

## Cytochrome C phylogeny



## Recent evolution of influenza virus



Protein differences versus separation time
(Dickerson 1971)


Constant rates of evolution.

Rate differs among proteins.

## Outline

- The pattern in molecular data
- Hypothesis of neutral evolution
- Molecular clock hypothesis
- Why neutral evolution in linear
- Generation time

The neutral theory of molecular evolution

1. Most mutations are harmful and are removed by selection.
2. Selectively neutral mutations are not removed.
3. Most molecular variation within species is neutral.
4. Same is true of differences between species.

Evolution is fastest in the parts of the genome that matter least.
"those amino-acids which are critical to the biological function of a molecule should be strongly conserved by natural selection. Other amino-acids may have general properties which make their presence desirable but not indispensable, and these residues should exhibit a lesser degree of evolutionary restraint. Other amino-aids may simply take up space." (Doolittle and Blombäck 1964)


Why clumping of invariant positions?


- Proteins fold
- Adjacent positions are close together on folded protein.
- Conserved regions bind with other molecules.

Some parts of Cyt-C protein vary more than others

- Some positions never change.
- Invariant positions not scattered at random.
- Hypothesis: invariant positions are functionally important.

Introns evolve faster than exons
(Fairbanks 2009)

Human sequence
GGCTTCTTCTACACACCCAAGACCCGCCGGGAGGCAGAGGACCTGCAGGGTGAGCCAACTGCCCATTGCTGCCCCTGGCCGCCCCCAGCCACCCCCTGCTCC GGCTTCTFCTACACACCCAAGACCCGCCGGGAGGCAGAGGACCTGCAGGGTGAGCCAACTGCCCATTGCTGCCCCIGGCCGC
$\begin{aligned} & \text { GGCTTCTTCTACACGCCCAAGGCCCGTCGGGAGGCGGAGAACCCTCAGGGTGAGCCGAGGGGGCGTCCCGGGAGCGGTCGGGGGAGTTTTTAAAGAGGAAAT } \\ & \text { Pig sequence }\end{aligned}$
$\longleftrightarrow$ exon intron

1. Verticals link identical sites in pig and human INS genes.
2. More identity in exon (at left) than in intron (at right).
3. Identity in splice junction-1st 6 sites of intron.

Introns were not discovered until 1977-long after the theory of functional constraint.

Pseudogenes evolve faster than functional genes


The genetic code (DNA version)

| First <br> Position | Second Position |  |  |  | Third <br> Position |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :--- | :---: |
| A | A | G | T | C |  |  |  |
|  | Phe | Ser | Tyr | Cys | A | (adenine) |  |
|  | Phe | Ser | Tyr | Cys | G | (guanine) |  |
|  | Leu | Ser | STOP | STOP | T | (thymine) |  |
|  | Leu | Ser | Stop | Trp | C | (cytosine) |  |

Few 1st-position changes are synonymous.

Weaker constraint in 2nd position.

Weakest in 3rd-position.
atg.tcg.ttt.act.ttg.acc.aac.aag.aac.gtg.att.ttc.gtt.gcc.ggt.ctg.gga.ggc.att.ggt
Met.Ser.Phe.Thr.Leu.Thr.Asn.Lys.Asn.Val.Ile.Phe.Val.Ala.Gly.Leu.Gly.Gly.Ile.Gly
61
tg.gac.acc.agc.aag.gag.ctg.ctc.aag.cgc.gat.ctg.aag.aac.ctg.gtg.atc.ctc.gac.cgc
att.gag.aac.ccg.gct.gcc.att.gcc.gag.ctg.aag.gca.atc.aat.cca.aag.gtg.acc.gtc.acc
181 . 1 Asn.Pro.Ala.Ala.Ile.Ala.Glu.Leu.Lys.Ala.Ile.Asn.Pro.Lys.Val.Thr. Val.Thr
tr.tac.ccc.tat.gat.gtg.acc.gtg.ccc.att.gcc.gag.acc.acc.aag.ctg.ctg.aag.acc.atc
Phe.Tyr.Pro.Tyr.Asp.Val.Thr.Val.Pro.Ile.Ala.Glu.Thr.Thr.Lys.Leu.Leu.Lys.Thr.Ile
${ }^{241}$ ttc.gcc.cag.ctg.aag.acc.gtc.gat.gtc.ctg.atc.aac.gga.gct.ggt.atc.ctg.gac.gat.cac
Phe.Ala.Gln.Leu.Lys.Thr.Val.Asp.Val.Leu.He.Asn.Gly.Ala.Gly.Ile.Leu.Asp.Asp.His
ag.atc.gag.cgc.acc.att.gcc.gtc.aac.tac.act.ggc.ctg.gtc.aac.acc.acg.acg.gcc.att
${ }^{\text {Gln. Ile.Glu.Arg.Thr. Ile.Ala.Val.Asn.Tyr.Thr.Gly.Leu.Val.Asn.Thr.Thr.Thr.Ala.Ile }}$
${ }_{\text {ctg.gac.ttc.tgg.gac.aag.cgc.aag.ggc.ggt.ccc.ggt.ggt.atc.atc.tgc.aac.att.gga.tcc }}{ }^{\text {t. }}$
eu.Asp.Phe.Trp.Asp.Lys.Arg.Lys.Gly.Gly.Pro.Gly.Gly.Ile.Ile.Cys.Asn.Ile.Gly.Ser
${ }_{\text {gtc.act.gga.ttc.aat.gcc.atc.tac.cag.gtg.cec.gtc.tac.tce.ggc.acc.aag.gcc.gcc.gtg }}$
Val.Thr.Gly.Phe.Asn.Ala.Ile.Tyr.Gln.Val.Pro.Val.Tyr.Ser.Gly.Thr.Lys.Ala.Ala.Val
${ }^{\text {gtc. aac.ttc.acc.agc.tcc.ctg.gcg.aaa.ctg.gcc.ccc.att.acc. ggc.gtg.acc.gct.tac.acc }} \stackrel{\mathrm{c}}{\mathrm{t}}$

541 c
Val.Asn.Pro.Gly.Ile.Thr.Arg.Thr.Thr.Leu.Val.His.Lys.Phe.Asn.Ser.Trp.Leu.Asp.Val
601 t c c
gag.ccc.cag.gtt.gct.gag.aag.ctc.ctg.gct.cat.ccc.acc.cag.cca.tcg.ttg.gcc.tgc.gcc
Glu.Pro.Gln.Val.Ala.Glu.Lys.Leu.Leu.Ala.His.Pro.Thr.Gln.Pro.Ser.Leu.Ala.Cys.Ala
gag.aac.ttc.gtc.aag.gct.atc.gag.ctg.aac.cag.aac.gga.gcc.atc.tgg.aaa.ctg.gac.ctg
gag.aac.ttc.gtc.aag.gct.atc.gag.ctg.aac.cag.aac.gga.gcc.atc.tgg.aaa.ctg.gac.ctg
Glu.Asn.Phe.Val.Lys.Ala.Ile.Glu.Leu.Asn.Gln.Asn.Gly.Ala.Ile.Trp.Lys.Leu.Asp.Leu
ggc.acc.ctg.gag.gec.atc.cag.tgg.acc.aag.cac.tgg.gac.tcc.ggc.atc.
Gly.Thr.Leu.Glu.Ala.Ile.Gln.Trp.Thr.Lys.His.Trp.Asp.Ser.Gly.Ile

## Genetic drift

Variant forms of a gene or a nucleotide site are called "alleles."
The "frequency" of an allele is its fraction $w / i$ the population.

Neutral alleles increase or decrease in frequency just by chance.
This is called "genetic drift."
Occasionally, one drifts to extinction and is lost.
Eventually, all are lost but one. The remaining allele has frequency $100 \%$ and is said to be "fixed" in the population.

If the surviving allele arose from a single mutation, then at this genetic locus, all copies of the gene descend from that ancestral mutation.

## Why neutral evolution is linear

In a population of size $N$ and mutation rate $u$, there are $2 N u$ new mutations each generation.

A fraction $1 / 2 \mathrm{~N}$ of these drifts to fixation.
Resulting rate: $2 N u \times \frac{1}{2 N}=u$.
Constant mutation rate $\Rightarrow$ const rate of molecular evolution.

## Outline

ADH in $D$. melanogaster

Nucleotides \& amino acids.

Most variants in 3rd position.

Only 1 (pos 578)
changes amino acid

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## Fixation probability of a new neutral mutation

What is the probability that a brand new neutral mutation, which exists only in a single copy, will eventually become $100 \%$ of the population?

In a population of size $N$, there are $2 N$ gene copies, one of which is our new mutant. Eventually, all but 1 will be lost.

If they are selectively neutral, each gene copy has the same chance $(1 / 2 N)$ of fixation.

The fixation probability of a neutral mutation is $1 / 2 N$.

## Synonymous versus nonsynonymous clocks



Within each protein, synonymous (S) sites evolve faster than non-synonymous ( N ) sites.

Evolution is linear in either case.

| Outline | The neutral theory again |
| :--- | :--- |

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Denton (1985, p. 287) argues this isn't so
"Since the rodent order diverged from the primate, it is practically certain that the line leading to mouse has undergone nearly 100 times as many reproductive cycles as that leading to man. If mutation rates are practically constant per generation how then could drift have generated equal rates of genetic divergence in mice and men?"
$27 / 30$
The body-size effect is not as large as Denton thought

- Most mutations happen during cell division. The mutation rate per generation depends on the number of cell divisions per generation. This number is larger for large animals than for small ones.
- Large animals have small populations; this increases fraction of mutations that are effectively neutral.
- For both reasons, the generation-time effect is smaller than Denton assumed.
- Clearly detectable only in 1980s.

Under strictly neutral evolution, the rate of evolution equals the mutation rate, $u$.

If $u$ were constant per generation, then the rate of evolution should scale with generation time. Large animals have long generation times and should evolve slowly.

He's right—large animals evolve more slowly

(Martin \& Palumbi 1993)
The neutral theory again
$26 / 30$

## Summary

1. Molecular differences accumulate at roughly constant rate.
2. Evolution is fastest where selective constraint is weak.
3. Supports idea that most molecular evolution is neutral.
4. Does not imply that neutral evolution at level of organism.
