NAS - Genetics + Origin of Species 1.31.97

Francisco Ayala - Intro + Sales of Book

Wally Gilbert - Origin of Genes

Introns Early } says both sides use same data to boost their
Introns Late } argument

1. Phylogeny - bacteria no introns
2. Homologous genes - intron position } Data - but interpretation
3. Correlation w/ 3D position } is up for grabs

Exon shuffling

- says introns should have "dramatic" impact of recombination rate - and allows mixing of different pieces.
- Exon theory of genes
- suggest that proteins are made up of "words" and it is easier to make a sentence out of words than random letters.

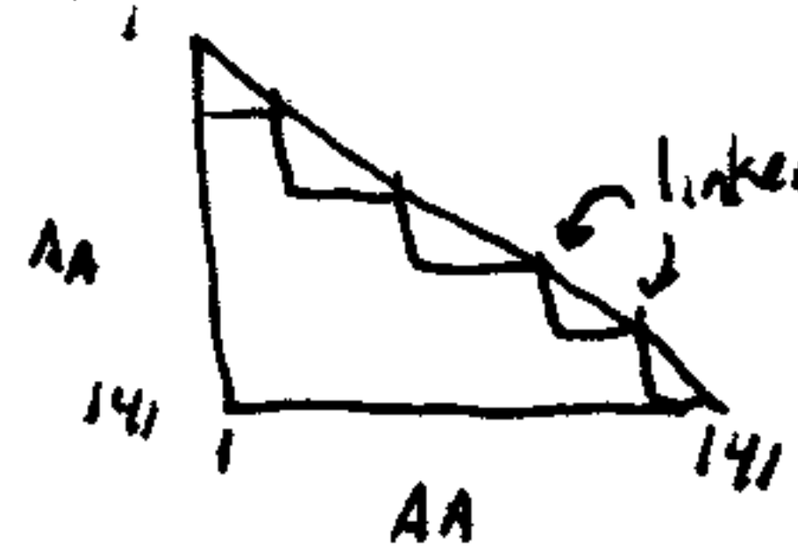
∴ would expect exons to correlate w/ structure

Intron Phase

- position of intron w/in codon
- suggests introns would not be in phase if introns inserted late.
- suggest separate exons should be in phase if exon shuffling important.
- in data ... there is an excess of symmetrical exons

Protein modules

- introns early predicts exons should represent "modules" in 3-D space.
- but hard to determine where the boundaries are.
- but if splice signals are important... phase may affect splicing
- but selection after insertion could affect position
- he suggests that introns late couldn't explain this w/o excess biochemical pleading
- are introns correlated at all w/ particular amino acids or flanking n.t. sequence
- are introns correlated w/ degree of aa conser



linker regions - positions between groups of aa that are very close together.

So.. data looks like there is a bias ... what else could

No sequence bias
No aa bias
No surface bias
No AGG or AGGT bias

} no obvious bias in regions near linkers

"Ancient introns" .. conserved positions → but if introns stay at same position must be some selection. So... why couldn't this selection have driven insertion of introns to these positions

Linker regions

~15 aa	21A°
~22 aa	28A°
~30 aa	33A°

with your ancient introns must need some selection to keep them in position so why couldn't late insertions do this

Lewontin suggests we need to know more information about splicing signals to know if there is residual bias.

M. Perugrino asked about whether splicing failure could explain phase correlations.