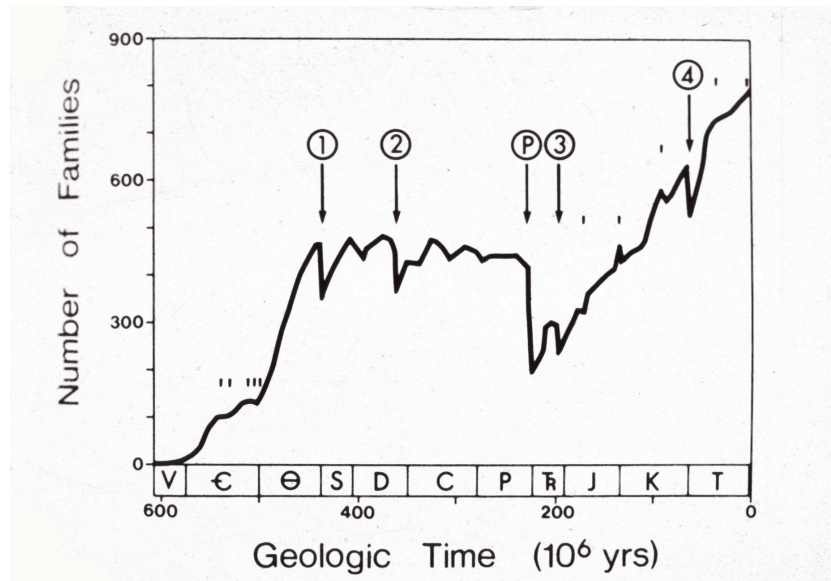


Ward Lecture 5 - Diversity through time, and Evo-Devo

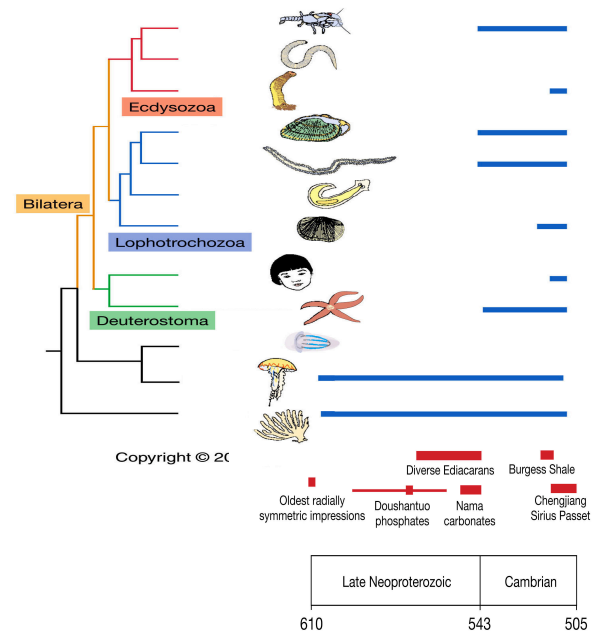
What is biological diversity, and what has been its pattern or trajectory through time?

For this lecture - read Ch.18 in addition to prior assignment



Cambrian Explosion redux:

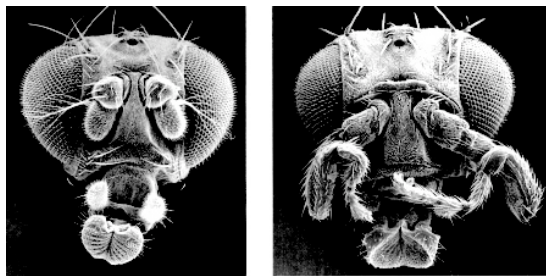
- So why was there such a sudden diversification of so many different kinds of body plans so fast?
- We can understand the need for so many body plans: predators, herbivores, etc
- But just how did they come about so quickly?
- **Answer: *Hox genes!***



Evo-Devo

- As the body of a multi-cellular org develops, a system is required to arrange cells in 3-D space and time
- For tissues and organs to develop, every cell in growing body has to be identified by location in relative to other cells and relative to time - this is called a developmental sequence
- Genes responsible for coding this information called *Homeotic loci*
- *These are Hom (invertebrates) or Hox (vertebrates) genes - collectively called Hox*

A *Drosophila* homeotic mutation, antennapedia - small genetic change, large effect.



This four-winged fly resulted from changes in three HOX genes



How Hox genes work

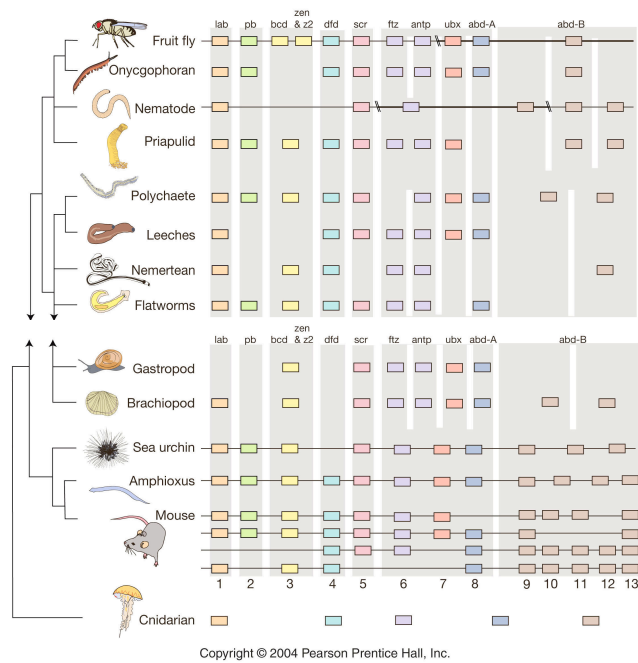
- They code for proteins that bind to DNA - and in so doing control the transcription of other genes on the DNA
- Key observation - fruitflies missing one or more Hox gene PRODUCTS- the enzyme coded by a specific Hox gene - could build legs or eyes in wrong place on body
- The cells that built the structures did not know where to grow them

Hox genes:

- All occur in groups. Total number of genes in each group, and number of groups, varies by taxa.
- There is a correlation between order of genes along chromosome and anterior to posterior location of gene products on embryo
- Hox gene products are regulatory proteins: they regulate the fate of cells in time and space- they do not make a structure, they regulate where it will be made

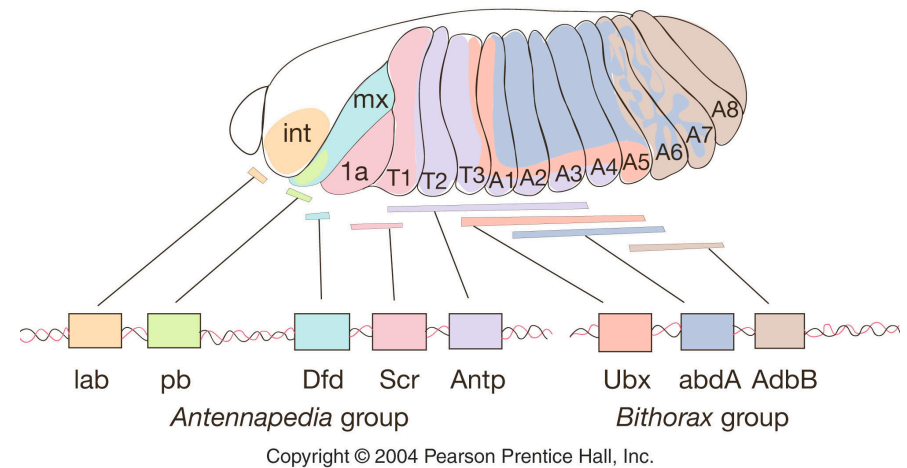
Hox genes and the Cambrian Explosion

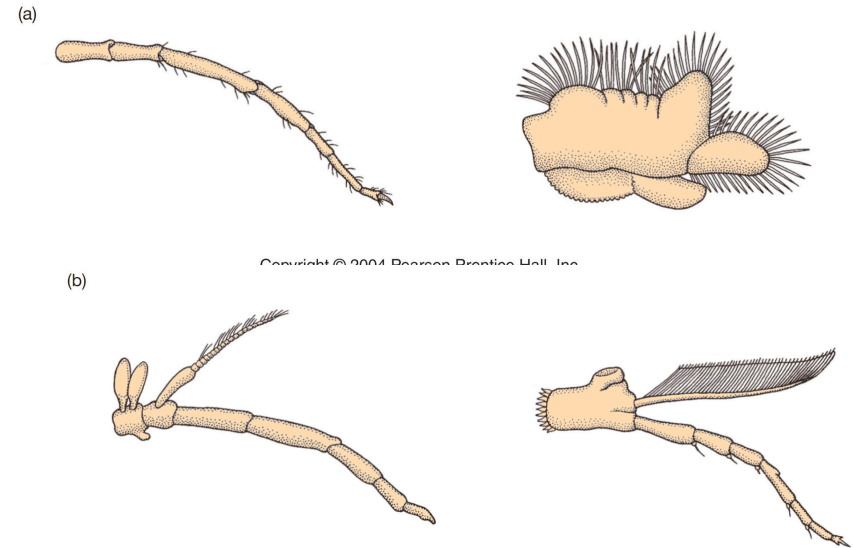
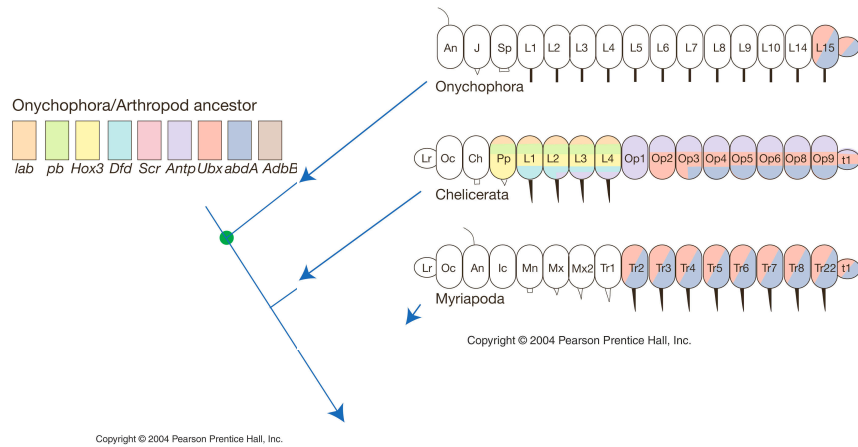
- Hox genes numbers increased through time
- Adding new Hox genes was involved in animal diversification
- But not just change in number, but change in function as well probably involved in building new body plans



Hox genes and the Cambrian Explosion

- Shifting zones of Hox gene expression can shape differences in body design
- This certainly happened in the fast formation of many arthropods involved in the Cambrian Explosion
- The Cambrian Explosion may have been ignited by an increase in the number of Hox genes and by shifting zones of extant H.Gs

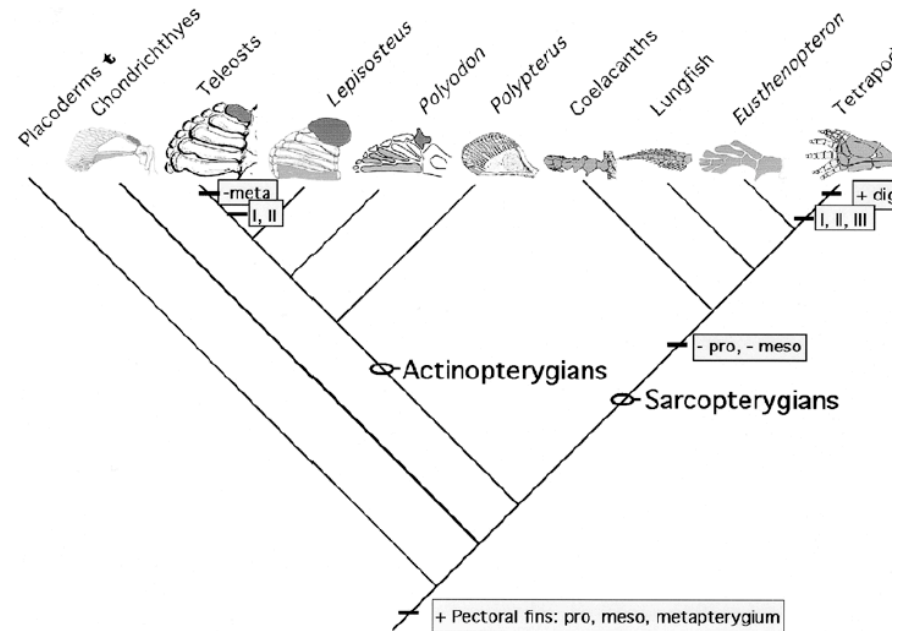


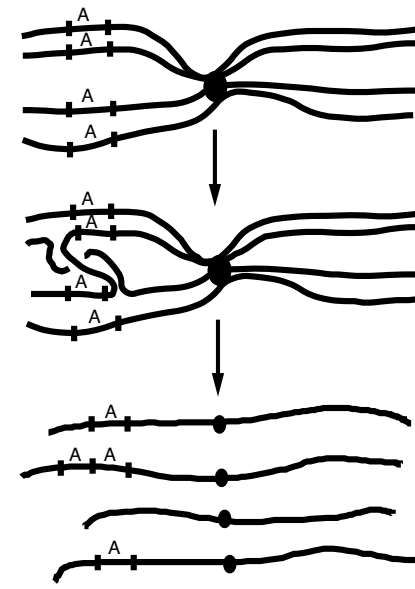
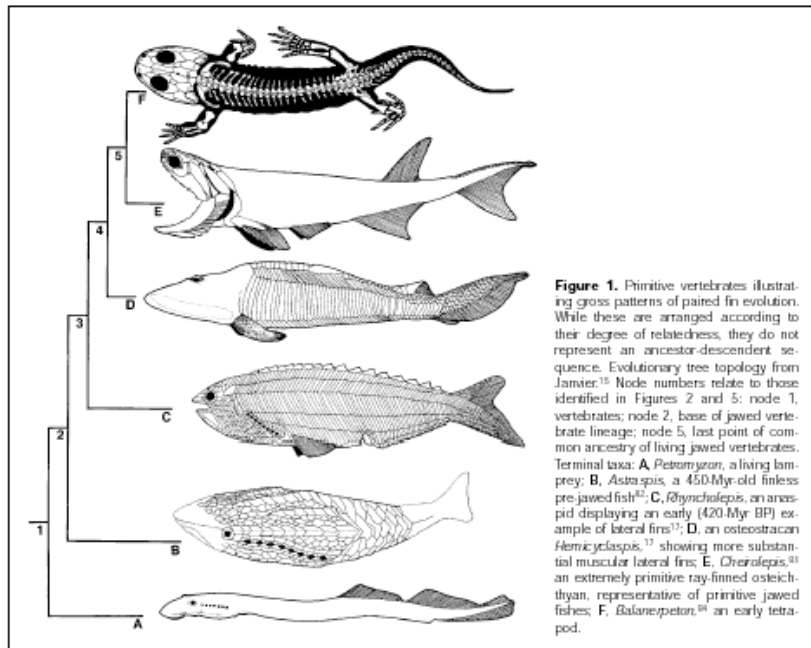


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Vertebrates have been no less clever with reshaping limbs

- Allowed vertebrate adaptations to water, land and sky
- They have done this while being locked into an ancient design of two pairs of limbs with generally no more than five digits
- How was this done?





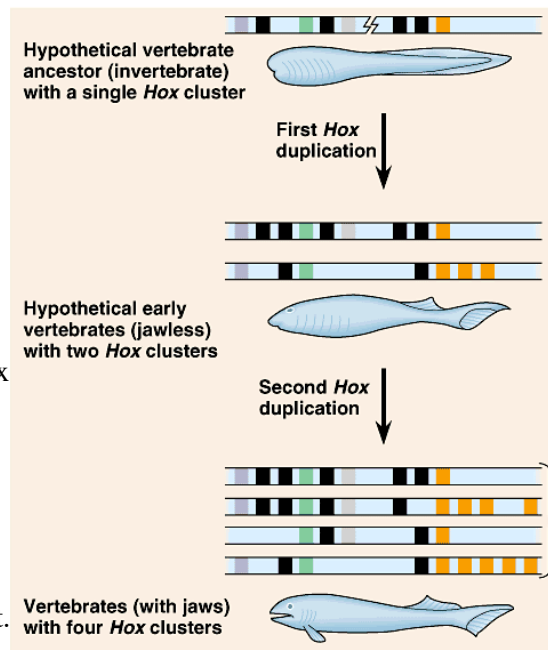
A gene is duplicated by unequal crossing-over, resulting in chromosomes with different numbers of gene copies in a population.

The complex of HOX genes appears to have contributed to vertebrate evolution and complexity in two ways:

First, there are more duplicated genes in the complex (yellow genes).

Second, the entire complex was duplicated twice yielding four sets of HOX genes, perhaps as part of polyploidization events in early vertebrates.

Some genes were then lost.



How did fins evolve into limbs, and these to the huge variety of structure we know in tetrapods today?

- Hox genes changed switches that allowed different parts of bones to change relative sizes
- Other genes produced more rapid growth-chief among these the BMP bone growth gene - increased BMP causes more growth

Mollusks - diversification by shell shape formation

- What is the genetic basis of shell coiling, shell ultrastructure?
- How quickly can shell shape change?
- How has it been done - an ongoing UW project

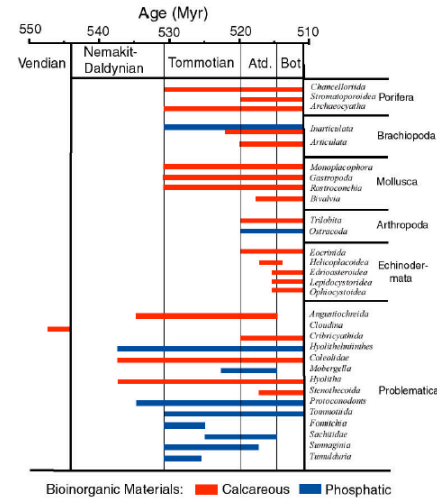


Figure 10.2. Stratigraphic ranges and first appearances of major fossil taxa that employ calcareous and phosphatic biomineralization. Not all families and problematic taxa are listed, nor are silica biomineralizing groups; for summaries of the stratigraphic range of these groups, see Beagren [11]. Note that the mineralogy of *Cloudina* is poorly constrained; Grant [19] inferred a primary mineralogy of high-magnesian calcite based on preferential dolomitization of shell layers. Data from Lowenstam & Margolis [6] and Beagren [11].

2 Major Questions:

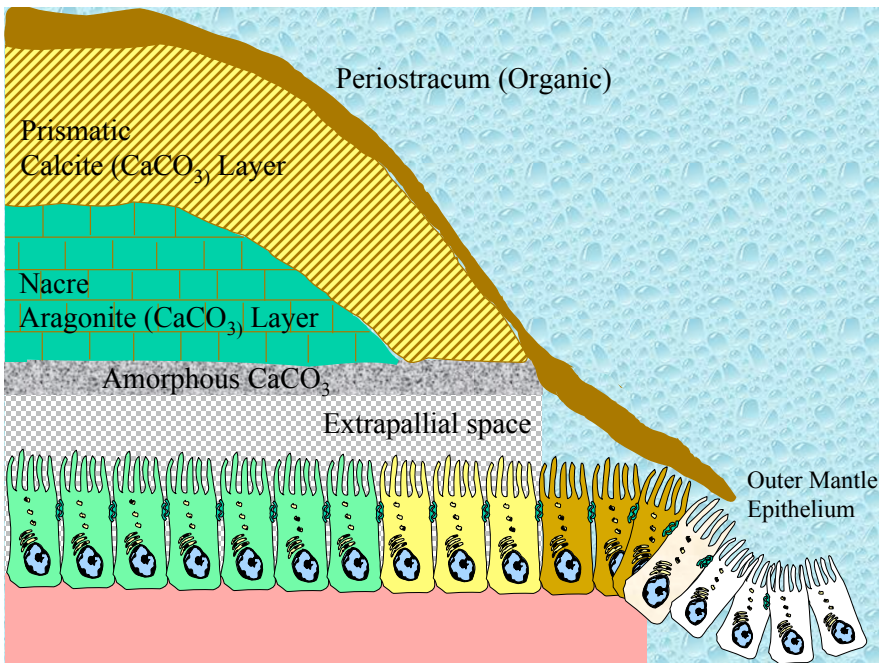
What are the genes controlling shell formation in lophotrochozoa?

Are the genetics of shell formation the same in different taxa?

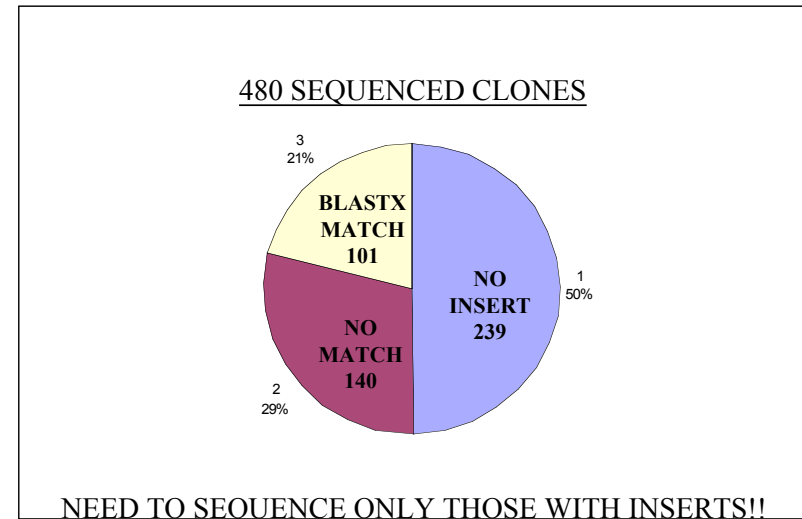
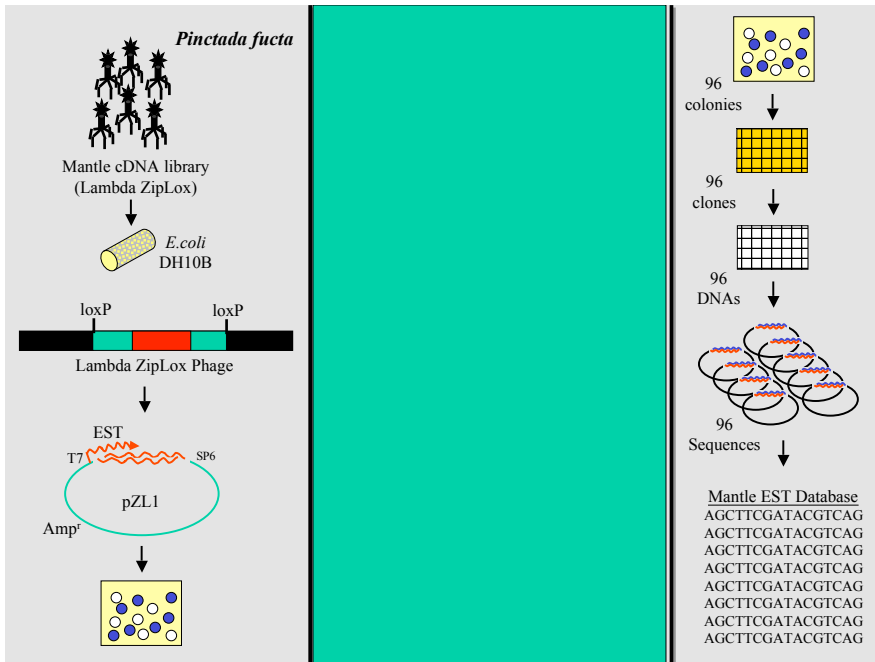
2 Major Initial (1-2yr) Approaches:

Study the function of candidate genes in embryos/juveniles of an experimentally tractable organism (*Problem: Few Candidates Known!*)

identify potential candidate genes for several taxa based on mantle EST's (*Problem: Expensive*)



1 Biochemical Approach	(e.g. Mantle Zones- Carbonic Anhydrase, Alkaline / Acid Phosphatases Oxidases)
Histochemical Stains	→ Mantle Histology
2 Physical Biochemistry Approach	(e.g. Epitaxial Crystal Growth Macromolecular Control)
In Vitro Biomineralization Scanning EM	→ Biophysical Model
3 Developmental Biology Approach	(e.g. Many studies - Molluscs, Brachiopods, Echinoderms)
Cell Lineage Tracers Scanning EM	→ Fate map of Shell
4 Genetic Approach	(e.g. sort Genetic and Environmental components of variation)
RAPD / RFLP markers chromosome maps	→ Track markers and shell variation in mating population (e.g. <i>Lymnaea</i> shell coiling gene) <i>(Physa Genetics????)</i>
5 Molecular Biology Approach	(e.g. Biomineralization Proteins)
Protein Isolation cDNA isolation	→ Macromolecules in All of Above (e.g. <i>en</i> , <i>dpp</i>) <i>(EST Analysis)</i>



**Pf EST BLASTX Matches
(approx. 75 different proteins)**

Interesting

cysteine dioxygenase
 adhesion glycoprotein?
 glutathione peroxidase
 growth factor? Fibulin?
 Lectin??
 myosin LC-adductor
 muscle(scallop)
 paramyosin (bivalve)
 ref(2)P????

Less Interesting

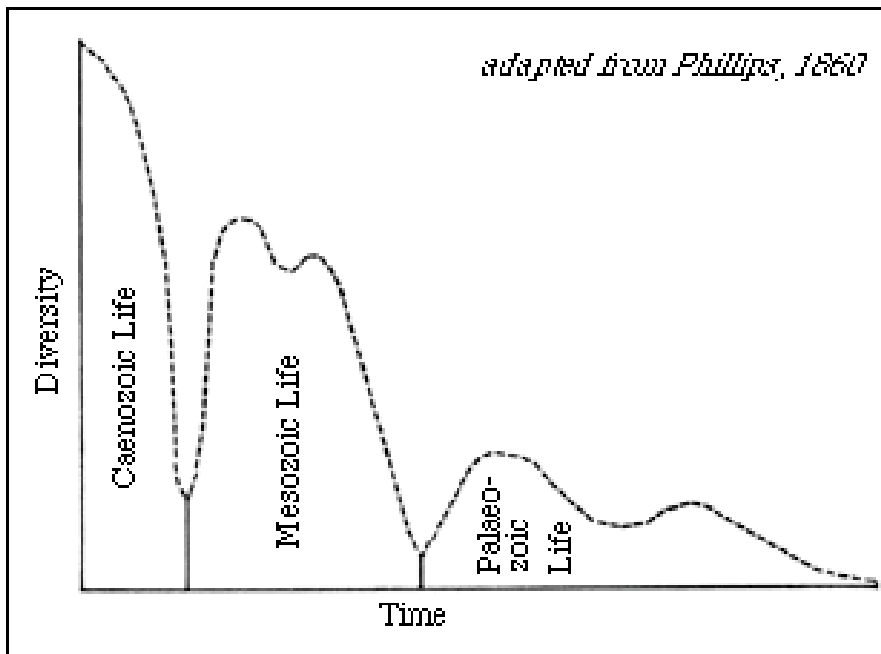
Actin 1 (2)
 Dynein light chain (2)
 NADH ubiquinone red (2)
 NDP kinase B (2)
 ubiquitin 1 (2)
 actin 2
 actin depolymerize factor
 adenosylhomocysteinase 1
 APC subunit 10
 collagen ??
 Collagen ??
 cytochrome P450
 EF-1 alpha
 EF-1 beta
 EF-1 gamma
 EF-2
 mito ATP synthase I
 PEP carboxykinase
 peptidyl-prolyl isomerase
 sec61 gamma subunit
 septin
 TRAP-gamma
 ATP synthase lipid BP
 cathepsin B
 metallothionein
 Transgelin? Calponin?
 tumor protein (TCTP)
 ubiquitin 2
 ubiquitin 3
 Zeta 1 COP

Boring

ribosomal protein P1 (6)
 ribosomal protein P2 (3)
 ribosomal protein L10 (2)
 ribosomal protein L35 (2)
 ribosomal protein L4 (2)
 ribosomal protein L15 (4)
 ribosomal protein L17 (2)
 ribosomal protein L21 (2)
 ribosomal protein L18
 ribosomal protein L11
 ribosomal protein L3
 ribosomal protein L30
 ribosomal protein L13a
 ribosomal protein L13b
 ribosomal protein L23
 ribosomal protein L27
 ribosomal protein L29
 ribosomal protein L35a
 ribosomal protein L36
 ribosomal protein L7a
 ribosomal protein L7b
 ribosomal protein S12 (3)
 ribosomal protein S14 (2)
 ribosomal protein S25 (2)
 ribosomal protein S29 (2)
 ribosomal protein S4 (3)
 ribosomal protein S3
 ribosomal protein S27
 ribosomal protein S17
 ribosomal protein S20
 ribosomal protein S8
 ribosomal protein S13
 ribosomal protein S24
 ribosomal protein S27a
 ribosomal protein SA

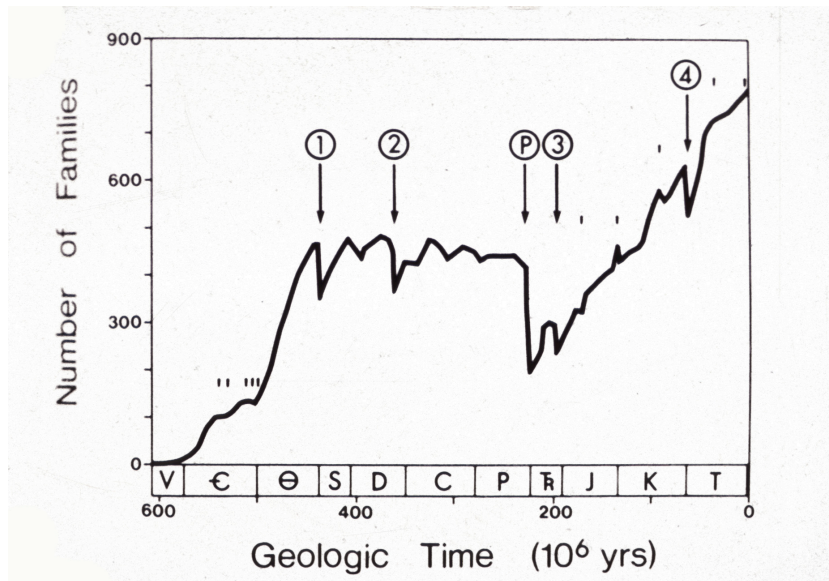
What else promoted diversification?

- New structures, new habitats, new niches- the keys to adaptive radiation
- Modernization - evolution took structures and made them better
- Geological changes independent of biology- such as oxygen levels and continental configurations



Jack Sepkoski data set

- Analyzed thousands of first and last occurrence data from Zoological Record (a publication)
- From these data compiled first Family level, then generic data for Phanerozoic
- Monumental effort - took twenty years!



Major findings

- 1. Burst of diversification in Cambrian (so called “Cambrian Explosion”),
- 2. Rough plateau of diversity for 200 million years,
- 3. Dip caused by Permian extinction,
- 4. Recovery, with present day diversity two to three times higher than anytime in Paleozoic

Would the diversity of all taxonomic levels equally represent actual changes in diversity through time?

- * What proportion of all phyla have been discovered?
- * What proportion of species have been discovered?
- What taxonomic level constitutes an accurate measure of significant diversity?

How would one go about estimating changes in the global diversity of life through time?

Is the fossil record equally complete for all types of organisms?

- * land plants
- * vertebrates
- * shallow water invertebrates
- * deep water invertebrates
- * plankton

Fig. 1. Comparison of genus diversity and proportional diversity of motile (active) and nonmotile (passive) marine metazoans through the Phanerozoic Eon; groups designated in Table 1

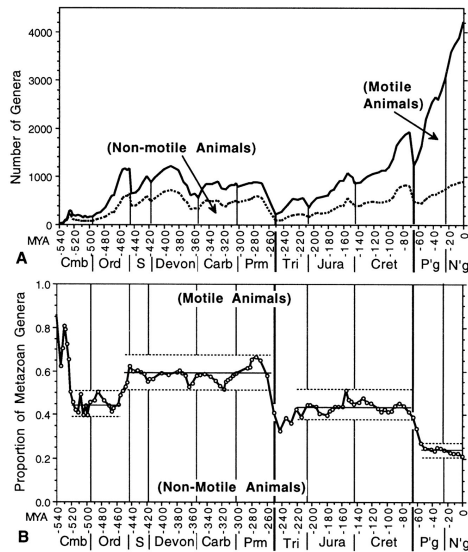
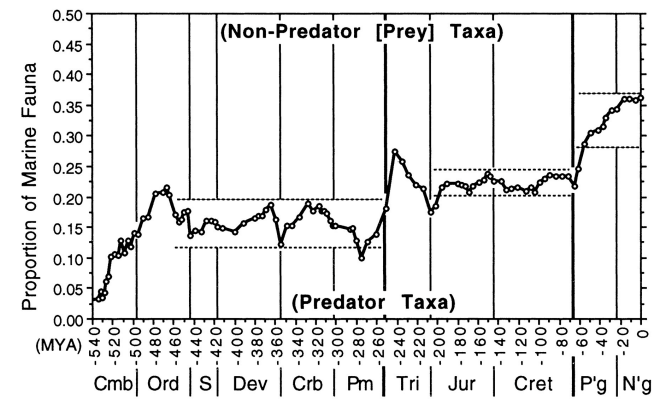


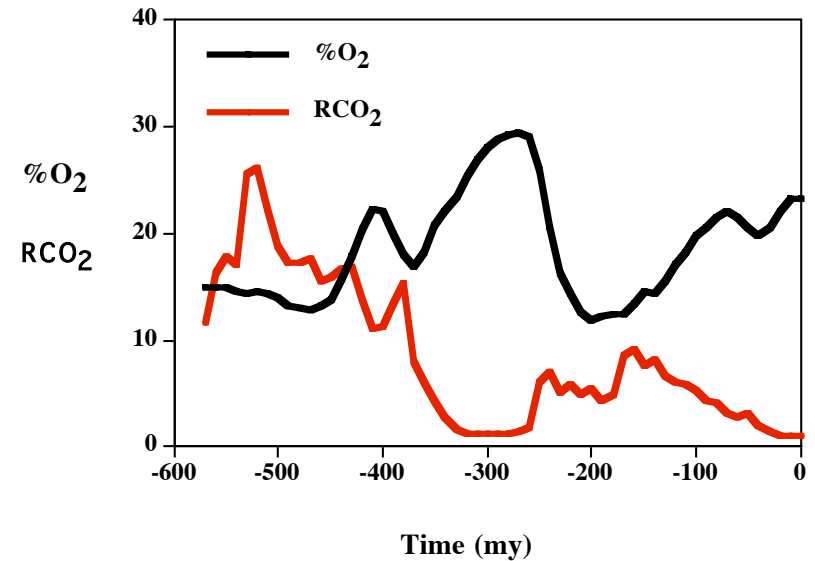
Fig. 3. The proportion of tabulated marine genera comprising predators throughout the Phanerozoic Eon



Bambach, Richard K. et al. (2002) Proc. Natl. Acad. Sci. USA 99, 6854-6859

Some really big changes

- The conquest of land by plants. First common vascular plants in Silurian and first forests in Devonian (400 mya)
- This stimulated the colonization of land by first invertebrates (Silurian) and later by vertebrates (Devonian)
- The evolution of the amniotic egg - allowed land vertebrates to be freed of water
- Similar breakthroughs in plant reproduction - evolution of gymnosperms in late Paleozoic, greening of all land areas



More greatest hits

- Evolution of endothermy in vertebrates - probably happened near end of Permian
- Evolution of advanced herbivory in vertebrates - late Paleozoic
- Evolution of vertebrate flight - sometime in late Paleozoic
- Evolution of mammals and dinosaurs - Triassic

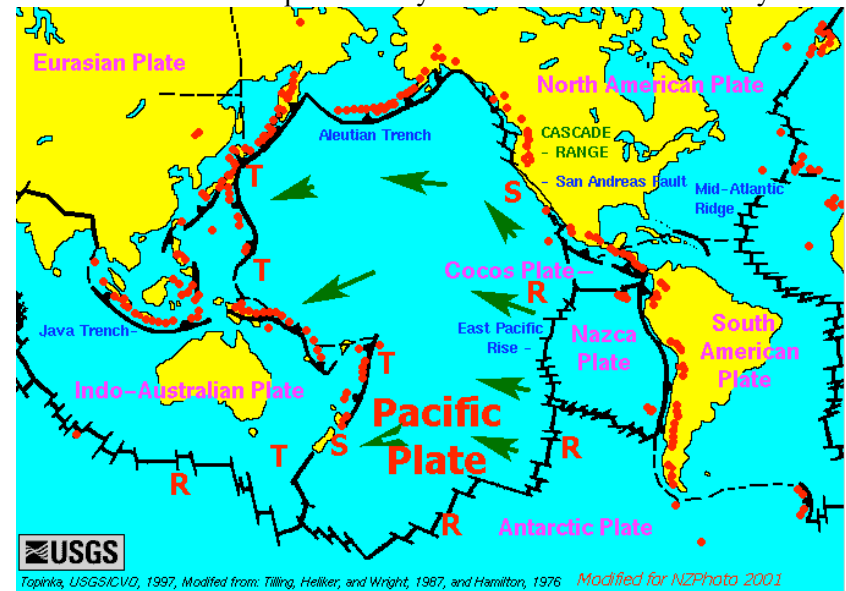
A really big driver of biodiversity:

- The evolution of angiosperms - flowering plants - occurred in early Cretaceous -120mya
- Stimulated great adaptive radiation of insects
- Caused major changeover in vertebrate faunas as well - as well as changing the balance of carbon cycle by annual leaf loss
- By end of Cretaceous 90% of flora was flowering
- First - Magnolia!

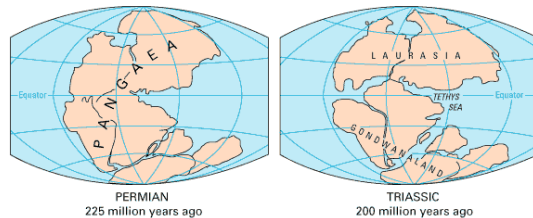
Influences on Diversity

- Diversity of organisms increases from pole to equator
- Continental size
- Continental shape - one large 'supercontinent vs. many smaller continents and islands
- Biological context - diversity of prokaryotes and Eukaryotes, role of sex in diversity
- Mass extinctions

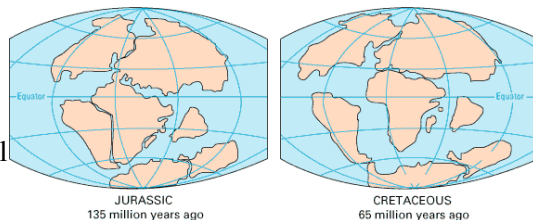
Plate tectonics and continental drift have seriously rearranged the continents over the past 250 Myr and continue to do so today.



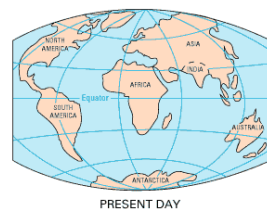
At one point all the continents are thought to have been fused into the supercontinent **Pangaea**.



The split into supercontinents **Laurasia** and **Gondwanaland** is thought to have led to the evolution of marsupials on Gondwanaland and placental mammals on Laurasia.



Only Australia remained isolated and hence retained both marsupials and monotremes (platypus and echidna)

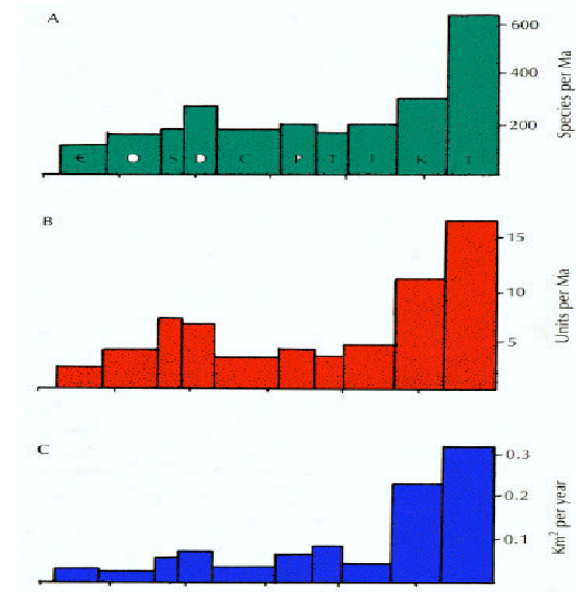


Could our diversity curves be all wrong?

- Null hypothesis: Diversity has been as high since the Cambrian as it is now - observed curve is artifact of fossil record
- How can this be tested?

Potential Factors Controlling Global Diversity

- Habitable Area
- Mass Extinctions
- Adaptive Radiations
- Ecospace Utilization
- Plate tectonics and Provinciality
- Biomass and Nutrient Levels



Biases

- Rock area sampled
- Age of rock
- Number of exceptional deposits through time
- Does % of fauna with hardparts change through time
- Paleontological interest in time intervals
- “Pull of the Recent”