Bio1B Evolution 2

Last lecture:
- Introduction to Craig & lecture outline
- Foundations
  - Pre-Darwinian background
  - Darwin: early influences, Beagle voyage
  - Wallace

Today
- Natural selection - principles, lines of evidence in the “Origin”
- Descent with modification
- Estimation & interpretation of phylogeny
- Some major insights about the “Tree of Life”
  - 3 kingdoms: Archaea, Bacteria, Eukarya
  - Assembling the eukaryote cell
  - Metazoan origins & relationships

On-line resources:
Understanding Evolution (UCMP): http://evolution.berkeley.edu/
Tree of life: www.tolweb.org/tree/

The Darwin-Wallace principle of Natural selection

- Individuals within a population vary for one or more characteristics (traits)
- Traits are (to some extent) inherited by offspring from their parents
- More offspring are produced than can survive
  => those with traits that improve survival/reproduction leave more offspring
  => these favorable traits will accumulate in the population over generations

Lines of evidence in the “Origin of the species by means of natural selection” (Darwin, 1859)

- Artificial selection as analogy to natural selection
- Biogeography: Nested geographic distributions
- Homology of traits modified for different purposes
- Population pressure

Homologous structures: variations on a structure present in a common ancestor
Anatomical homologies of embryos

Chick embryo
Pharyngeal pouches
Post-anal tail

Human embryo

Pharyngeal pouches
Fish - gills
Mammals - ears, throat

Molecular homologies - new insights invisible to Darwin

- Genetic code
- Transcription & translation machinery
- Colinear segmentation (Hox) genes
- etc etc.

Descent with modification by natural selection + extinction

The current view of the phylogenetic hierarchy
(Understanding Evolution web site)

cf. Aristotle’s scala naturae
What evidence do we use to estimate the tree of life?

**General principles:**

- Taxa (species, genera etc.) are grouped by shared-derived traits.
- Taxa should be monophyletic.

**Examples of shared-derived traits that group major lineages of vertebrates**

- Character table
- Phylogenetic tree

**Key concepts in tree thinking**

- J and K are sister taxa.
- D, E, G, and H are grouped by shared-derived traits.
- B is the most recent common ancestor to D, E, G, and H.

**DNA sequence variation**

Fitting observed patterns of sequence variation at homologous (aligned) sites to a phylogenetic hypothesis.

(see also Fig. 26.8)
Methods for estimating phylogeny from molecular data

- Parsimony - minimize #changes on tree
- Maximum likelihood, Bayesian (data + model of sequence evolution)
  - Find tree that is most probable given the data

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(a) Percentage differences between sequences

(b) Comparison of possible trees

15% 15% 20% 15% 5% 25% 15% 10%

John Huelsenbeck, IB & MVZ "curator of trees"

Estimating divergence times from a phylogeny

- Branch lengths are proportional to amount of change (Fig 29.19)
- **Molecular clock:**
  - Zuckerkandl & Pauling 1960s
  - Some genes evolve at approx constant rate
  - Absolute rate can be estimated from fossils at (or near) nodes
  - This calibration can be used to estimate other divergence times in tree
  - See text for caveats!

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Cool stuff - understanding metazoan origins (Nicole King, MCB)

See also Fig. 32.3
Surprise 2

Eukaryotic cells were assemble via endosymbiosis - mitochondrial & chloroplasts are modified symbiotic bacteria

Each has a (small) genome separate from the nucleus