National Academy of Sciences

Colloquium

On

"Tempo and Mode in Evolution"

Revised Program

January 27-29, 1994

Arnold and Mabel Beckman Center

100 Academy Drive, Irvine, CA 92715

Name Badges will be required for all functions.
(Badges will be distributed at the desk in the Atrium of the Beckman Center)

Thursday, January 27

7:30 - 10:00 pm. Welcome Reception.

Friday, January 28

7:30 am. Buffet Breakfast in Refectory.

9:00 am. - 1:00 pm. **SESSION I. Early Evolution**

9:00	*Introduction and Chairperson*	*Walter M. Fitch (UC Irvine)*
9:10	**Phylogenies from Function: A Possible History of Replication**	*Nancy Maizels (Yale)*
10:00	**The Root of Life**	*Ford Doolittle (Dalhousie)*
10:50	**Break**	
11:10	**Proterozoic Eukaryotes: Evidence for Accelerating Rates of Evolution**	*Andrew Knoll (Harvard)*
12:00	**The Earliest Life**	*William Schopf (UC Los Angeles)*

1:00 - 2:00 pm. Lunch in Refectory.

2:00 - 6:00 pm. **SESSION II. Microevolution**

	Chairperson	*John C. Avise (U of Georgia)*
2:00	**Dynamics of Adaptation and Divergence in Bacterial Populations**	*Richard Lenski (Michigan State U)*
2:50	**Genome Organization**	*Daniel Hartl (Harvard)*
3:40	**Break**	
4:00	**DNA Polymorphism: Selection and Drift**	*Richard R. Hudson (UC Irvine)*
4:50	**Patterns of Chloroplast DNA Evolution**	*Michael Clegg (UC Riverside)*

Friday Evening

6:00 pm. Cocktails in the Atrium.
7:00 pm. Dinner in the Atrium.

8:15 pm. *Introduction: James W. Valentine (UC Berkeley)*
Banquet Lecture: Stephen Jay Gould (Harvard)
Pattern, Rate and Mode of Morphological Evolution

Saturday, January 29

7:00 am. Buffet Breakfast in Refectory.

8:30 am. - 12:30 pm. **SESSION III. Macroevolution**

	Chairperson	*Wyatt W. Anderson (U Georgia)*
8:30	**On the Origin of Phyla**	*James W. Valentine (Berkeley)*
9:20	**Plants, Biomechanics, and the Invasion of Land**	*Karl Niklas (Cornell)*
10:10	Break	
10:30	**Tempo and Mode in Human Evolution**	*Henry McHenry (UC Davis)*
11:20	**The Role of Extinction in Evolution**	*David M. Raup (U Chicago)*

12:30 - 1:30 pm. Lunch in Refectory.

1:30 - 5:30 pm. **SESSION IV. Patterns and Rates of Molecular Evolution**

	Chairperson	*Francisco J. Ayala (UC Irvine)*
1:30	**Molecular Biogeography**	*John C. Avise (Georgia)*
2:20	**Molecular Genetics of Speciation**	*Francisco J. Ayala (UC Irvine)*
3:10	Break	
3:30	**Molecular Clocks**	*Walter M. Fitch (UC Irvine)*
4:20	**Molecular Analysis of a Chromosomal Phylogeny in Drosophila**	*Wyatt W. Anderson (U Georgia)*

Van Shuttle Service between Irvine Hyatt and Beckman Center

(Vans will be waiting at the Main Lobby Entrance to the hotel).

Thursday

Hyatt to Beckman Center: Vans will leave every 15 minutes from 7:00pm to 8:15pm
Beckman Center to Hyatt: Vans will leave every 15 minutes from 8:30pm to 10:00pm

Friday

Hyatt to Beckman Center: Vans will leave every 15 minutes from 7:00am to 8:45am
Beckman Center to Hyatt: Vans will leave every 15 minutes from 9:00pm to 10:15pm

Saturday

Hyatt to Beckman Center: Vans will leave every 15 minutes from 6:30am to 8:15am
Beckman Center to Airport/Hyatt: Vans will leave every 15 minutes from 5:00pm to 6:15pm

Driving Directions to the Beckman Center

From Orange County Airport. Take MacArthur South; right at University Avenue exit; right at second light (California Ave.); first right at Academy Drive.

From Irvine Hyatt. Take Union; left on Main; left on Jamboree; left on MacArthur; right at University exit; right at second light (California Ave.); first right at Academy Drive.

From LAX. 405 FWY south to 73 FWY; right at University exit; right at second light (California Ave.); first right at Academy Drive.

From San Diego. 5 FWY to 405 FWY; Jamboree exit; left on Jamboree; left on MacArthur; right at University exit; right at second light (California Ave.); first right at Academy Drive.

From Riverside. 91 FWY to 55 FWY to 73 FWY; right at University exit; right at second light (California Ave.); first right at Academy Drive.

Beckman Center: **Telephone (714) 721-2200; Fax (714) 721-2288**
Irvine Hyatt: **Telephone (714) 975-1234; Fax (714) 852-1574**

Organizing Committee

Walter M. Fitch, co-chair *Francisco J. Ayala, co-chair*
Wyatt W. Anderson *John C. Avise* *James W. Valentine*

I) Fitch Intro
- GG Simpson - Tempo & Mode in Evolution

II) Nancy Marzels

Lynn Margulis book - its a good book if you only look at the pictures.

- All cells share essentially the same biochemistry
-
- tRNA & replication
- RNA world
  - catalytic RNA - suggests a solution to chicken & egg problem (Cech Altman Pace)

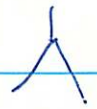
smallest catalytic unit { UUU / GAAACp } Kazakov & Altman

- possible problem - RNA doesn't show up in Miller-Urey experiments

* - suggests these are conserved because of the # of interactions

- replication
  - problems ① loss of ends ② specificity
  - solution to ① - telomeres - circular genome - circularize for replication
    T4, - terminal redundancy - primer protein

like tRNA



phage Qβ –

Qβ Replicase

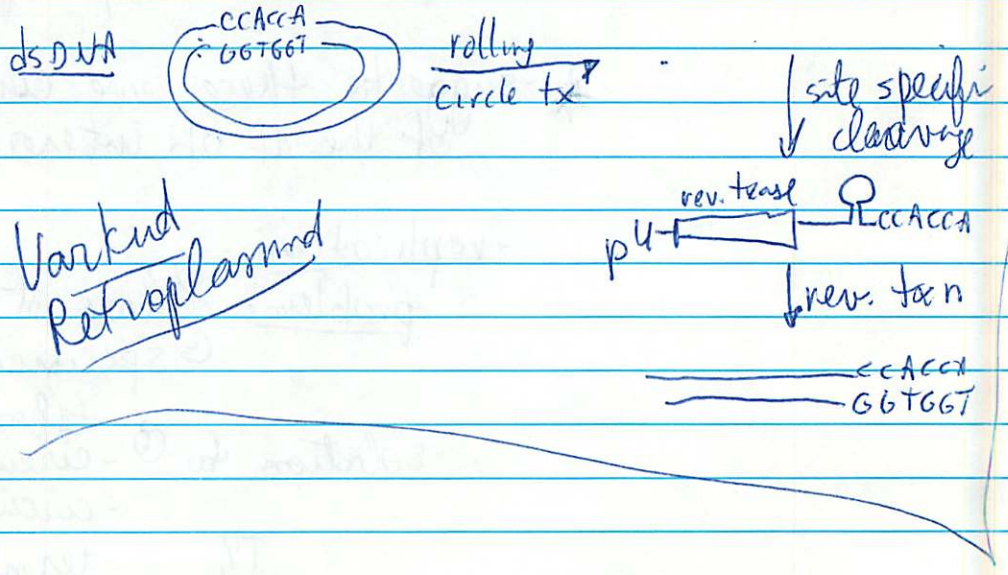
phage pol – (II)(Tu)
ribosome (S1)(Ts) } Elongation Factors

Suggests that some Viruses are v.v. old

- Genomic Tag Model
  - 3' terminal tRNA-like structures substrates for replicases
  - present in lots of viral genomes

- Suggests that tRNAs have two domains

- Allambourity - nt plasmids in N. crassa



Varkud Retroplasmid

Retroviruses

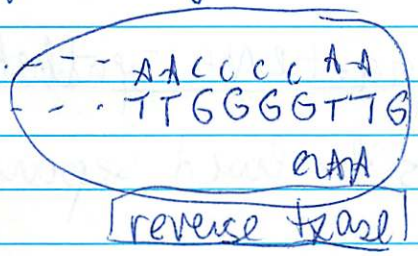
RNA — tRNA primes ⟶ DNA

Cauliflower mosaic virus

tRNA primer to make cDNA

Telomerase

- RNA component is a built in template for adding GGGGTT to end



Polymerases

How did tRNA get into protein synthesis

- a charged tRNA (say with a basic aa.) could better interact w/ (-) RNA

- suggest that early prot. synthesis could have been to better make such changes

- RNAs can recognize aa. specifically

Translation
- tons of factors
- suggests it must have arisen stepwise

replication
↓
tRNA
↓
aa tRNA synt.
↓
ribosome

1) modern tRNA synthetases are diverse in size & structure.
2) aa. does not interact w/ cognate anticodon

Two types of aa-tRNA synthetases
- suggests evolved separately

Summary
① tRNA early in replication

WF Doolittle - Root of Life

Reconstructing Pre-Progenote Evolution
1) molecular fossils
2) cellular fossils (current)
3) comparative molecular biology

cenancestor: the most recent common ancestor of all living things

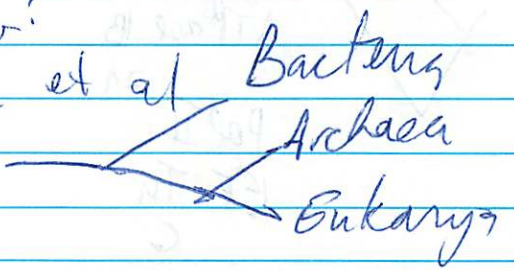
was the cenancestor a progenote

Progenote Concept

- Woese - suggested cenancestor was progenote

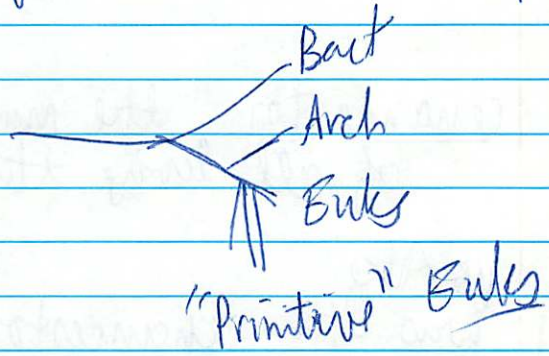
Exon theory of genes apparently still endorsed only by Wally Gilbert

Rooting - how?
Iwaabe et al



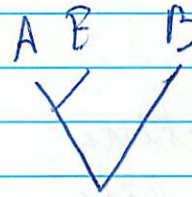
Map of genome

- similar operons
- suggests progenote was ink so simple



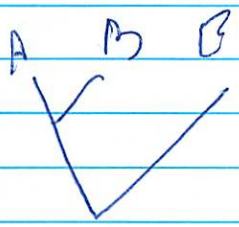
But - problems w/ rooting

i) EF hard to align



Argmosucc.
ATPase B
2A
Pol II
EF Tu
G
Hmg CoA
Ribo L2
L23
RNA pol B

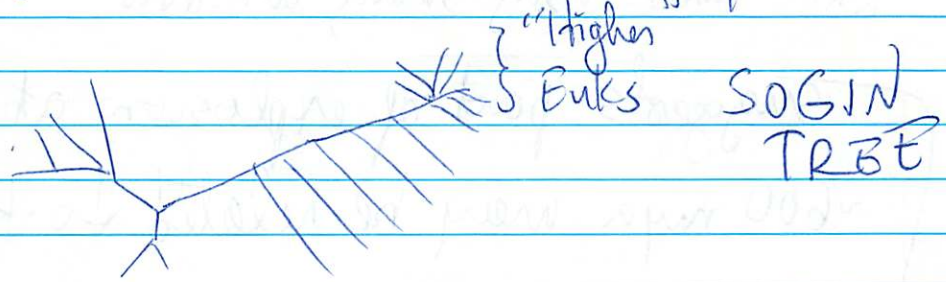
Enolase
FeMnSOD
PGK
GAPDH
MDH
Glut syn
Trp B
II C
GDH

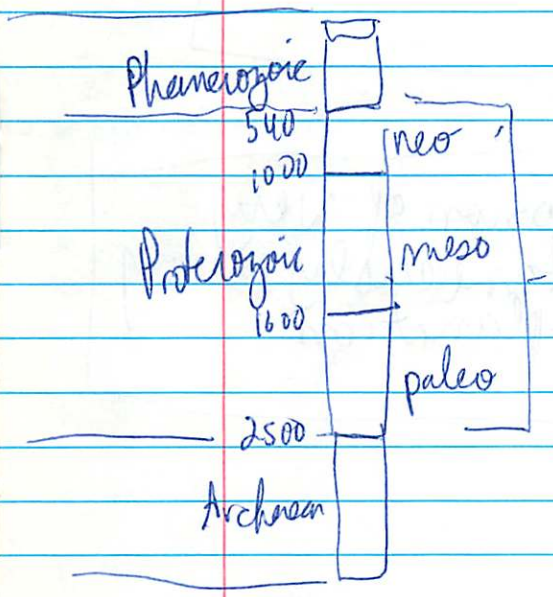


Citrate syn
Glut syn I
Isoleucyl tRNA synthetases
Gyrase B
Hsp 70
Trp A
E

GDH
Aspartate aminotransferase

Andy Knoll - Proterozoic Eukaryotes - Harvard





Fossil Eukaryotes

- ~17-1800 mya & before
- 1st 5-600 mya after this fossil diversity is low
- 900-1000 mya - 1st real morphological diversity of unicellular forms
- 1000-1100 - multicellular show up
- most of these forms disappear ~600 mya

~600 mya - new more morphologically complex forms show up

- most of these are gone by ~560 mya when animals show up

what about using sliding window?

suggests part of explosion at ~600 mya may be related to the origin of meiosis

also suggests that explosion of very distinct groups simultaneously may have an ecosystem explanation

Bill Schopf - UCLA

Emphasizes importance of extinction

Claims two separate "regions" of evolution of life

Tachytelic - Fast Morphological Change

Bradytelic - Slow " "

Hypobradytelic - " "

Cyanobacteria

- suggests they have been Hypobradytelic

- Problems
  1. morphology may not reflect internal
  2. not many fossils
  3. not many morphological characters
  4. not always match between rRNA & morphology

- Results up to 3.5 bya
  - fossils of certain types virtually identical to modern ones

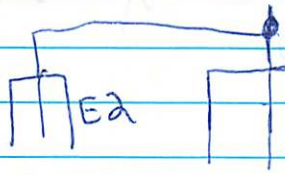
How explain - why so slow

1. strictly asexual
2. ecological generalists - but used groups not species
3. difficult to exterminate

No mutation
Don't evolve 'cause they can't evolve

Richard Lenski - [redacted] - Mich. St.

Dynamics of Adaptation and Divergence in Bacterial Populations

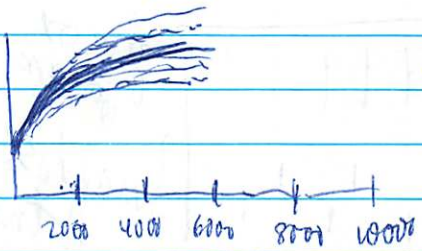


- same environment
- multiple replicates

E. coli

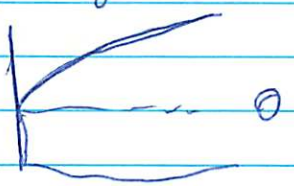
- strain they use is rec⁻
- all mutations are new
- serial dilution

Size of

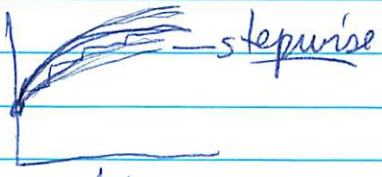


← all 12 generations do similar things

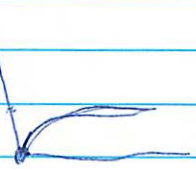
among pop SD for cell vol.



relative fitness

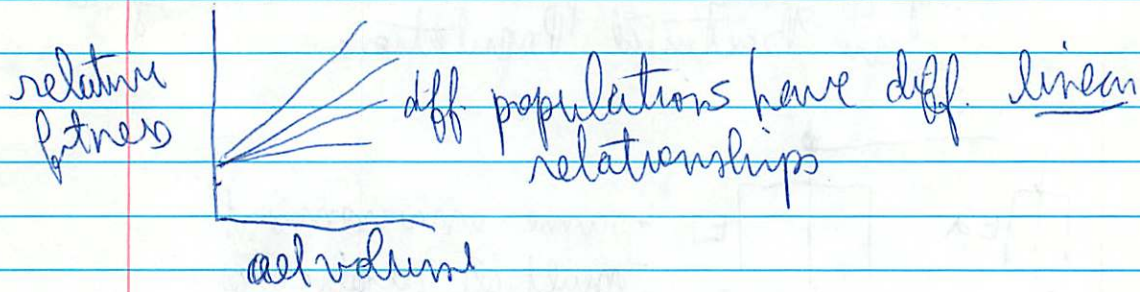


variation

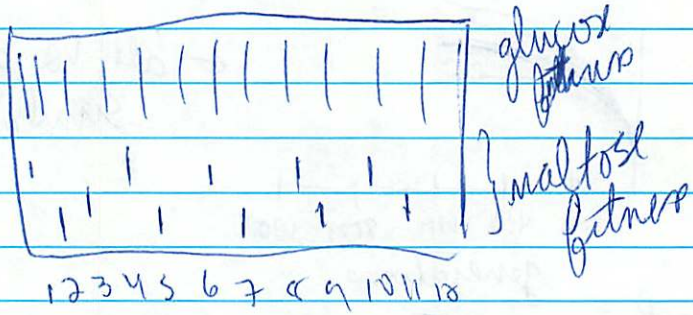


Adaptive Landscape

Covariance of Fitness & Morphology



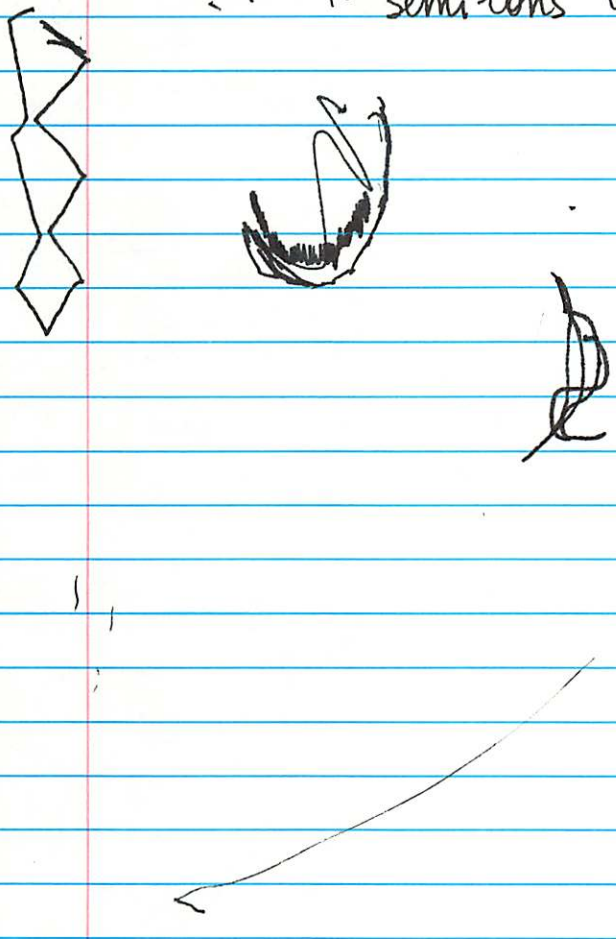
Thinks diff. orders of mutations are important

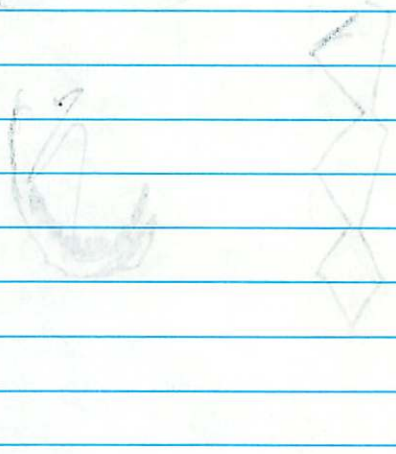


Dan Hartl - Genome Organization - Harvard

Polytene Chromosomes

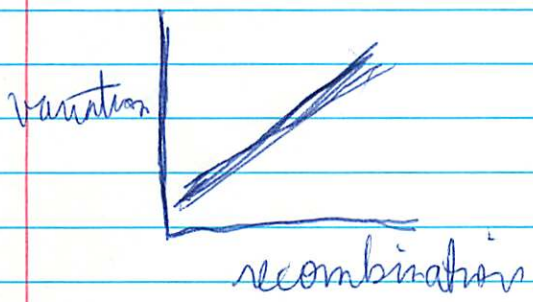
- patterns conserved w/in species
- " " semi-cons among closely related speeils





Hudson - UC Irvine

Recombination



Explanations

① mutation rate & recomb. associated - says no rec. betw. species are not high variation

② hitchhiking

- variation deep in regions of low recomb. because area of "sweep" is higher

③ background selection

- region of genome w/ tight linkage in which deleterious mutation rate is high should have low variation.

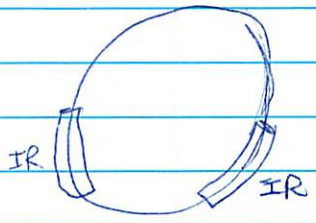
Michael Clegg - Chloroplast DNA - UC Riverside

Plants
- nuclear
- mitochondrial
- chloroplast - origin ~1 bya
  - land plants 500 mya
  - flowering plants 200 mya

Chloroplast Genome
- ~80 orf
- all tRNAs & rRNAs

Liverwort
Rice
Black pine

Tobacco complete sequence
- operons
- similar order to bacteria
- some group II introns
- IR

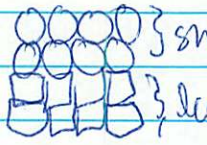


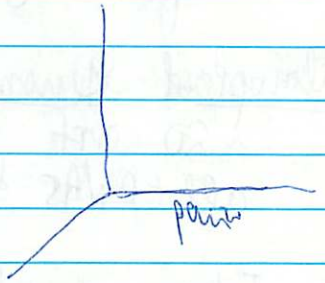
	Liverwort	Tobacco	Rice
tRNA	32	30	30
rRNA	4	4	4
ORFs	83	~30	~80

∴ General chloroplast genetic evolution appears to be conservative

what about w/ species or individual variation

Rubisco





Gould - Harvard

Many Darwinisms
- e.g. uniformitarianism

- paleontologists are there for documenting evolutionary history

Simpson's T & M in E 1944

- says 1st book to address process & mechanisms not just evolution as an entity

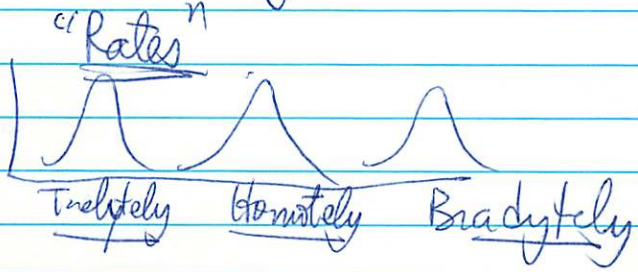
- only one picture of an organism

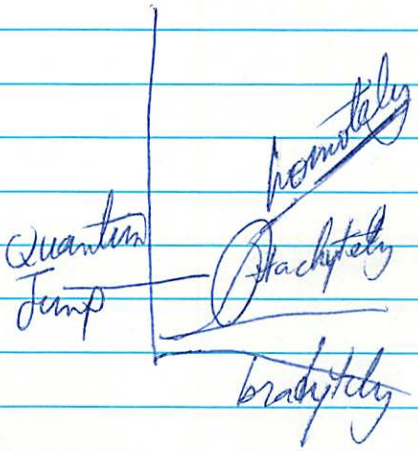
- study of Tempo quantitatively

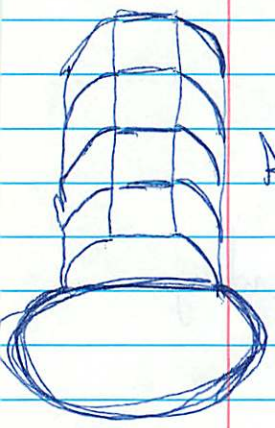
- can use Tempo to infer mode

3 Modes
1. speciation
2. quantum evolution
3. phyletic evolution

"Rates"

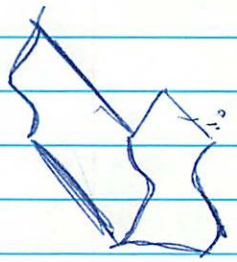






Levels of selection

Agrees w/ - DH
- individual
- group
- species
- Dakk



Henry McHenry UCDavis

Simpson & Human Evolution

Human Paleospecies

5 Australopithicus species

- including A. aethiopicus from 1 skull

Homo

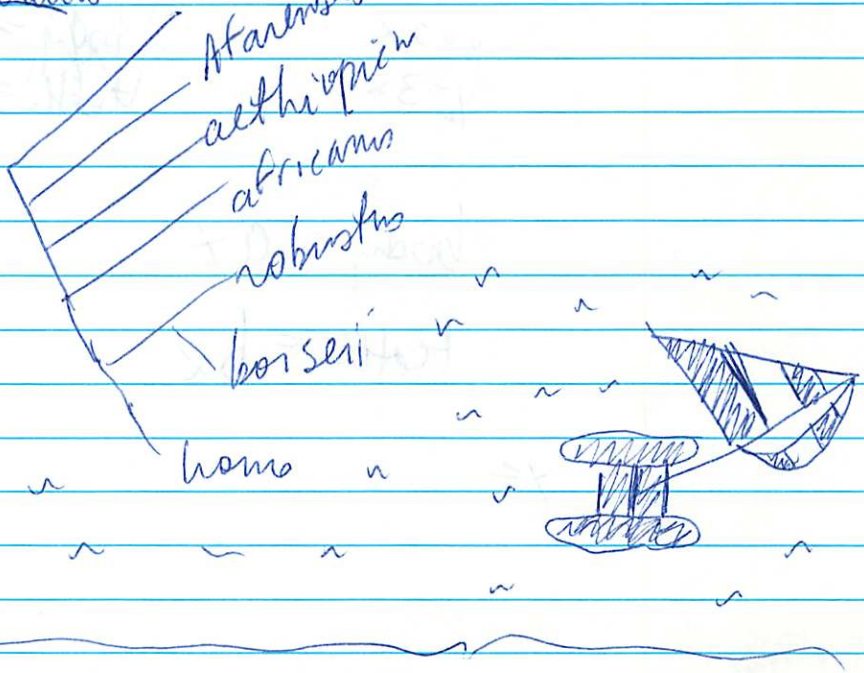
Homo habilis

Homo erectus - 1st ~ 1.8 mya - 0.25 mya

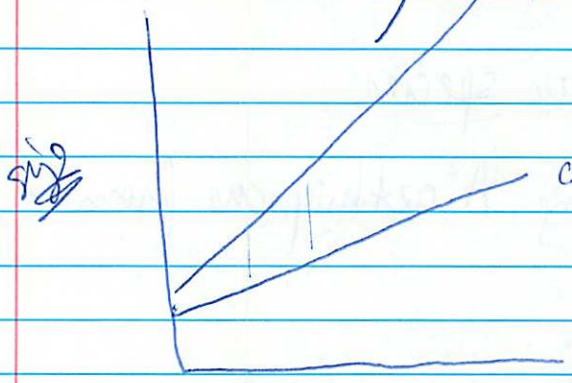
H. sapiens - 0.4 mya

70+ Cranial traits out

Cladogram



If a trait is variable and a new mutation shows up and spreads →



$y = mx + b$

$y_1 = 2x$

$y_2 = 3x$

body = 3x
teeth = 2x

body = ax

teeth = bx

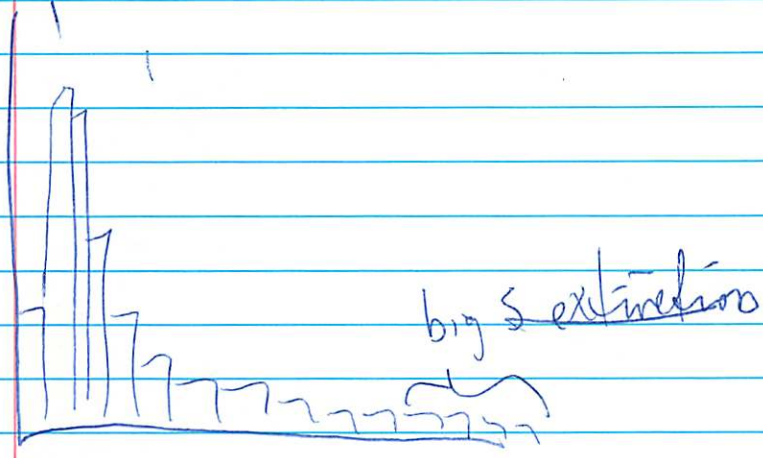
teeth/body

b/a

$y =$

David Ramp (being read by

frequency



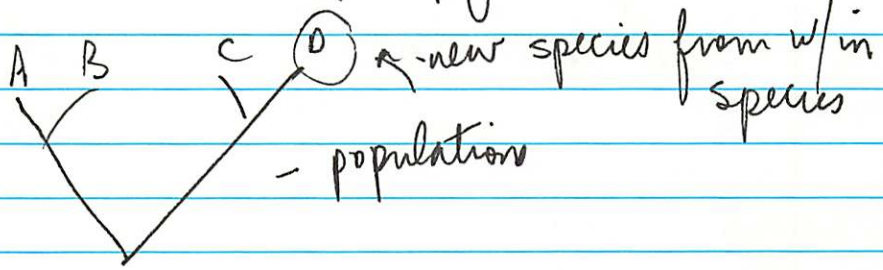
% species killed in X yrs

- says clustering cannot be explained by random phenomena

<- what about wave height phenomena >

John Avise

Speciation
- species themselves are paraphyletic



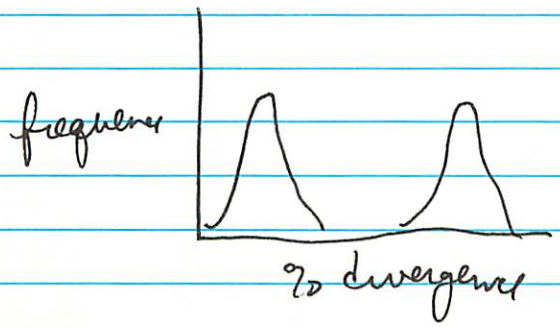
Intraspecific evolution

Coalescence

~~[illegible]~~ Pocket Gopher = 1st study

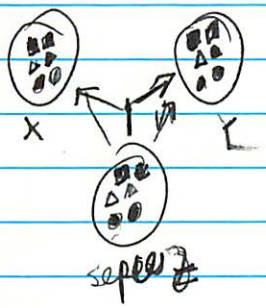
MA
- overlay phylogenies on geographic map
- relatively physically proximal

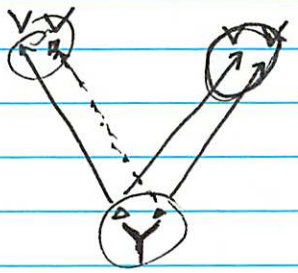
Snow Geese
- ♀ return to where born
- ♂ meet ♀ in winter in US & return w/ ♀



1) current biology doesn't tell much about genetic relatedness
2) current genetics doesn't tell much about biology

Francisco Ayala - Molecular Genetics of Speciation





with genes duplicated prior to divergence - gene phylogenetic split predates species split

- e.g MHC

what affects - transmission of polymorphism
t = time to fixation to new allele
N - effective pop. size
S - selection effect

IF allele is effectively neutral ($Ns < 1$)
$t = 4N$

- Other crop-species alleles

Bottleneck?

Fitch: Molecular Clocks

Definition:
- ~~for a replacement~~
- for a molecular clock the events (either replacements or substitutions) must be regular

Problem - don't observe replacements just comparisons

Solution
→ Z & P 1962 ① assume replacements = differences
② but not true

→ Margoliash & Smith 1965
- $r = -n \ln(1 - d/n)$
- assumes infinite # of sites

invariable - cannot w/o loss of fcn
vs
unvaried - does not

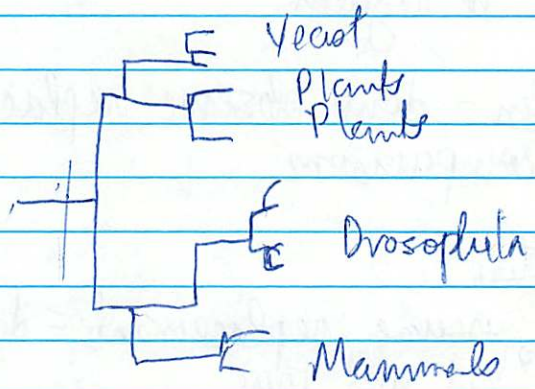
Jukes & Canton 1969
- how many sites possible
- $r = -19/20\, n \ln\left[1 - (20/19)(d/n)\right]$ a.a.'s
- $r = -3/4\, n \ln\left[1 - (4/3)(d/n)\right]$ nucleotides

- but what about invariable sites

Fitch & Margoliash 1967

- may be many invariable positions

SOD



Conditionally invariable positions
Sequence dependent invariable

SOD
Ayala - # aa subs not linear w/ time

Simulation of Covariation

Wyatt Anderson

Inversions

- Have a parsimony network of inversions
- Amyfast - on inversion