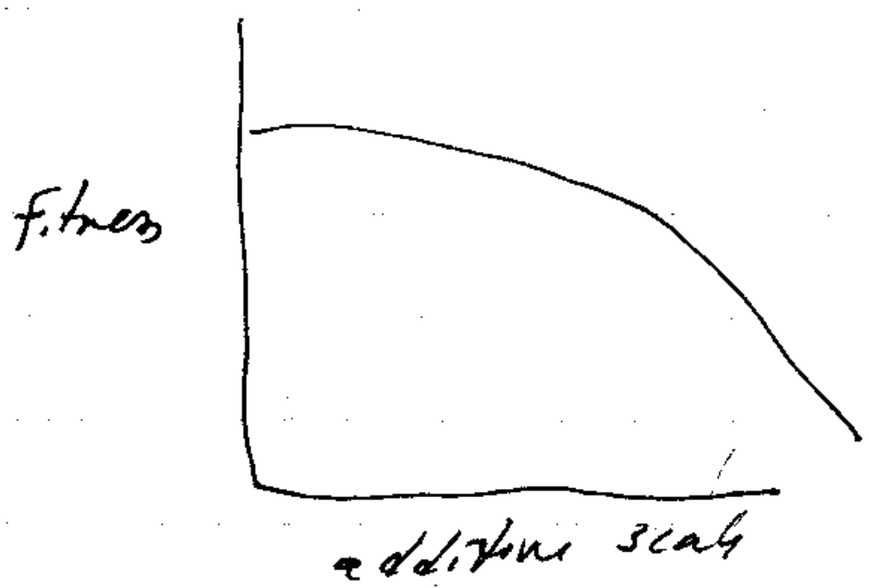


heterozygotes ↓ ↙ dominance parameter

$b_{12} = h_1 b_{11} + h_2 b_{22}$

X

The worse an allele is -- the more recessive it is.
(generally the case in Drosophila)

Asymmetry

Two types of GF

Tm1 — $X_1 Y$ — Tm2 — $X_2 Y$ — — Tf — — X_1, X_2

speciation — $A_1 A_2$ — $A_1 A_2$ — A_1, A_2

over time of speciation first one of then other of then 2 become invariable

- dont always become invariable at same time of genetic separation

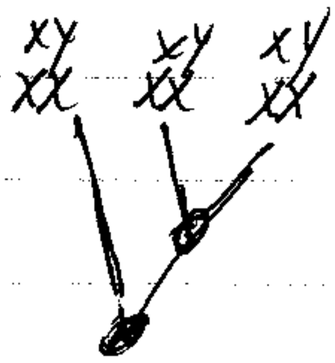
$X_1 * Y$
$A_1 A_2$ dead

$X_1 * X_2$
$A_1 A_2$

contingency recessive
- if $A_1 A_2$ then $X_1 *$ is recessive lethal

- the ratios of Tm/Tf

... w/ longer separation of Tm1, species the closer $T_{m1} + T_{m2}$ should be to each other



- or if $X_1 * Y$
$A_1 A_2$

SYNTHETIC LETHAL

M. Turrelli - Haldane's Rule

Haldane's Rule - heterogametic sex is inviable/ sterile if one is

- Muller's
  - heterogametic have only one allele for all X loci thus it is homozygous for recessive deleterious alleles

- Coyne (Cun.?) - tested
  - Flies

hybrid	X_1Y	X_1X_2 hybrid
	A_1A_2	A_1A_2
	sterile	fertile

- so if due to homo-recessive a ♀ w/ ~~[illegible]~~ X's from same species should be sterile

- but not great test bec. ♂ ♀ have diff. loci determing fertility

- so should do this test w/ viability ... bec. same loci affect viability

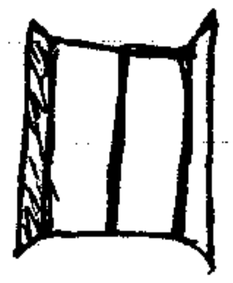
- Why are hybrids inviable?

$$aa \times AA \rightarrow Aa \quad \text{viable}$$
$$BB \times bb \rightarrow Bb$$

$$Aa \times Bb \rightarrow \begin{matrix} A & A \\ B & B \end{matrix}$$ - inviable because A & B don't interact well

(7) ~~Jordan Fox~~ - Freq. Data & selection

Frequencies ⟶ (difficult than to infer) Process



Difficulties

① don't know about # equil.
② don't know about history of selection

*- but says if know phenotypic effect of genotype can do O/E -- but assumes this has been constant

(8) Mark Krote - Sampling & Inference when a gene is Under Selection

Goal - char. type & intensity of selection if any

HCA

- fewer than expected homozygotes (but not many)
- neutrality can frequently be rejected by Watterson test
- assumed to be under balancing selection
- so need NULL SELECTION model

Watterson model

Hugh Salmon – UCB

Finds features that distinguish one sequence from another

s.#	1	2	3	4	5	6
check sequence	A	A	C	B	A	A
others	A	A	B	A	A	A
	A	A	B	A	A	B
	B	A	B	B	A	B
	C	A	A	A	B	B
	B	A	A	A	B	A

- can be used this degeneracy?

ART WEISS - U C Irvine

Genetics of Defense in Depth

- the fitness curve for a resistance allele depends on the tolerance

- Goldenrod & beetly

Susan Edmonds - UCSD ... Urchin Genetic Structure

- sampling diff. ages important
- multiple markers important

S. Franciscanus

S. purpuratus

- in some pops. adults & recruits have sl. diff. isozyme pattern
- allozyme - significant Heterozy,
- and - low Hetero

Karen Marchetti - why do ♂ have multiple song chars

Warblers ♂
- brightly ♦ patches
- song

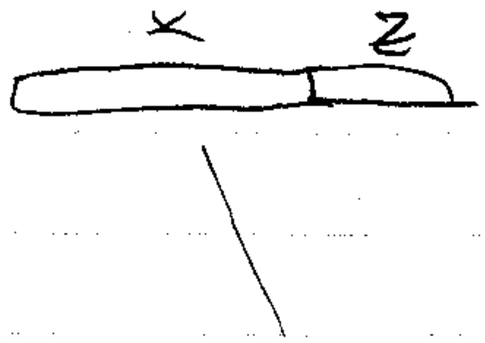
why multiple?
① ♀ choice may differ from ♂ compet.
② ♀ may choose many
③ diff. chars may reflect diff quality
④ variable ♀ choices
⑤ diff signal content

measurements

manipulation of color patch size

IS COLOR PATCH SIZE CONSTANT?

WHAT ABOUT ♀ SEEING THROUGH PAINT?



Grant Pogson - Comparing Protein & DNA Polymorphism

Comparing DNA & protein
- intra-locus
  - e.g. Adh (MacDonald & Kreitman)
- inter-locus
  - e.g. Karl & Avise (1992)
  - argue that diff in pattern of allozyme vs. DNA is due to selection

Uniformity of process

Drift	Equal ??	Mutation?
Migration	Equal	
Inbreeding	Equal	
Selection	Variable	
Mutation?		

Markers
- transcribed (use cDNA RFLPs)
- mutation rate $10^{-6} - 10^{-7}$
- BUT THIS IS BIASED TOWARDS ABUNDANT GENES

Heterozygotes

Agents

Overdom.
Multi-locus dom
Incl Alleles
Impacting

Markers

Assoc. overdom.
Inbreeding
Somatic aneuploids

Is gen. flow important

① gen flow should affect all loci equally

② so polymorphism should be same at all loci

HOW SELECT FOR RARE CONAS

MUTATION?

CALPEG 1994

Trevor Price

see Felsenstein 1985 {
- w/ biological correlations, it is generally assumed that phylogeny must be taken into account to determin significance of association

- unless of course selection is very effective and quick -- that is all things are optimized

- another problem is if another character affects the trait - only one of only

- Felsenstein method corrects for phylogeny

BUT THESE ARE STILL VERY CLOSE RELATIVES
- but Trevor says nothing affects only one variable (leg, brain & body size both affected by same selection)

- SO CONTRASTS (FELSENSTEIN) ASSUMES PHYLOGENY IS TOO IMPORTANT