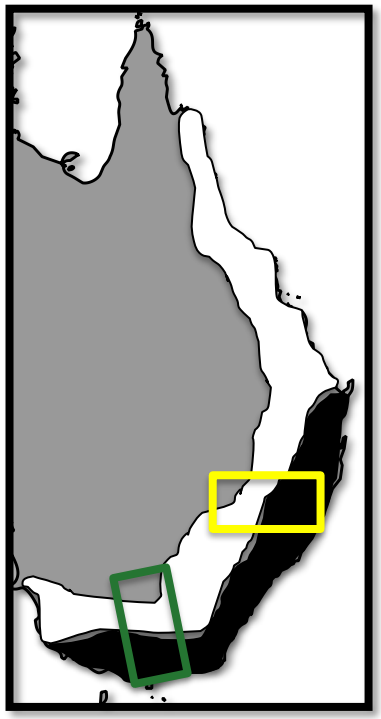


so any N-S pattern will look like it could be driven by climate

Need to test whether association of mtDNA with climate remains significant after accounting for ('partialling-out') the automatic correlation of climate with geography

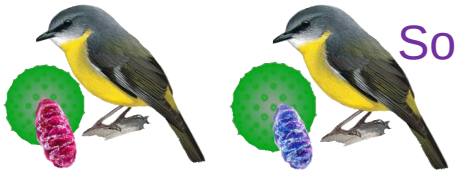
eg using distance-based redundancy analysis (dbRDA)

Testing for nuclear genes with mitochondrial functioning being ‘dragged along’ with mtDNA during introgression



- Two transects across mtDNA split
- True replicates (different nuclear backgrounds)

Northern transect



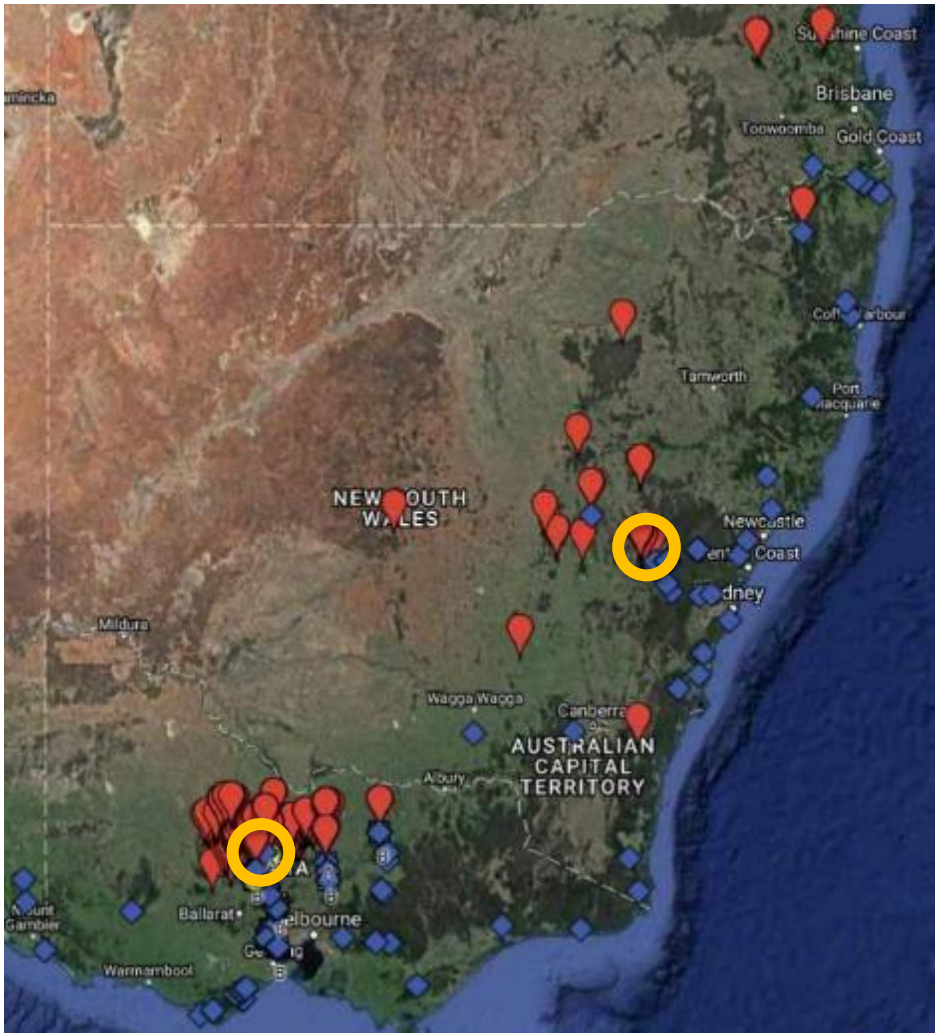
Southern transect

Nuclear genomewide marker scan >64,000 SNPs from short DNA sequences

Finding nuclear genes that differ between mitolineages

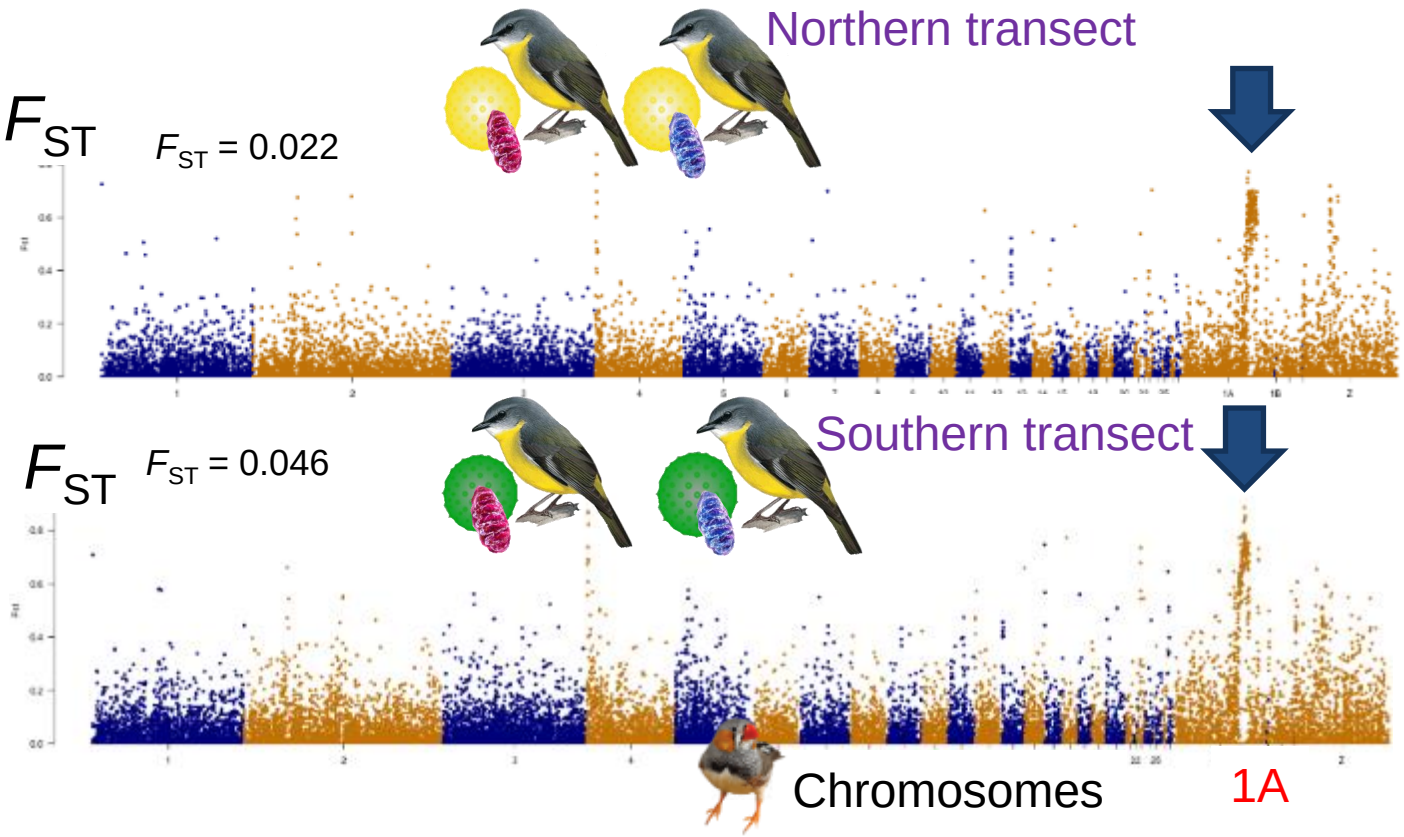
i.e. seeking high F_{ST} between adjacent inland and coastal robins

(This is a GWAS - genome wide association study)



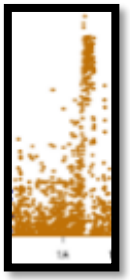
Morales HE, Pavlova A, Amos JN, Major R, Kilian A, Greening C and Sunnucks P (2018) Concordant divergence of mitogenomes and a mitonuclear gene cluster in bird lineages inhabiting different climates. *Nature Ecology & Evolution* 2, 1258–1267

Genomewide differentiation between inland and coastal mitolineages



Outliers have average F_{ST} > 0.48

This chromosome 1A ‘island of divergence’ is special



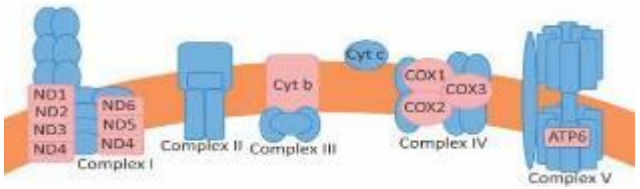
(1) ~15 million nucleotides long containing ~340 genes

(2) inherited as if one giant gene with two alleles

(3) inherited along with mitochondrial DNA, even though the rest of the nuclear genome is not

(4) Contains 32 genes that have functions in the mitochondrion (a significant excess)

including 4 OXPHOS genes



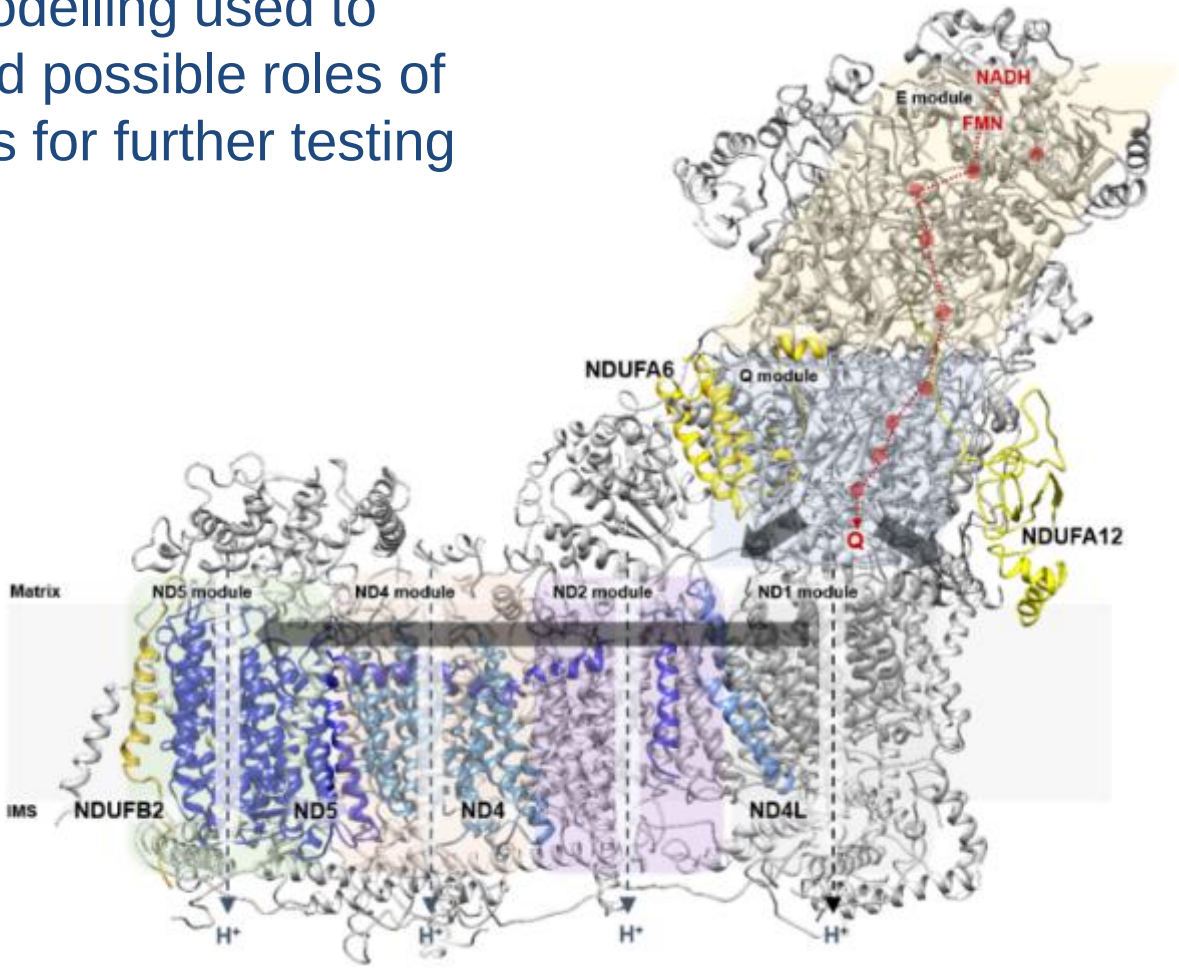
Three of these OXPHOS genes are partners of the mtDNA ones also showing signals of positive selection

Chris Greening

Protein modelling used to understand possible roles of candidates for further testing

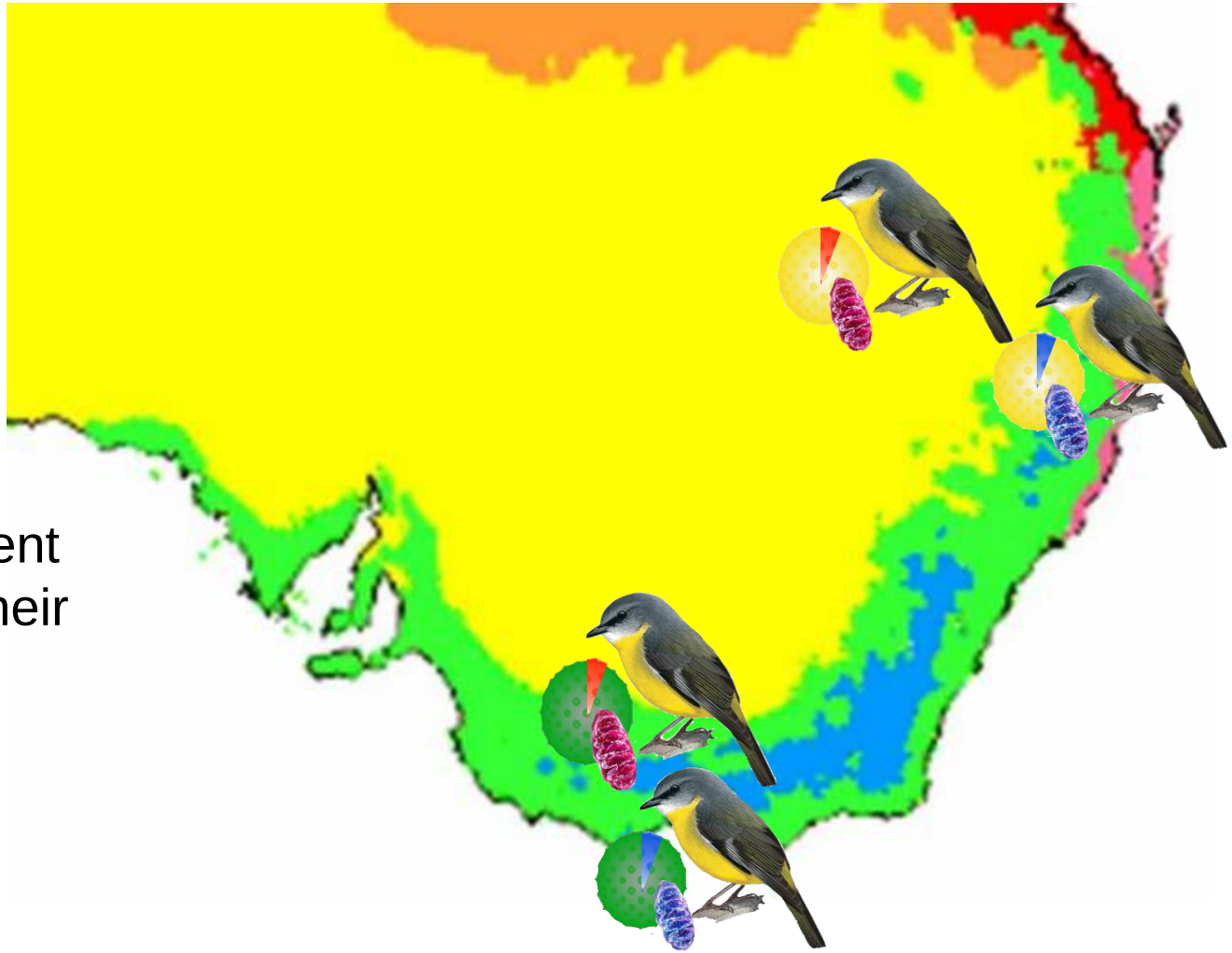
Nuclear mitochondrial gene products from in the 1A island in **YELLOW**

Mitochondrial gene products evidence for positive selection (ND4, ND4L and ND5) in **PURPLE**



Summary

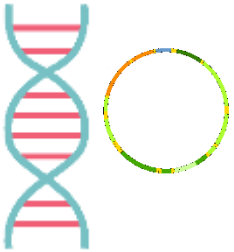
Two distinct mtDNA groups that also have set of putatively co-adapted nuclear genes

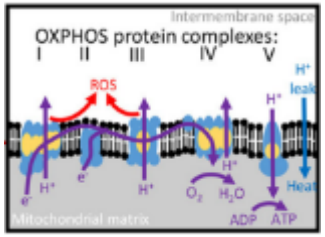


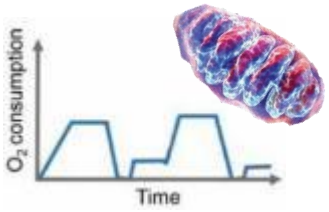
If adaptive, they should have different biology suited to their environments

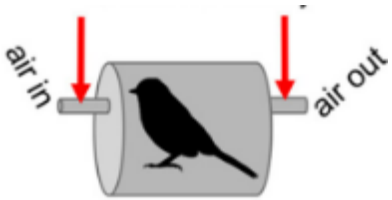
Local adaptation What to look for?

Genomes → OXPHOS → mitochondrial → metabolism









→

Some main items to measure that yield predictions

In a feasible design across an environmental gradient, with lineages side-by-side:

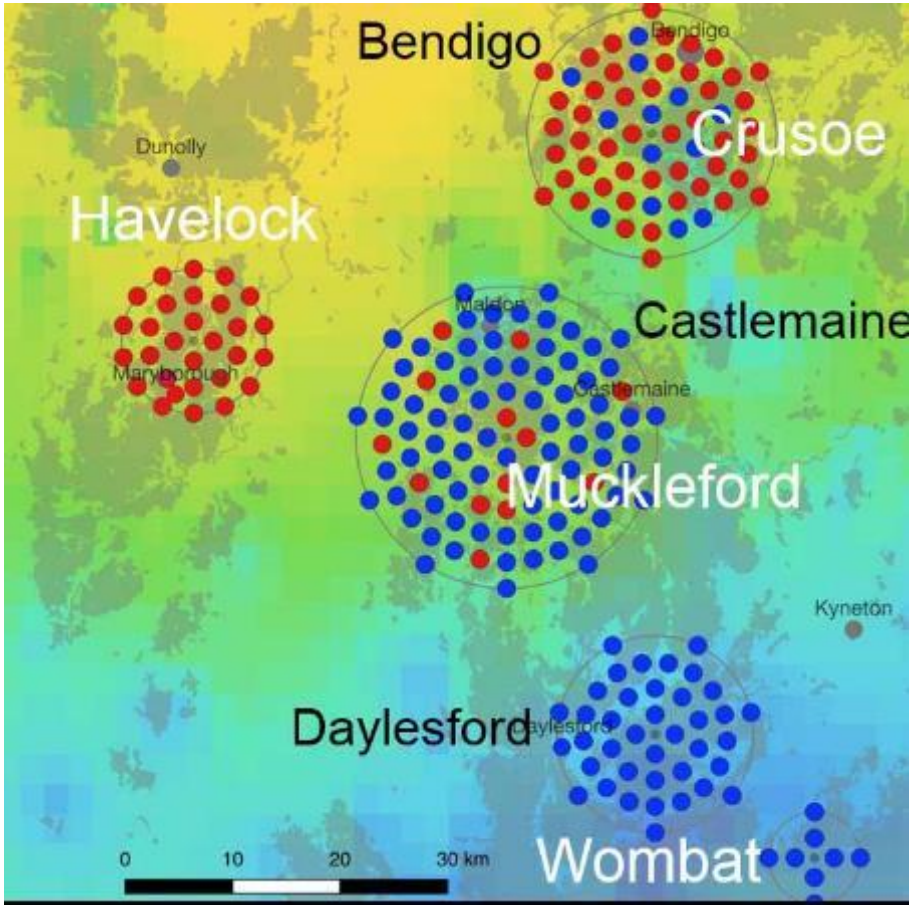
(1) Mitochondrial function

(2) Metabolism

(3) Environments

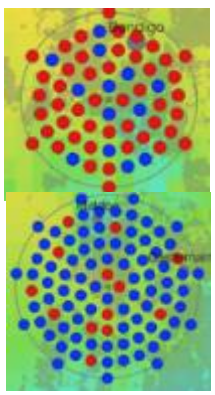
(4) Gene flow between the lineages

(5) Fitness x environment indicators



(The lineages should evolve to recognize and not breed with each other

Do females choose a mate of the same mitolineage?



Hons: Jessica Walters

Parentage analysis to find out:

- How often do mitolineages interbreed?
- Are there sex-specific consequences for their offspring?

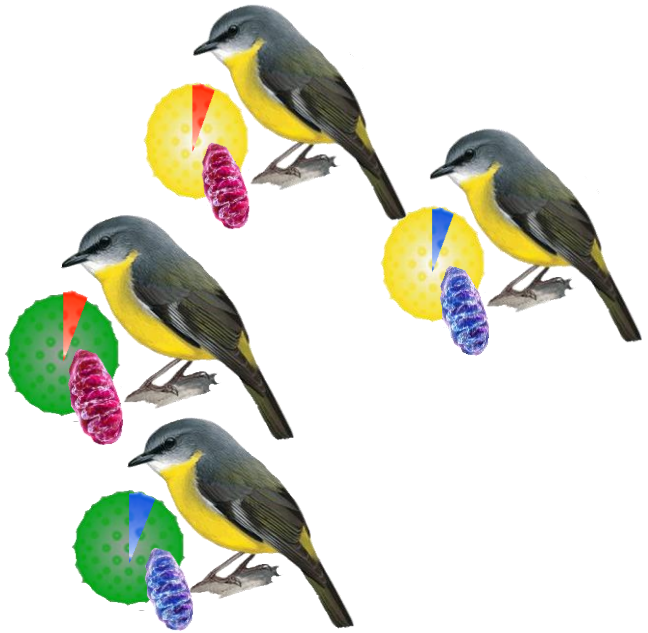
Apparently no preference for mating with own lineage, but…

…admixed parents ♀♂ or ♀♂ have almost no daughters

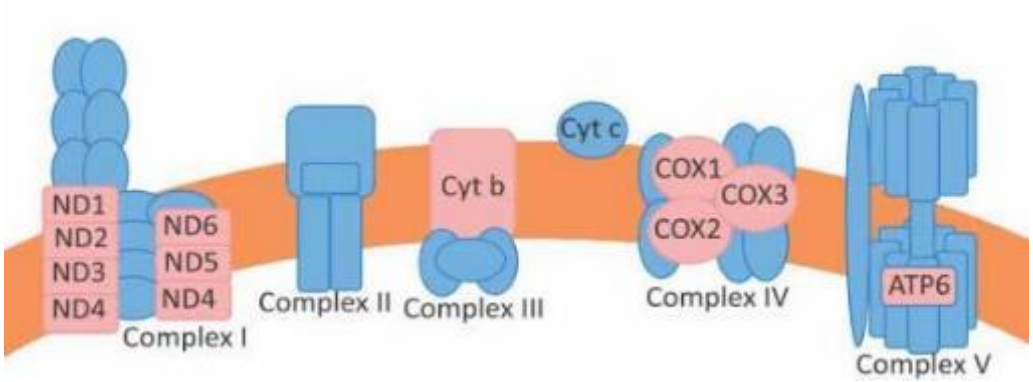
That is, strong selection against hybrid females

Implications

Inland and coastal Eastern yellow robins may be speciating by climate adaptation



through mitonuclear interactions



Hill (2015) Mol. Biol. Evol. 32(8):1917–1927

Next lecture – more on selection/adaptation