

## Acknowledgements

Collaborators:

**Daniel Hartl**  
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Comments  
& support:

**Lewontin & Hartl**  
**labs**

**Dick Lewontin**  
**Mark Siegal**

**Mutation - first cause of evolution,  
ultimate cause of genetic variation**

### **Estimation problem**

- **Direct measurement**

Problem: mutation is too infrequent

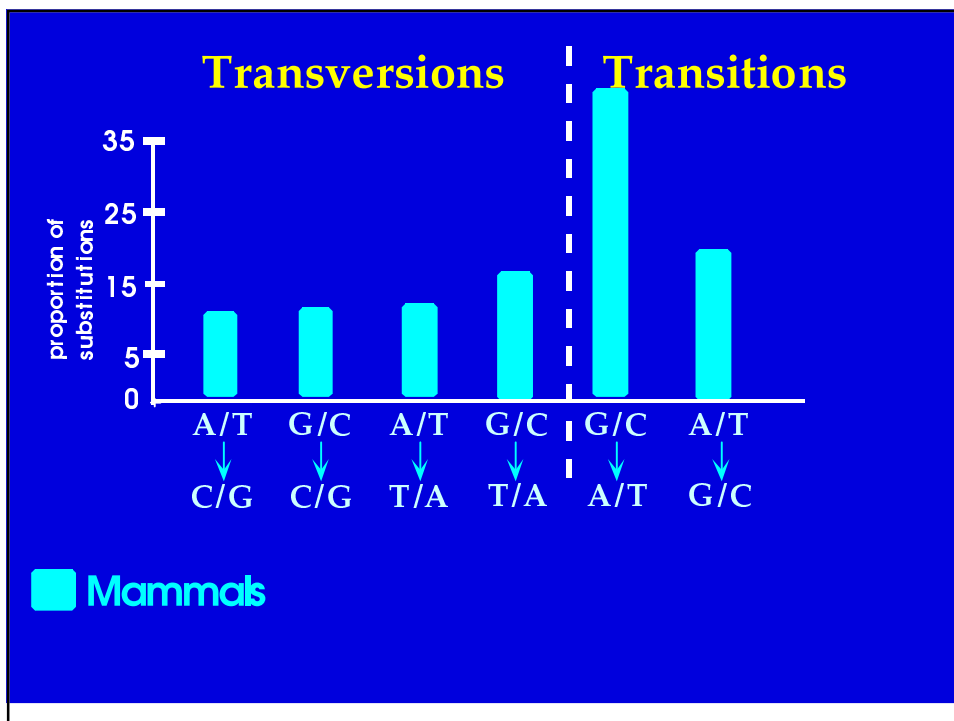
- **Inference from the observed variation**

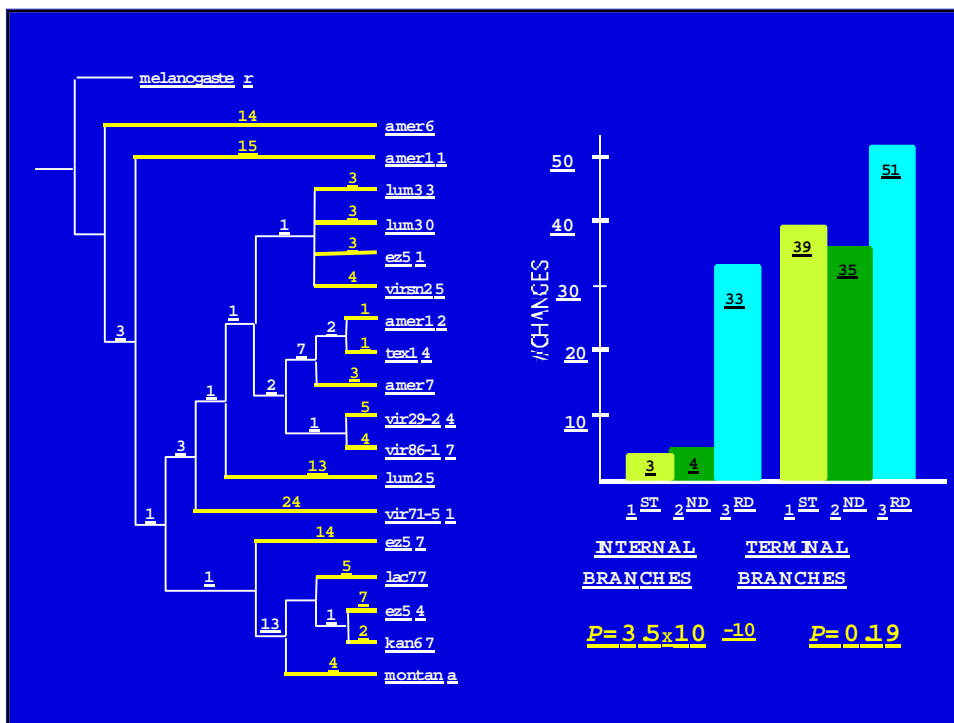
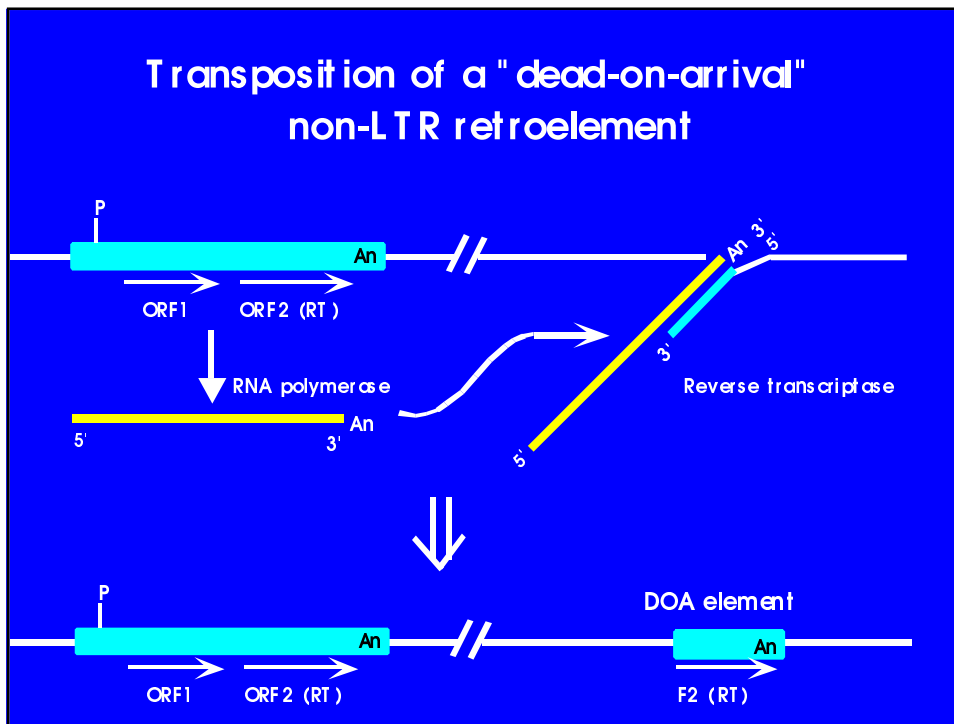
Problem: natural selection bias

## Estimation solution

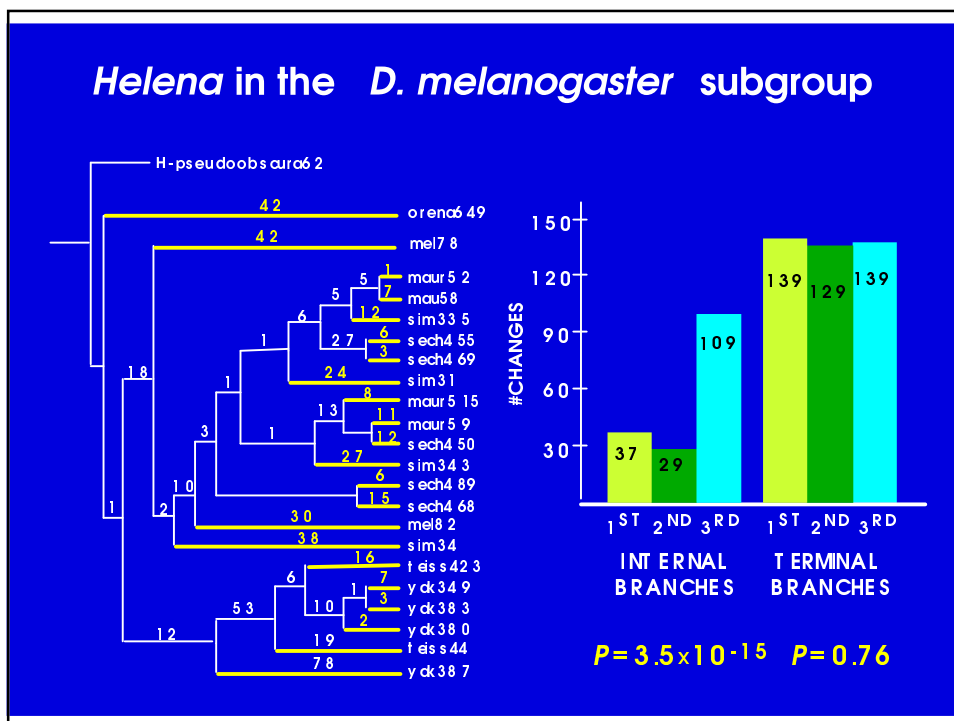
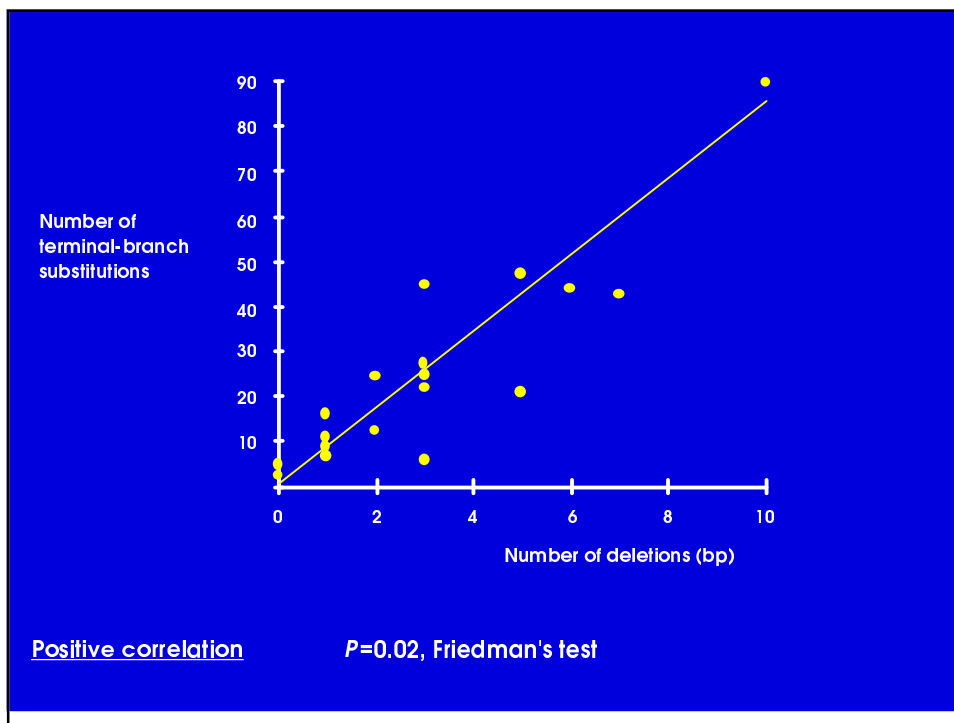
**Pseudogenes** → no functional constraints, ought to reflect mutational biases (Li, Gojobori, and Nei 1981)

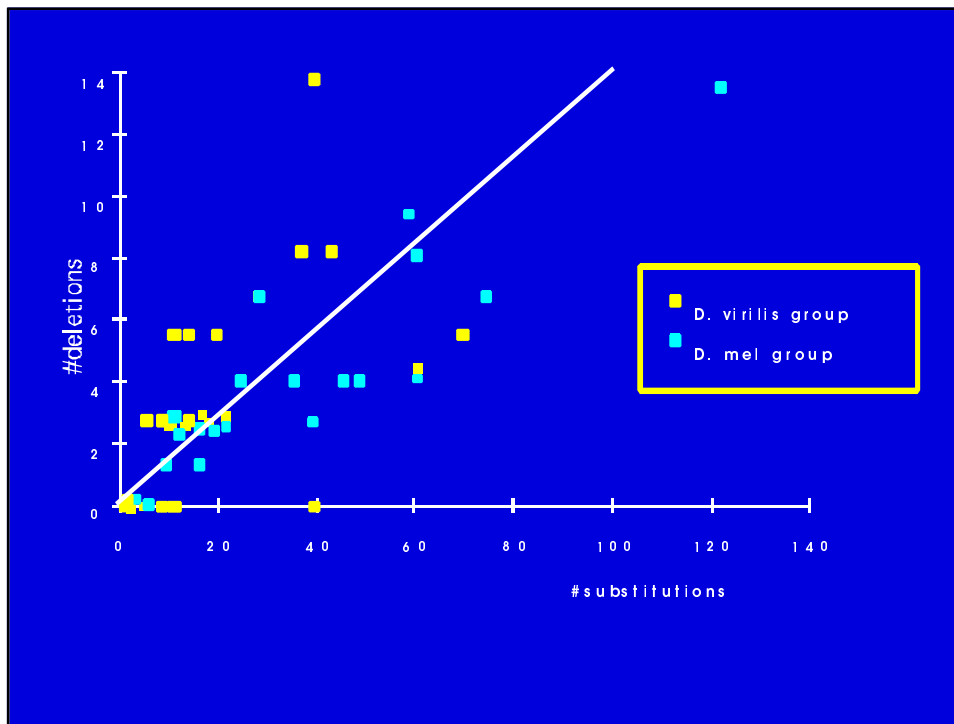
**Problem** → pseudogenes absent in many taxa





Mutational Patterns and Evolution of GC Content in Eukaryotes

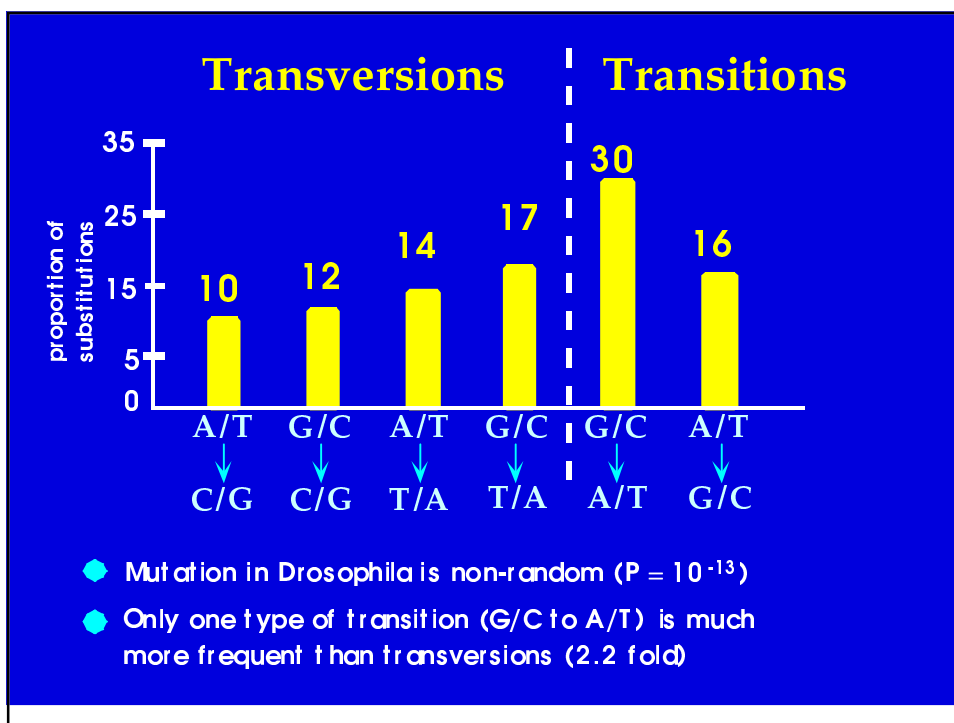
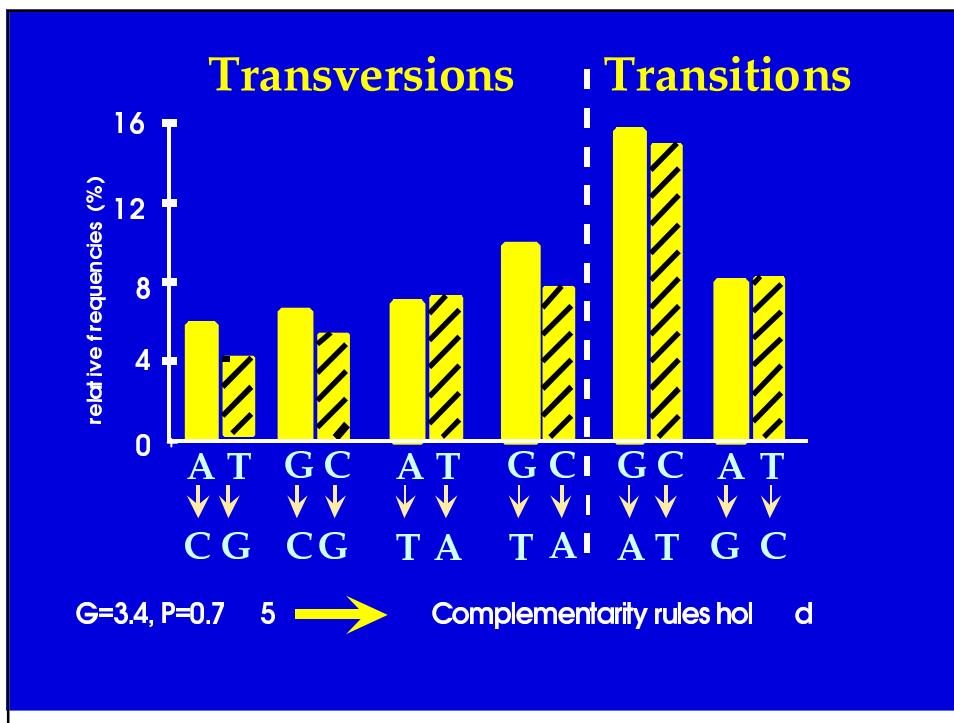




## How good are the raw data ?

585 substitutions in 1680 positions

- Large number of observed events ensures good statistical power
- Low proportion of sites substituted in each copy of *Helena* (average 1.5%; range 0.07-6.6%) avoids the problem of multiple hits



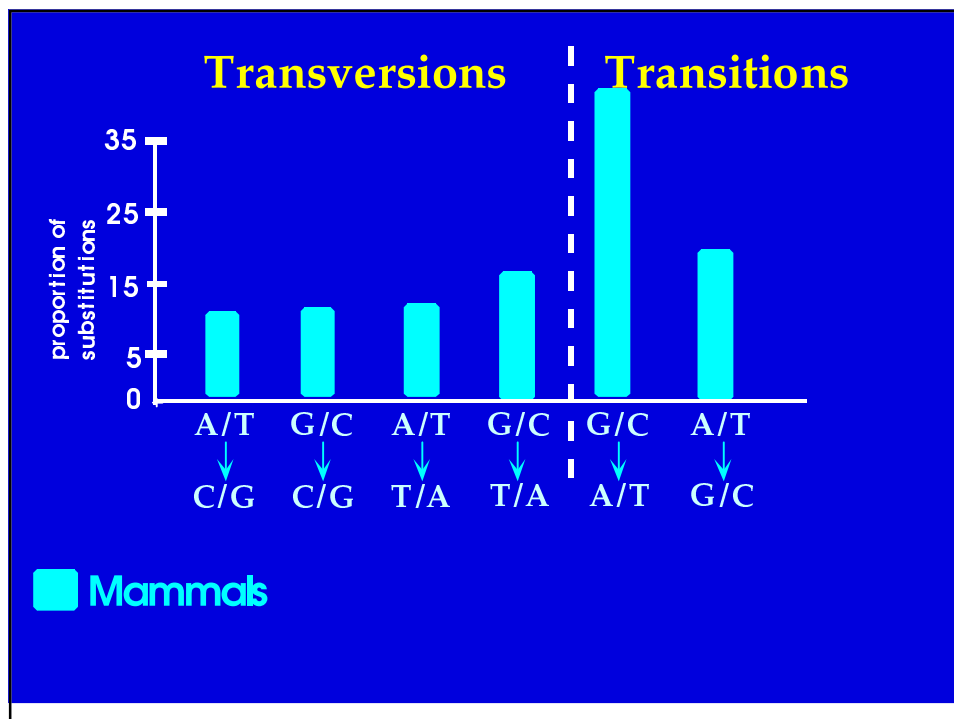
## Equilibrium predictions

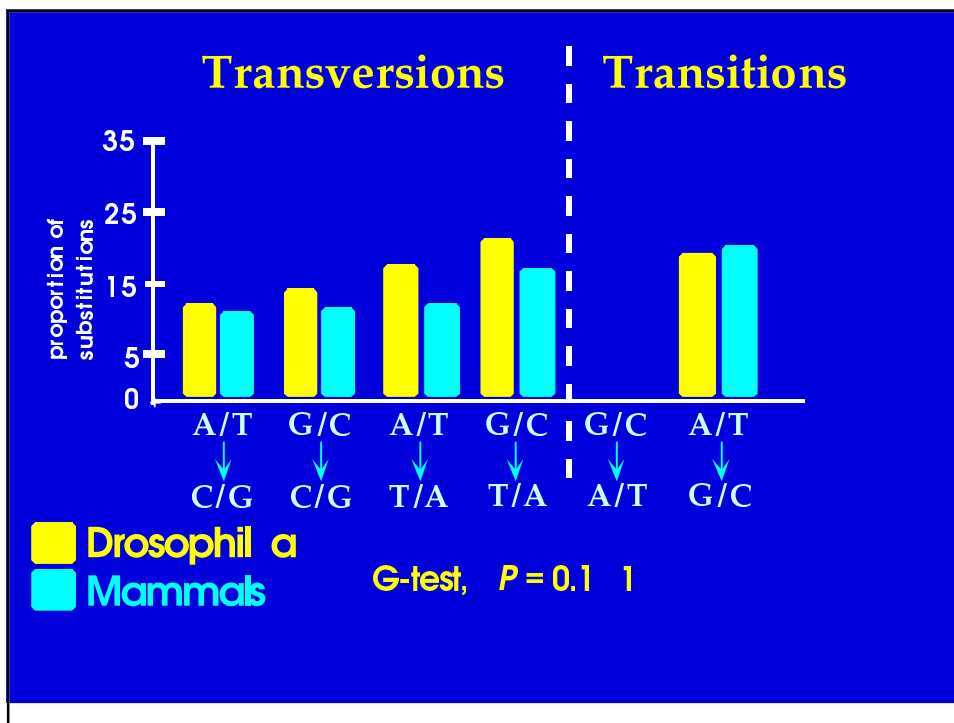
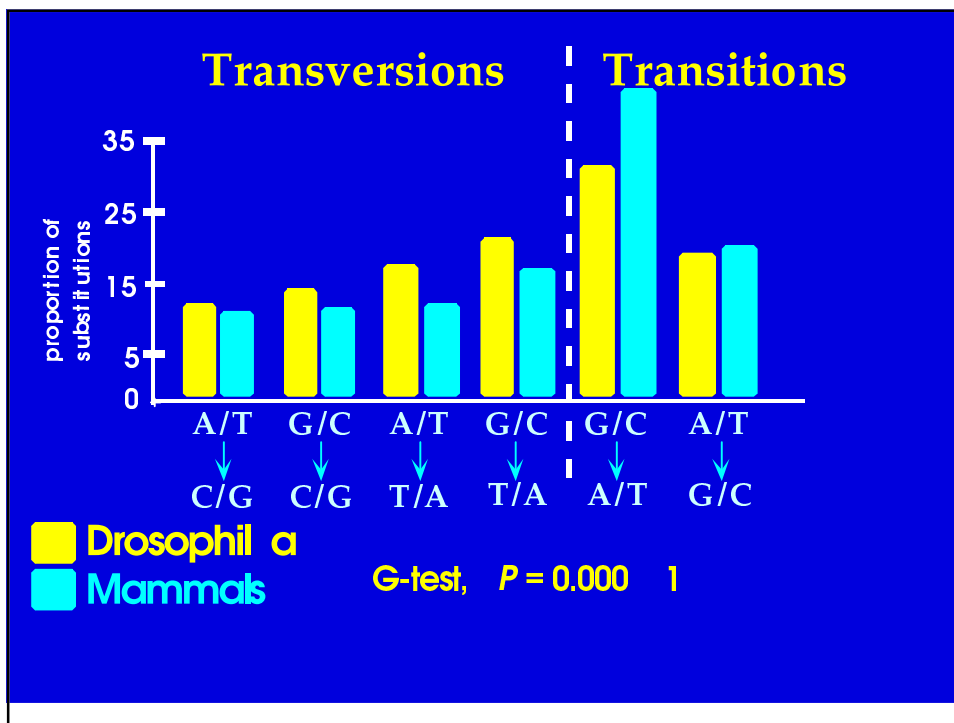
Using relative frequencies of point mutations it is possible to predict equilibrium AT content of the neutral portion of *Drosophila* DNA



AT content = **64.8%** (95% conf. interval, 60-69%)

This is consistent with the AT content of *Drosophila* introns ( **60-65.5%** )

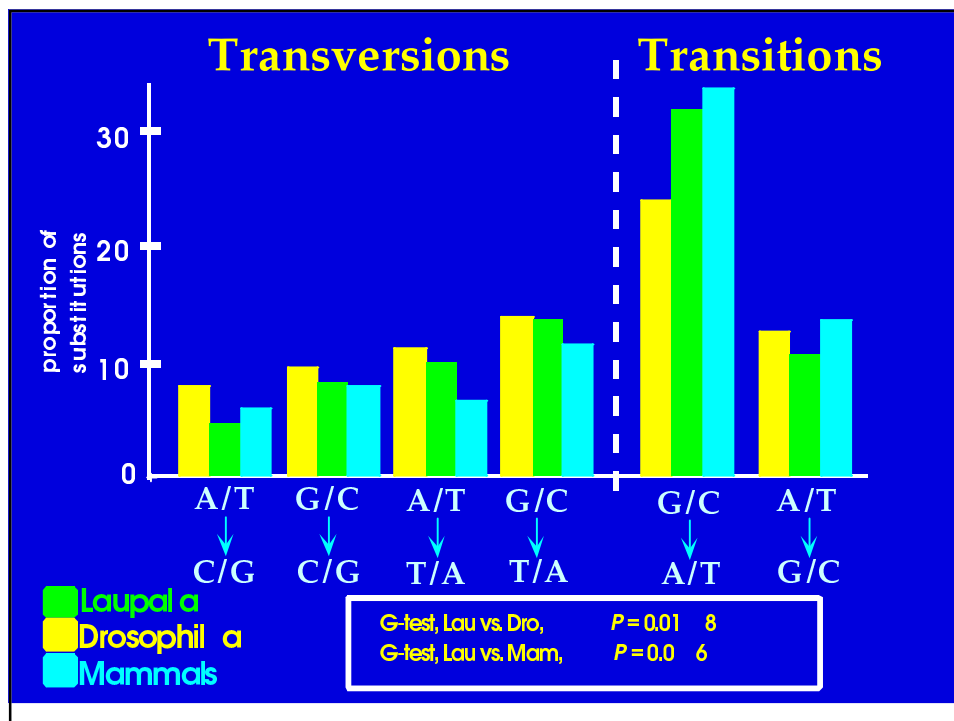






## Hawaiian crickets, Genus *Laupala*

- Endemic to Hawaii
- 37 recognized species
- Not well studied molecularly
- Large genome size (1800 MB vs 160 MB in *Drosophila*)



Mutational Patterns and Evolution of GC Content in Eukaryotes

