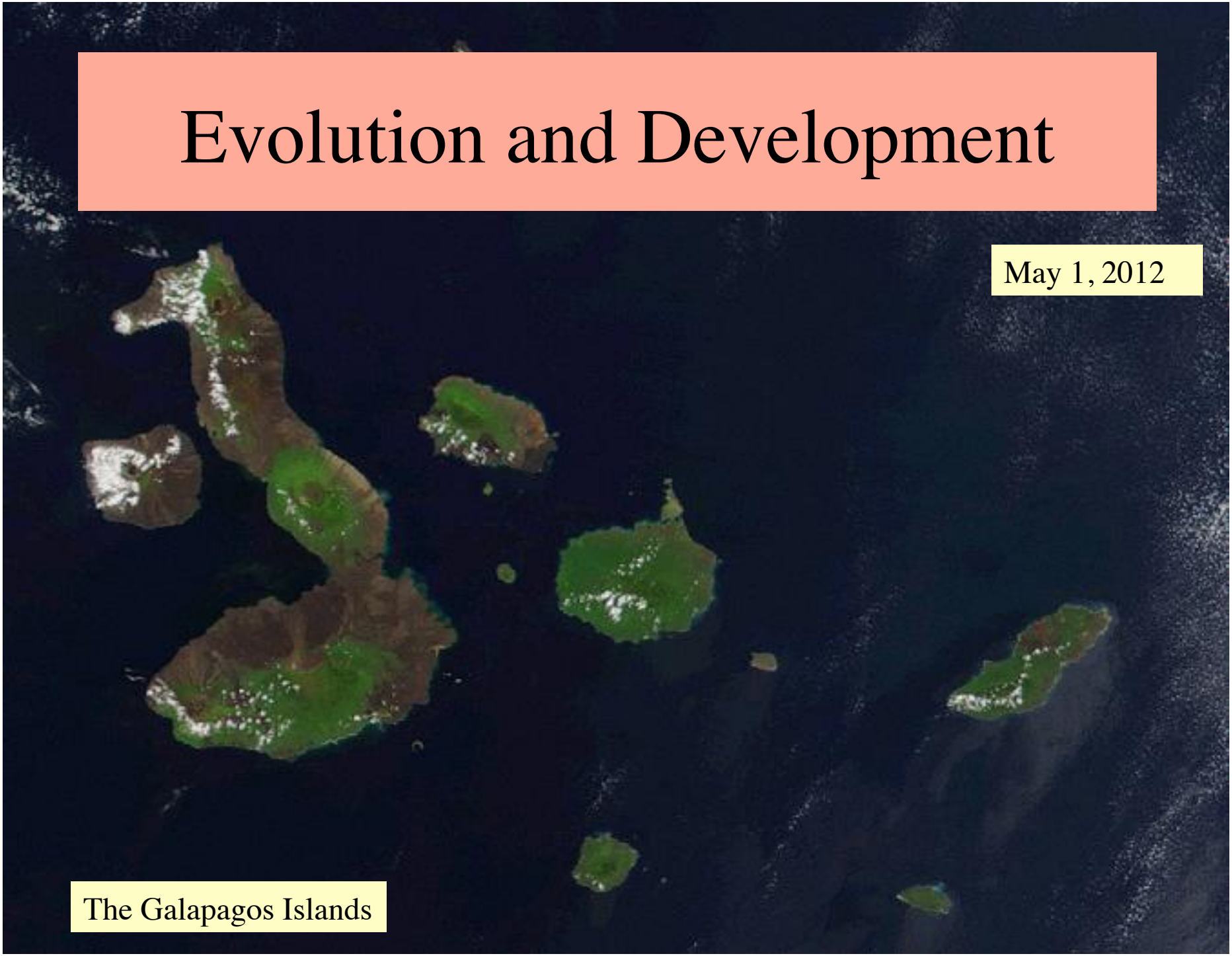
Evolution and Development



May 1, 2012

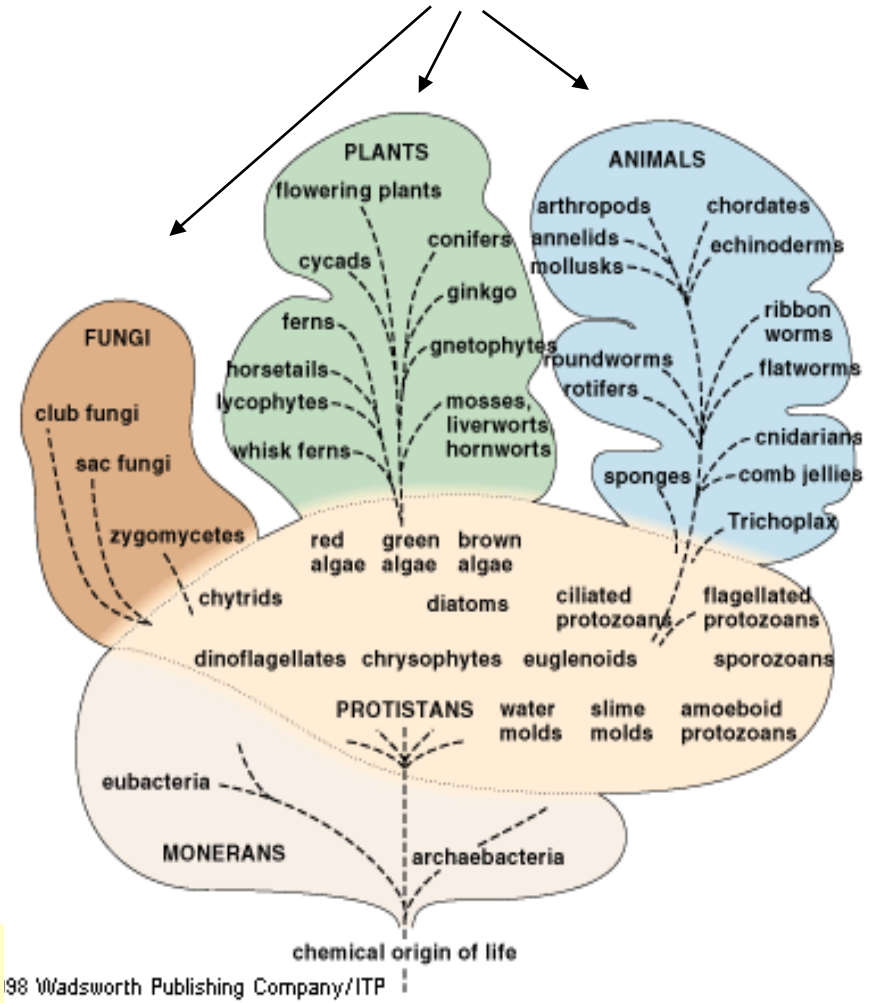
The Galapagos Islands

Life is the result of evolution

Classified based on similarities

- **Monera**
  - Archaebacteria
  - Eubacteria
- **Protista**
- **Fungi**
- **Plantae**
- **Animalia**

Evolution says these differences are due to common ancestry



"our classifications will come to be, as far as they can be made so, geneologies"
-Darwin

Evolutionary theory- “modern synthesis”

1. Evolution driven by single-base-pair changes at a slow, generally uniform rate

2. Many changes are neutral; stochastic processes have important influence

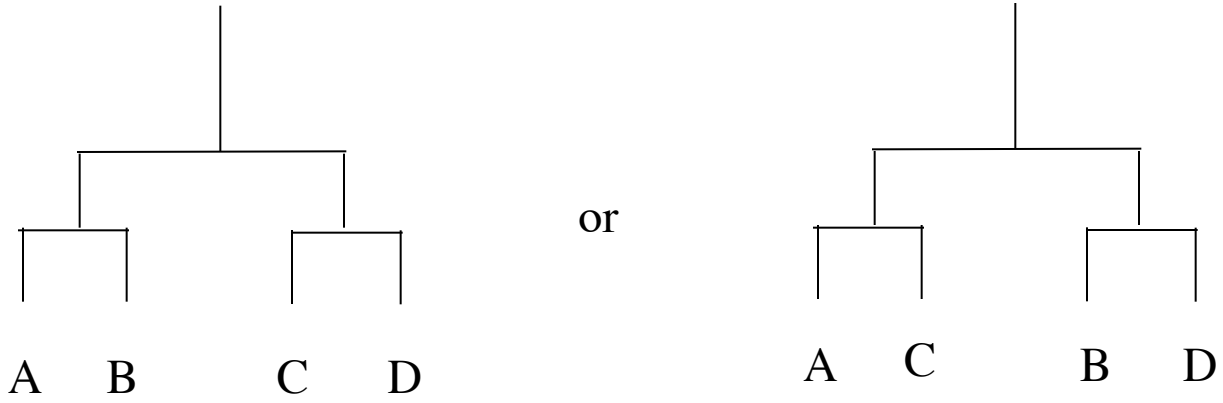
3. evolution of proteins by single amino acid changes the major driving force

4. gene duplication/divergence a major source of evolutionary novelty

These assumptions allowed evolution to be studied as a branch of applied mathematics

The search for the correct taxonomy ToL

One precise pattern of ancestry actually occurred- the problem is there is no reliable record of that ancestry beyond limited fossil data. Can it be deduced from indirect, evidence?



A: traits 1, 2, 4, 5
B: traits 1, 2, 4, 6
C: traits 1, 3, 4, 5,
D: traits 1, 2, 3, 6,

But in reality there are thousands of traits and millions of species

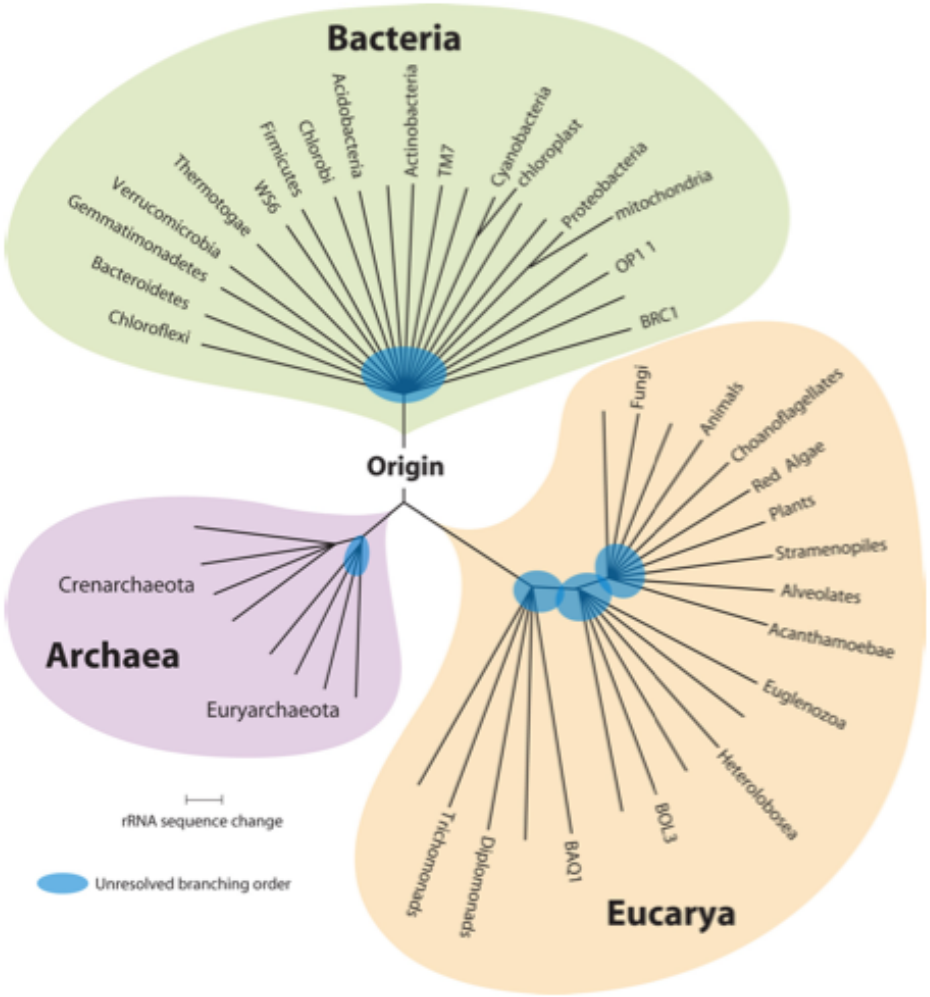
Assumptions and more assumptions

Classical taxonomy: weighs traits based on knowledge of species

Cladistics: weighs traits equally

Tree building algorithms: also mathematical- and flawed

Molecular phylogeny- an improvement?



A ToL based on rRNA sequences

Assume sequence changes are equal on average over time.

Small rRNA sequence highly conservative and universal, can be used for deep phylogenic comparisons

Paleontology provides some independent dates of branchpoints

Origin of life (i.e. the cell)	-4000 Myr
Development of eukaryotes and colonial organisms	-2000 Myr
Earliest metazoans	-550 Myr
Most metazoan phyla present	--510 Myr

Molecular based branchpoint dates generally don't agree with fossilt record.
Molecular date for metazoan origin: 800-1200 Myr instead of 600 Myr

The evo-devo research program: bring biology back to evolutionary studies

We can understand how metazoan organisms are related by understanding developmental programs. (real genotype-phenotype)

Closely related organisms will have fewer changes in their programs than distantly related organisms. (rational weighting)

Highlights how much we still have to learn about development, and the need to expand beyond model organisms, however.

The assumptions of the "modern synthesis" and "molecular clocks" are wrong

Not uniform at all

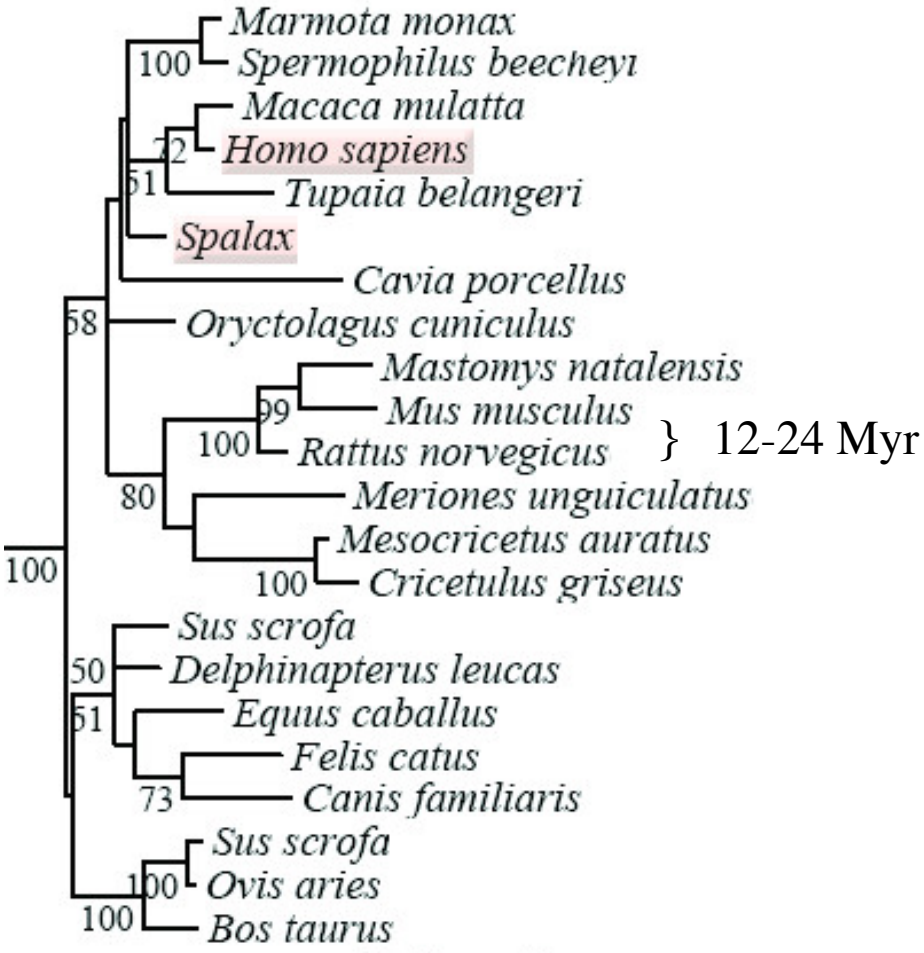
Fossil evidence: does not show uniform change, but punctuated equilibrium

Mass extinctions, duh

Large differences in evolutionary rates between groups

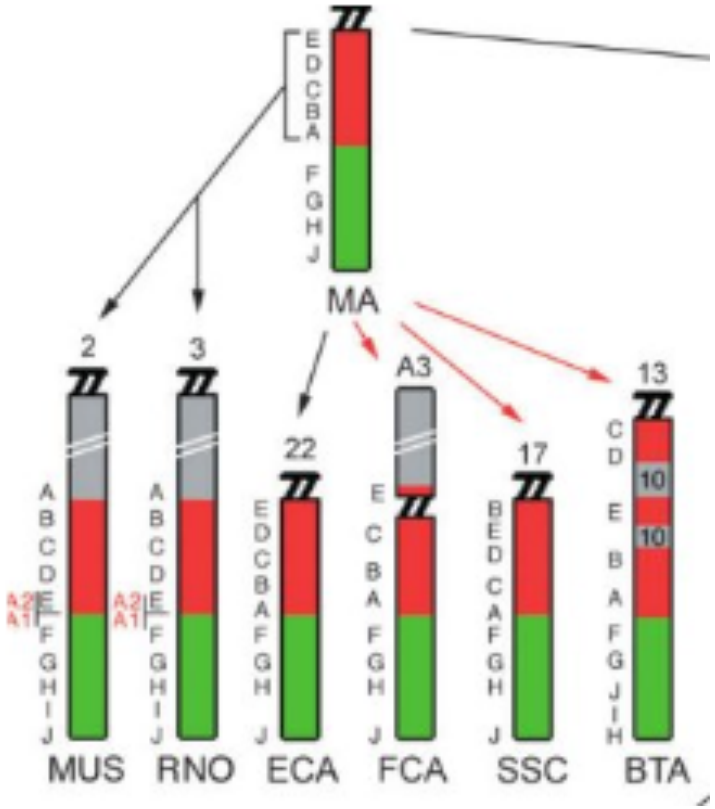
Evolution is relatively fast; so organisms stay in equilibrium with selective forces until the forces undergo a change, due to changes in climate, competition, etc.

Example: slow karyotypic evolution in mammals



} 12-24 Myr

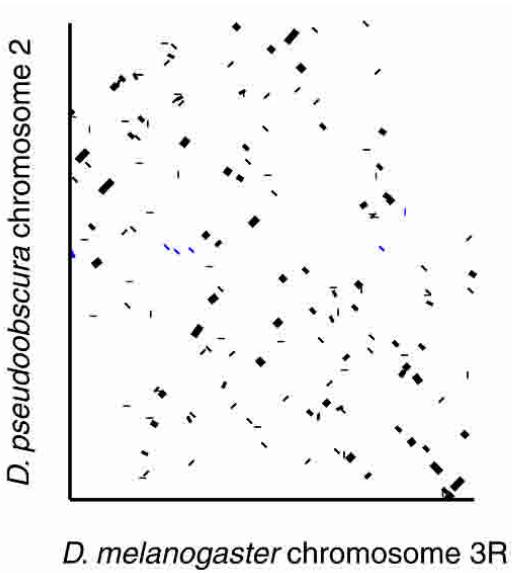
Chromosome 20

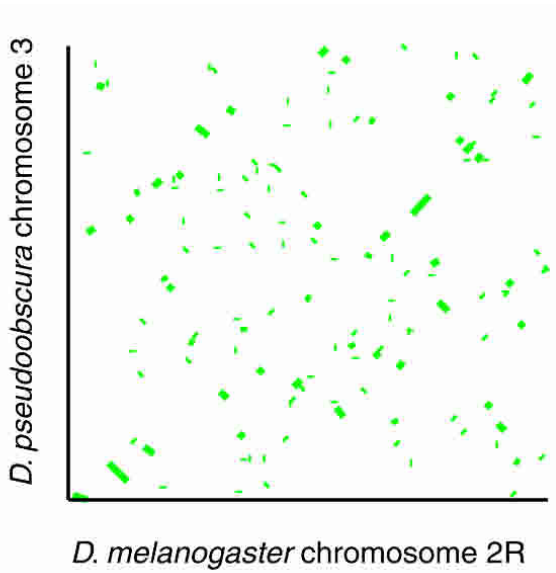


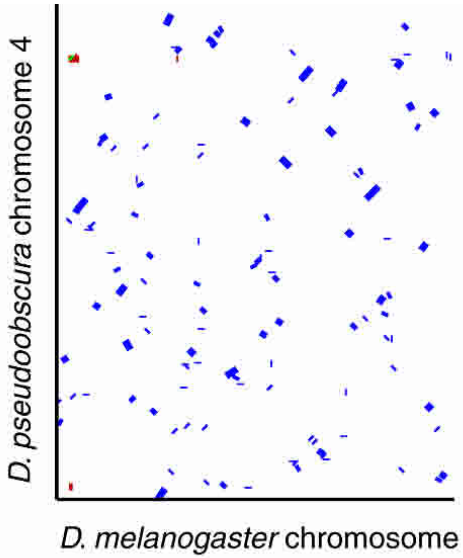
mouse rat horse cat pig cow

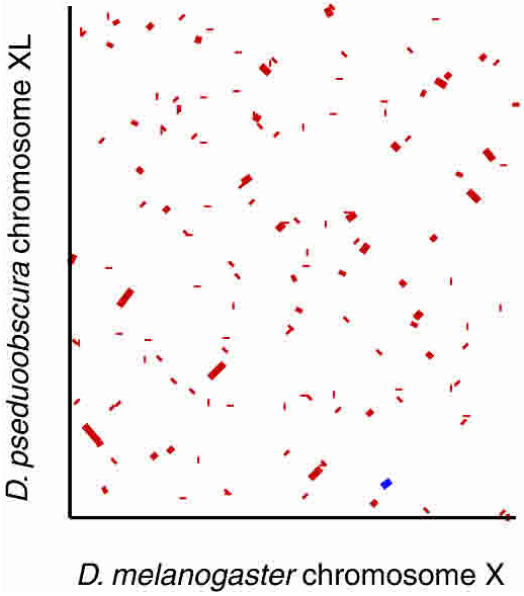
50 large rearrangements estimated between mouse and rat in entire genome

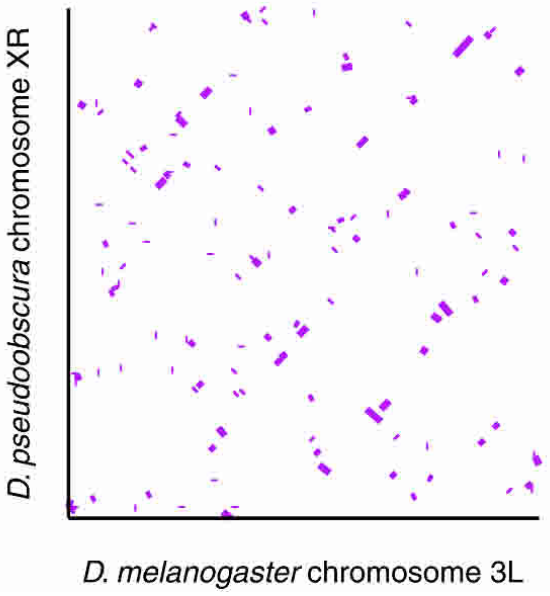
Fast karyotypic evolution in Drosophilids



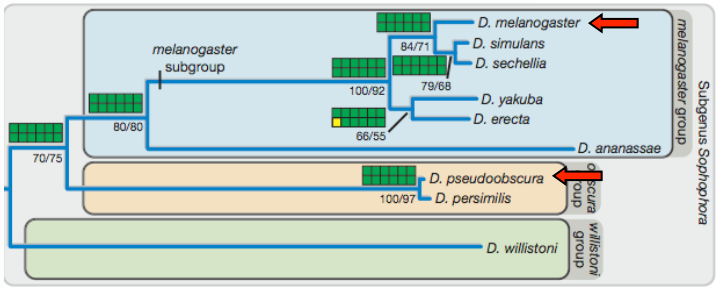








Separation: 25-30 million years



22-56,000 inversions fixed within the genus Drosophila

Point mutations and protein evolution are important, but genome rearrangments and regulatory evolution is more importnat

Transposable elements are a major source of genetic variation driving evolution

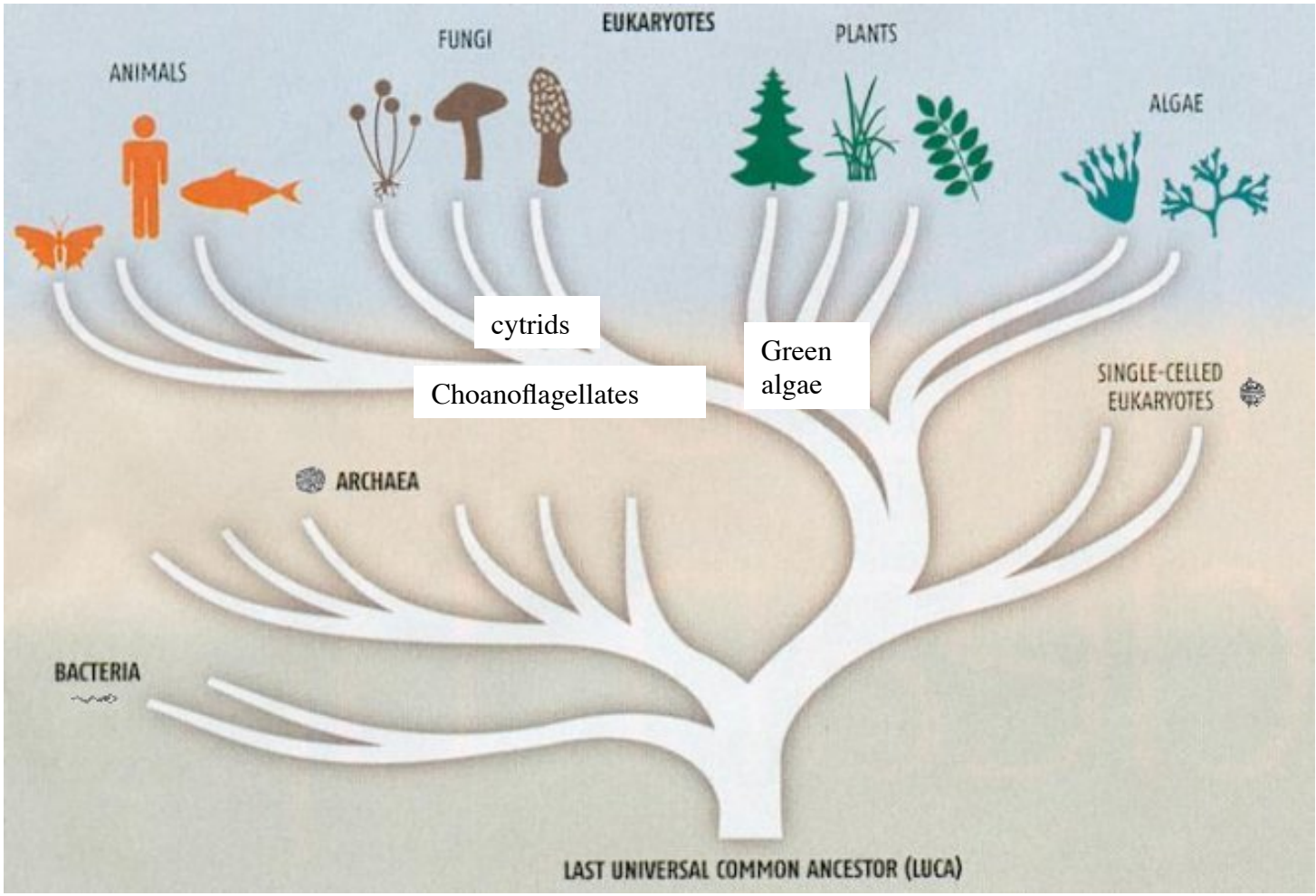
Individual humans differ by multiple CNVs; they are more readily associated with phenotypes/disease than point mutations

Transposons generated ~50% of human DNA; they are responsible for the rapid karyotypic evolution in insects; many examples are known of transposons associated with alleles conferring benefit; evolution drug resistance in bacteria since antibiotics a prime example

Origin of multicellularity

Fungi much closer to animals than to plants

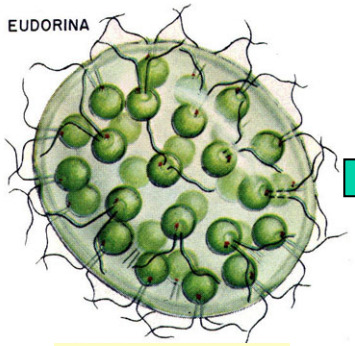
Lower fungi: slime molds, etc. Not closely related to fungi; instead arose from chytrids, choanoflagellates



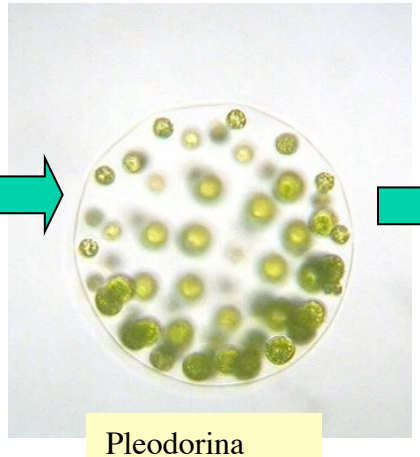
Colonial green algae

Origin of plants?

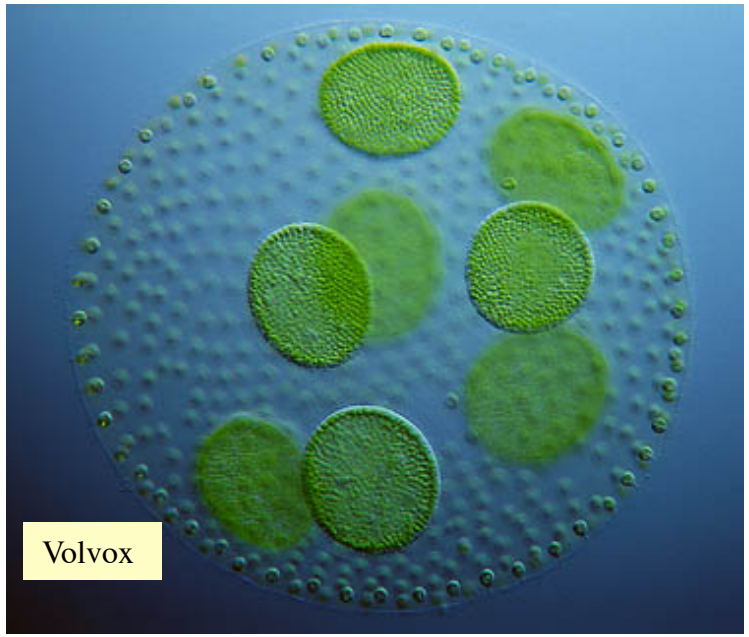
Chlamydomonas



Eudorina



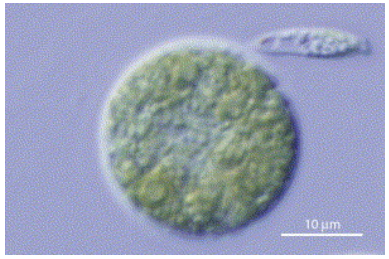
Pleodorina



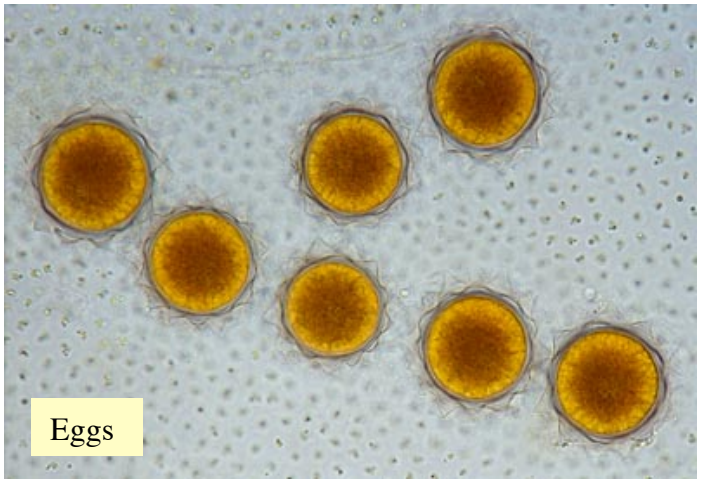
Volvox

A male specific gene in Pleodorina, PlestMID, expressed only in sperm nuclei, is related to the abundant mat- mating type gene, MID, of Chlamydomonas.

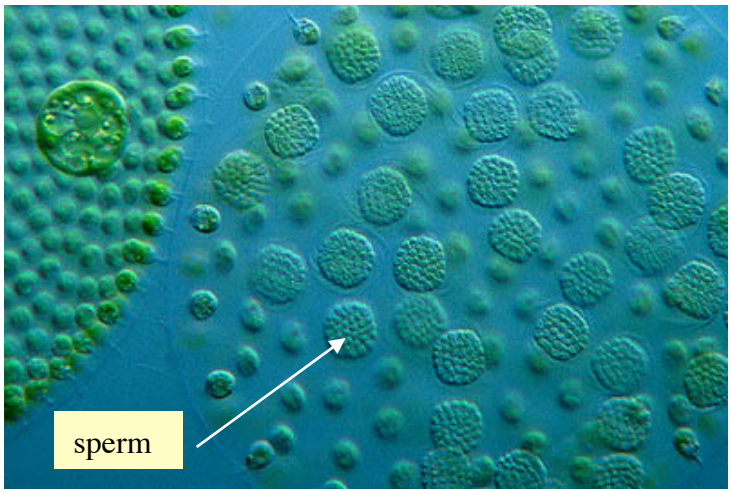
Earliest gamete specialization (size difference); colonies of different sex = sex determination



Pleodorina egg and sperm



Eggs



sperm

Genomes begin to encode a developmental program

Accrection of a developmental program, beginning with a spore, or zygote

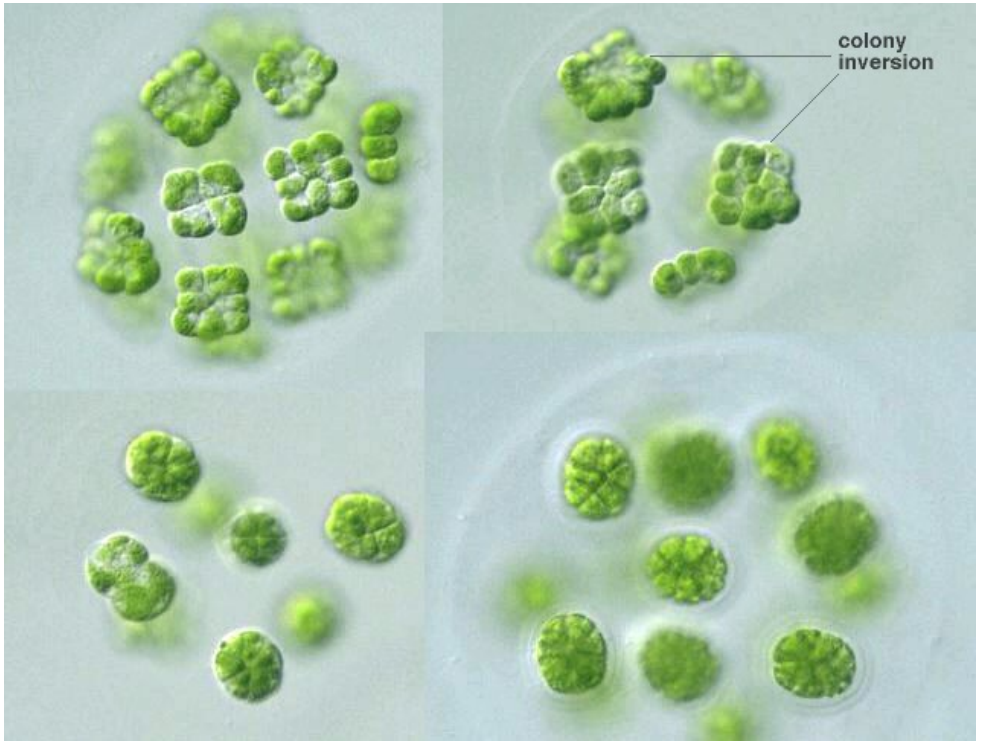
Volvox development:

1. germ line/soma separation
2. gastrulation-like "colony inversion"

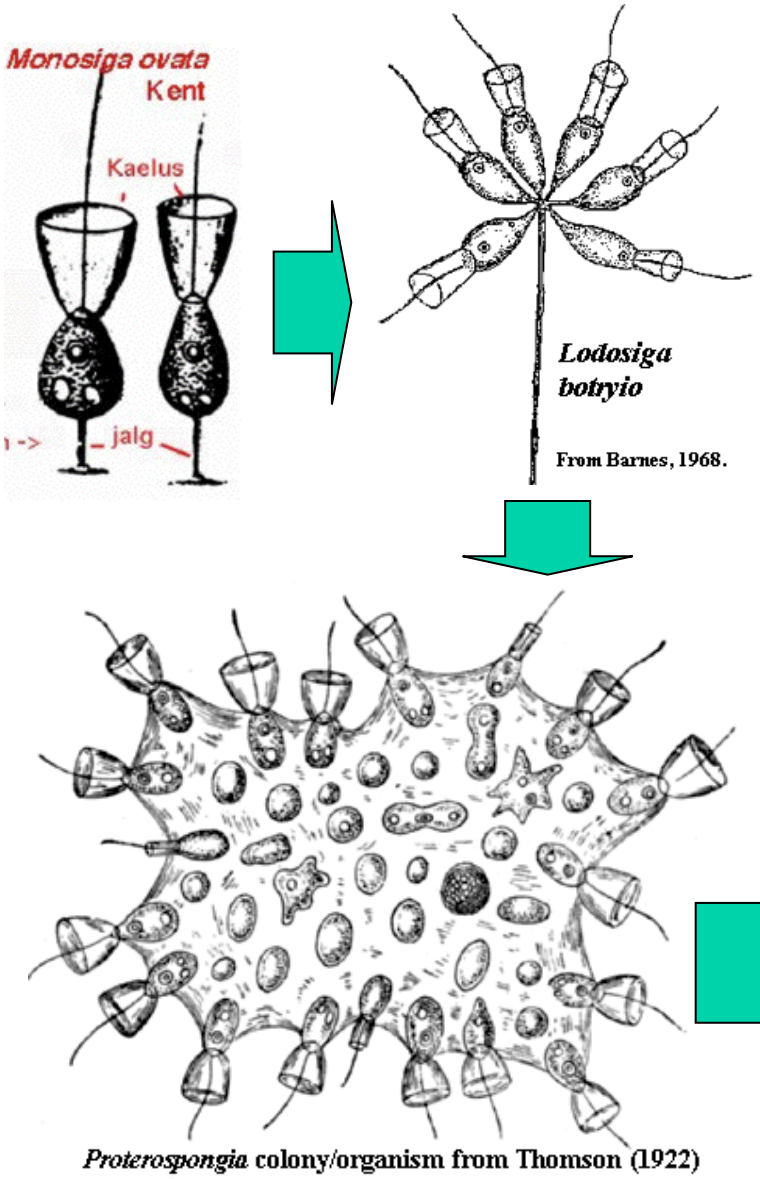
coincidence or parallel evolution?

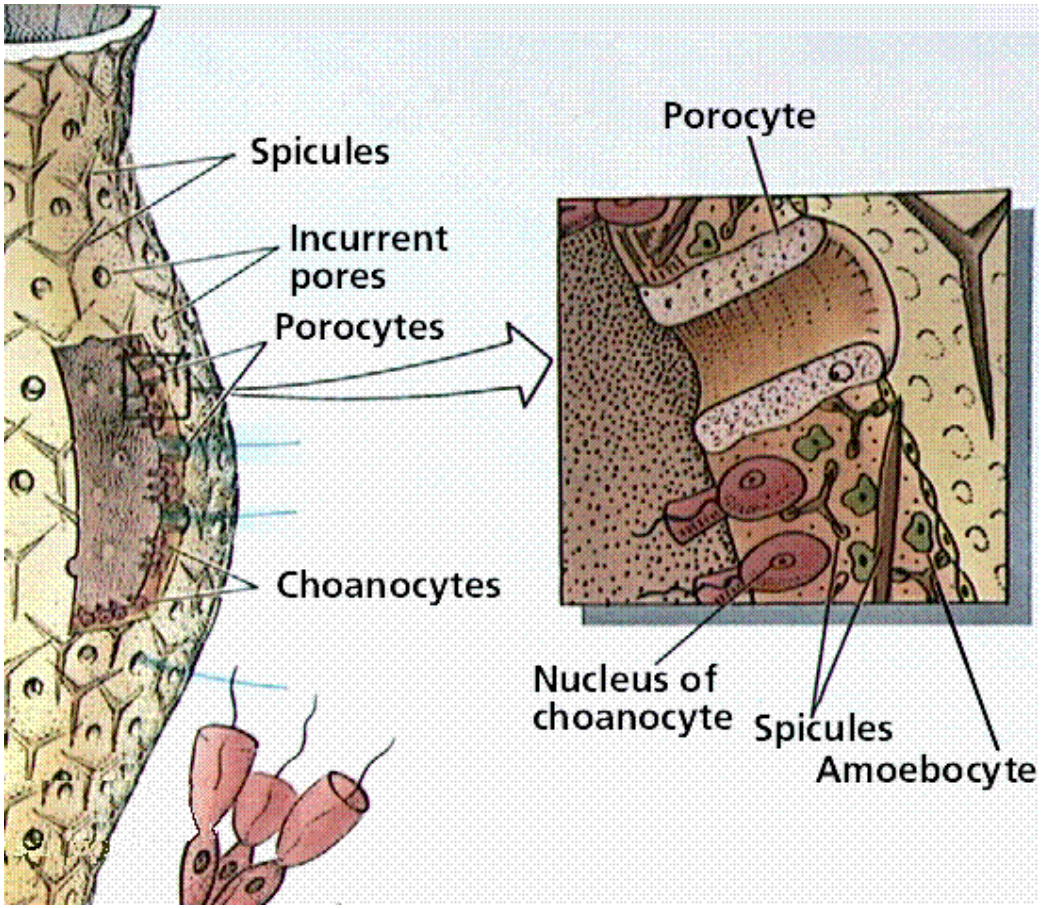
Need to understand the genetic basis of these programs to compare

RegA represses germ cell diff in somatic cells, probably by controlling chloroplast development; expression translationally regulated (see Babinger et al. Development 133, 4045)



Origin of sponges from Choanoflagellates





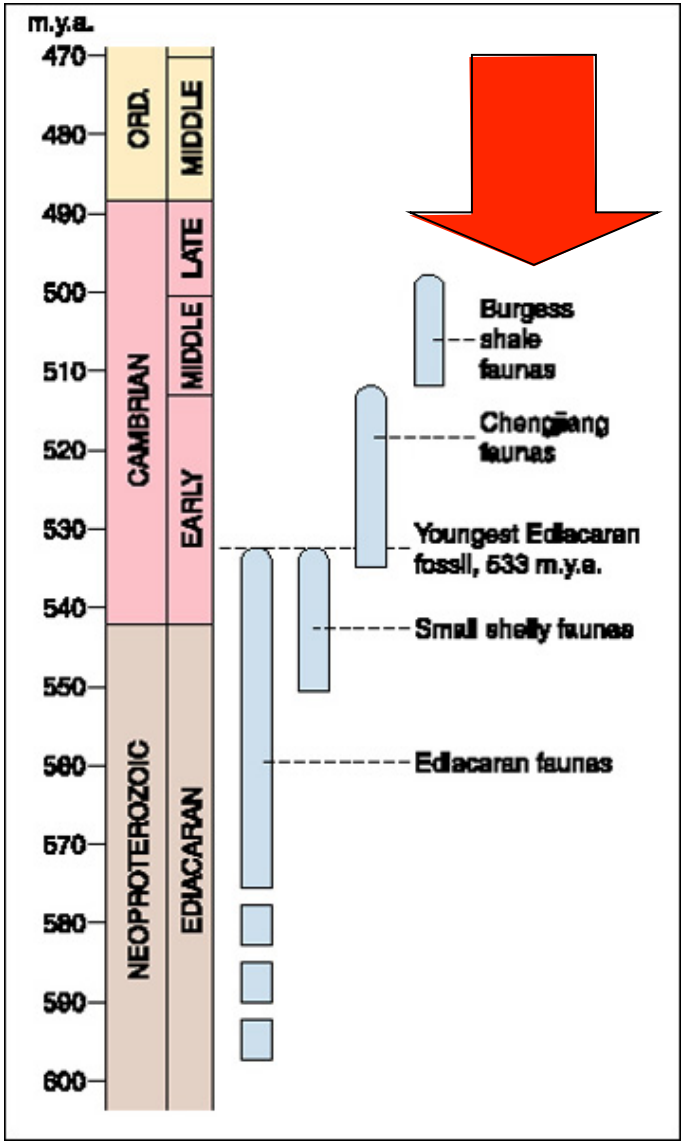
How many sponge developmental genes are present in each "intermediate" form?

The Cambrian explosion

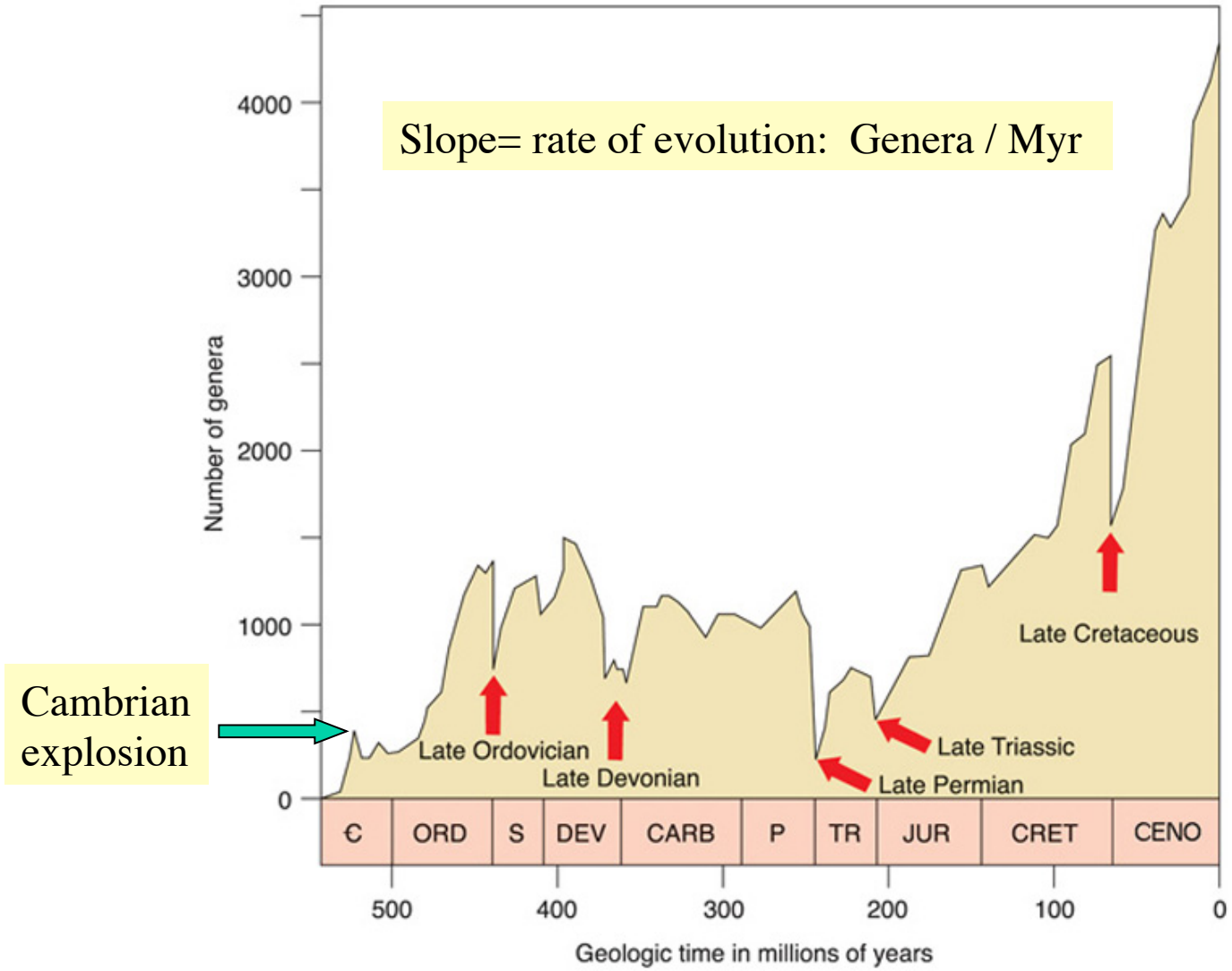
Burgess shale creatures

All life- marine

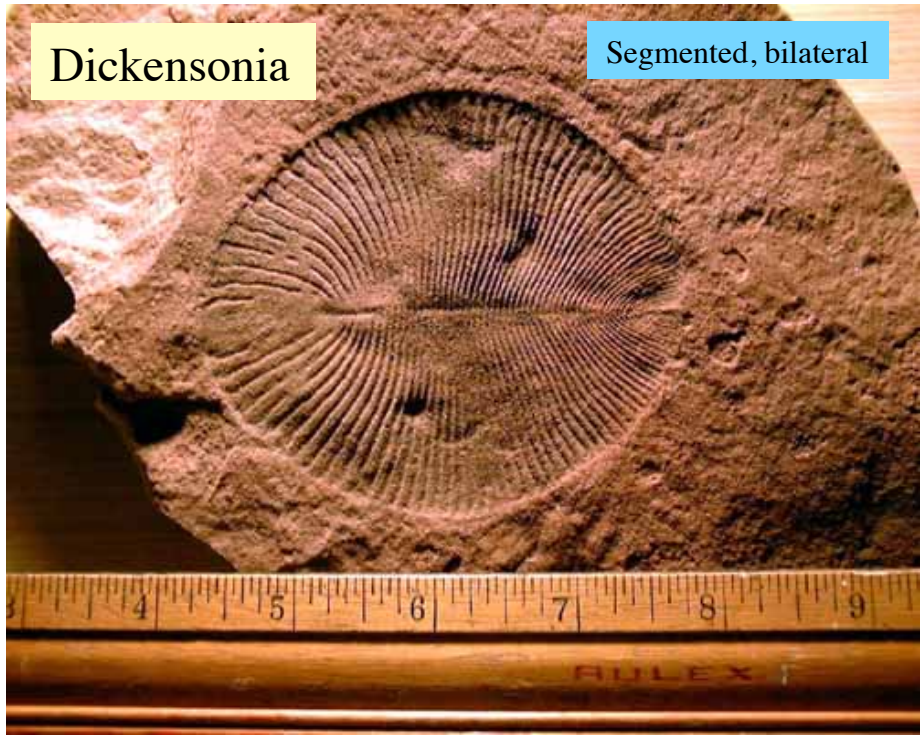
Presence of all major marine phyla

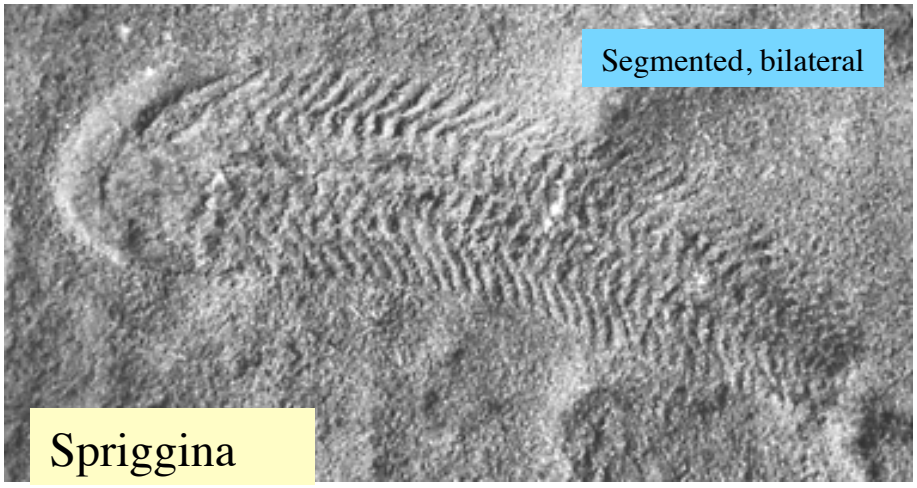


The Cambrian explosion-was it so special?

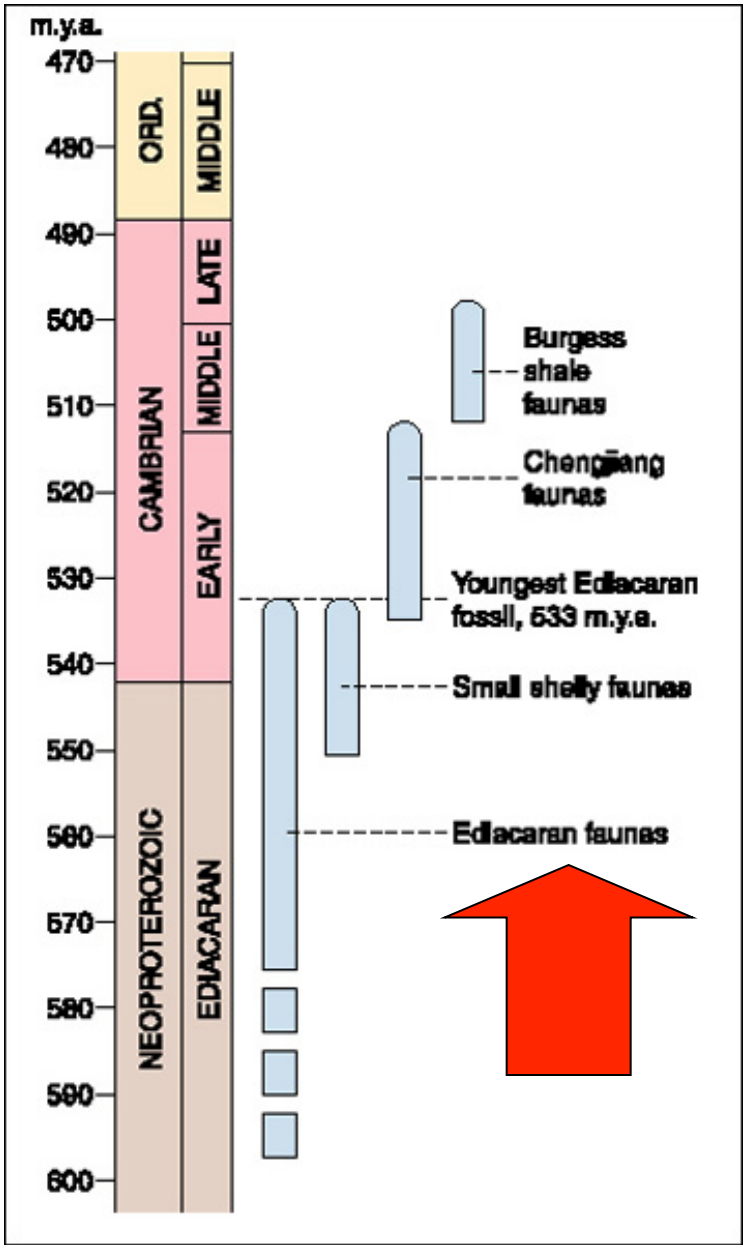


Pre-cambrian metazoans

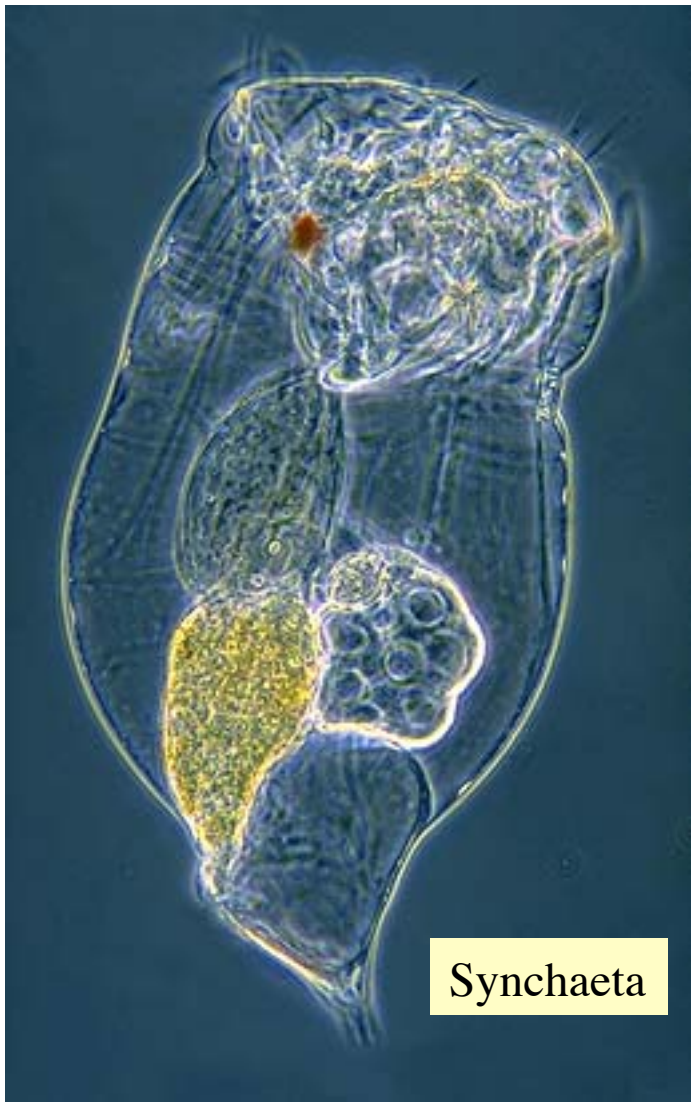




Edicaran animals

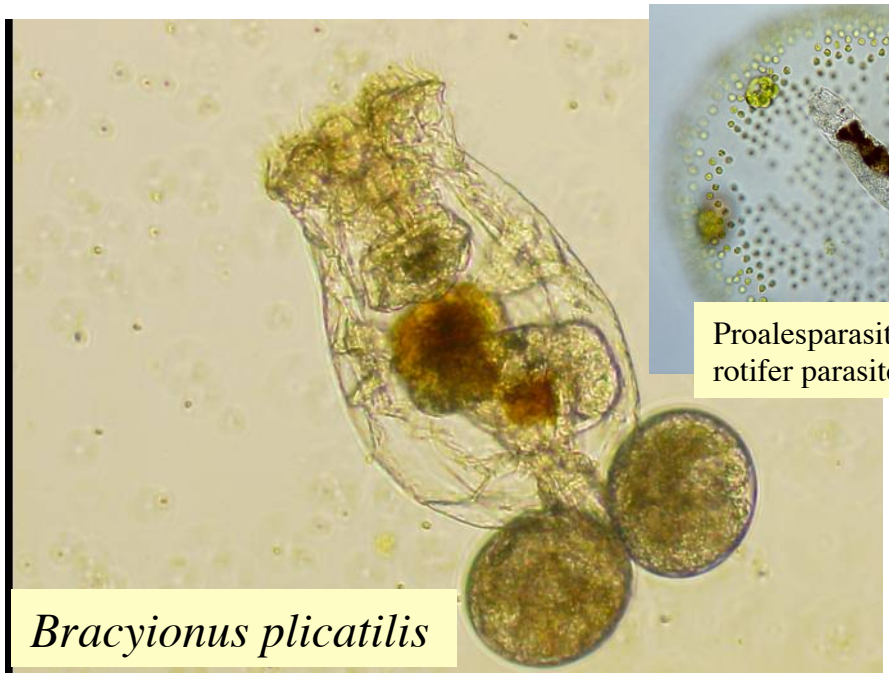


Other possible metazoan sources



Synchaeta

Rotifers: 50 μm to 3 mm



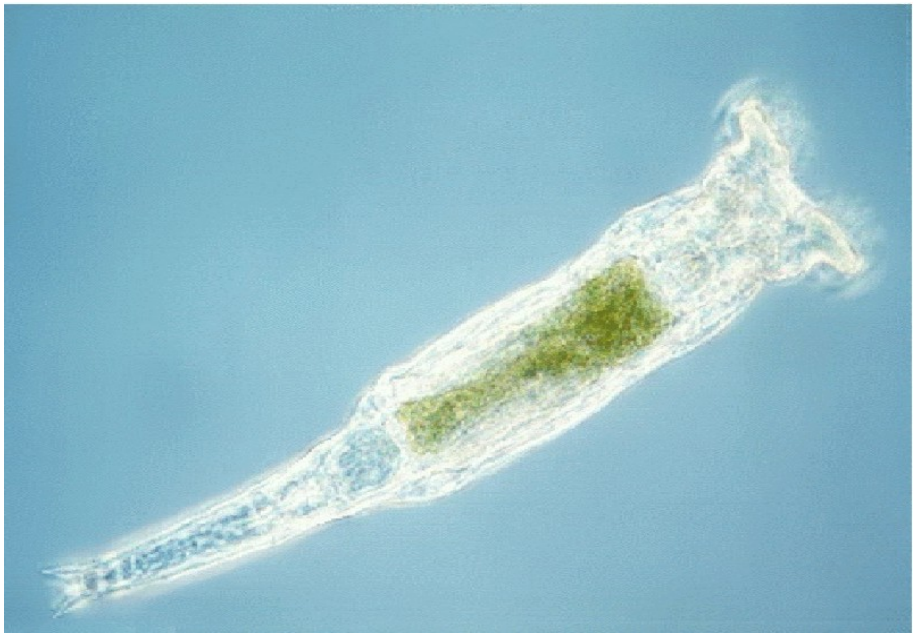
Bracyionus plicatilis

Proalesparasita: Volvox rotifer parasite

Current species classified as flatworms, (based on rRNA) but a distinct group

Don't fossilize

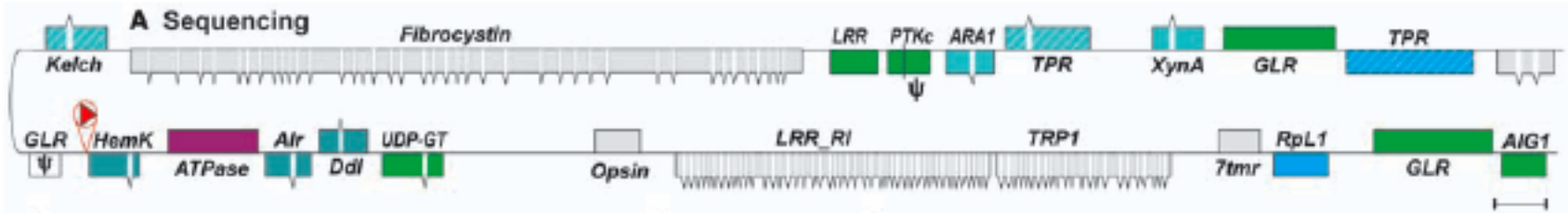
Unusual reproduction and genomes



>80 Myr evolution of the Bdelloid group without sexual reproduction

Horizonal gene transfer, **widespread in bacteria today**, may have played a big role in assembling a functional metazoan developmental program, from both primitive algal, rotifer and chanoflagellate sources

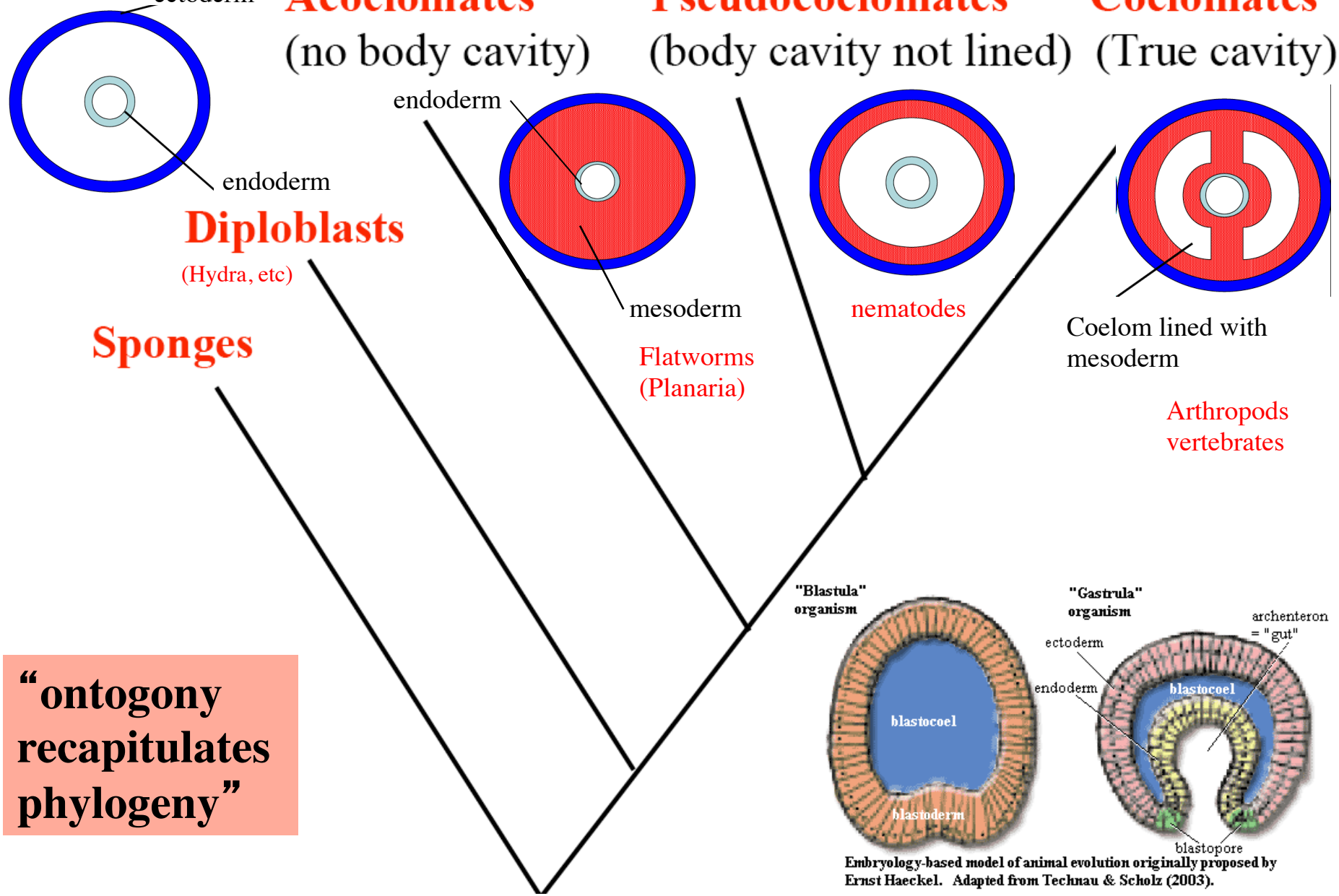
Presence of abundant horizontally transferred genes: Science 320, 1210 (2008)



metazoan bacterial fungal plant

Adineta vaga

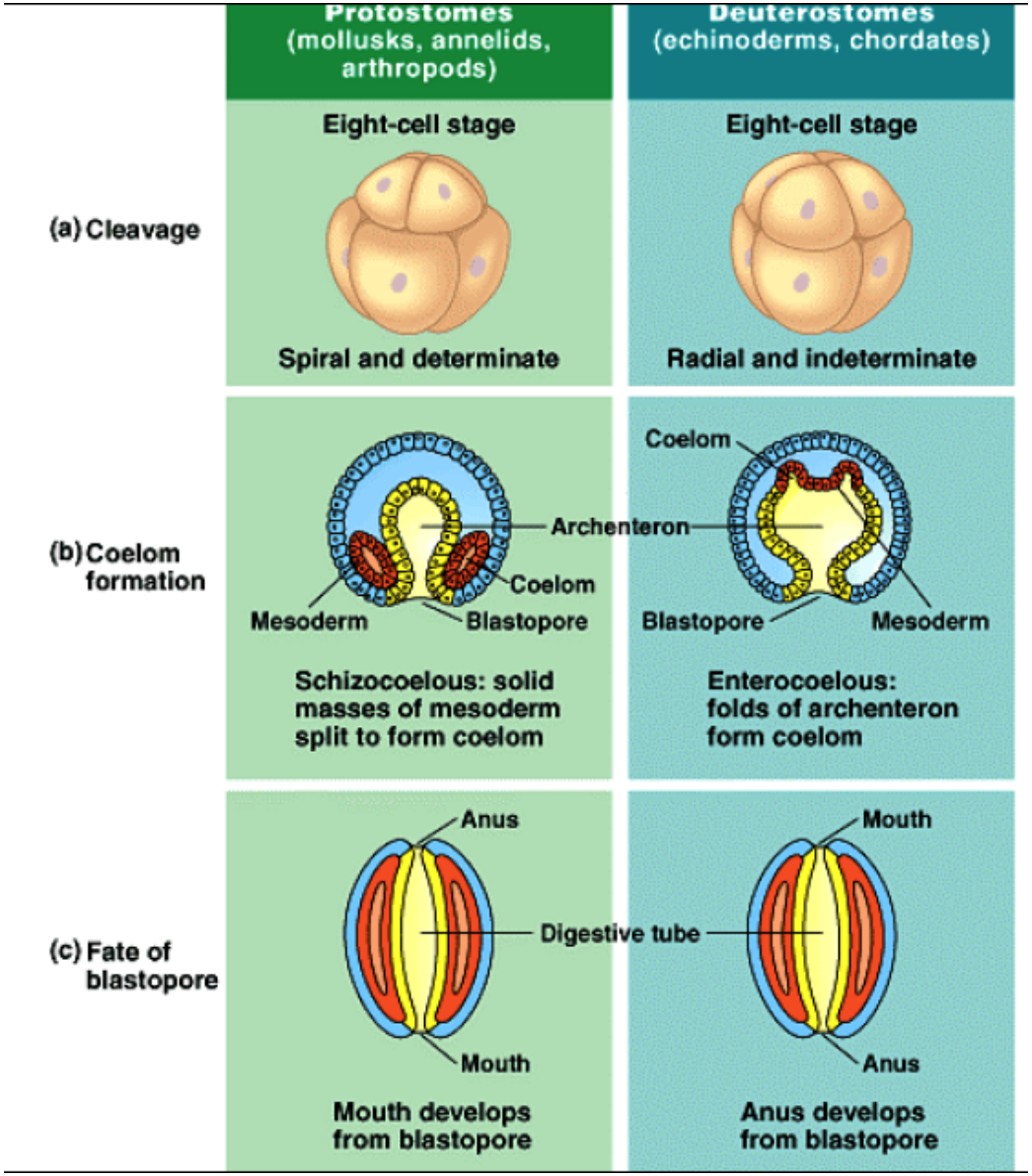
Grouping animals based on body structure



"ontogony recapitulates phylogeny"

Embryology-based model of animal evolution originally proposed by Ernst Haeckel. Adapted from Technau & Scholz (2003).

Classification based on blastopore fate

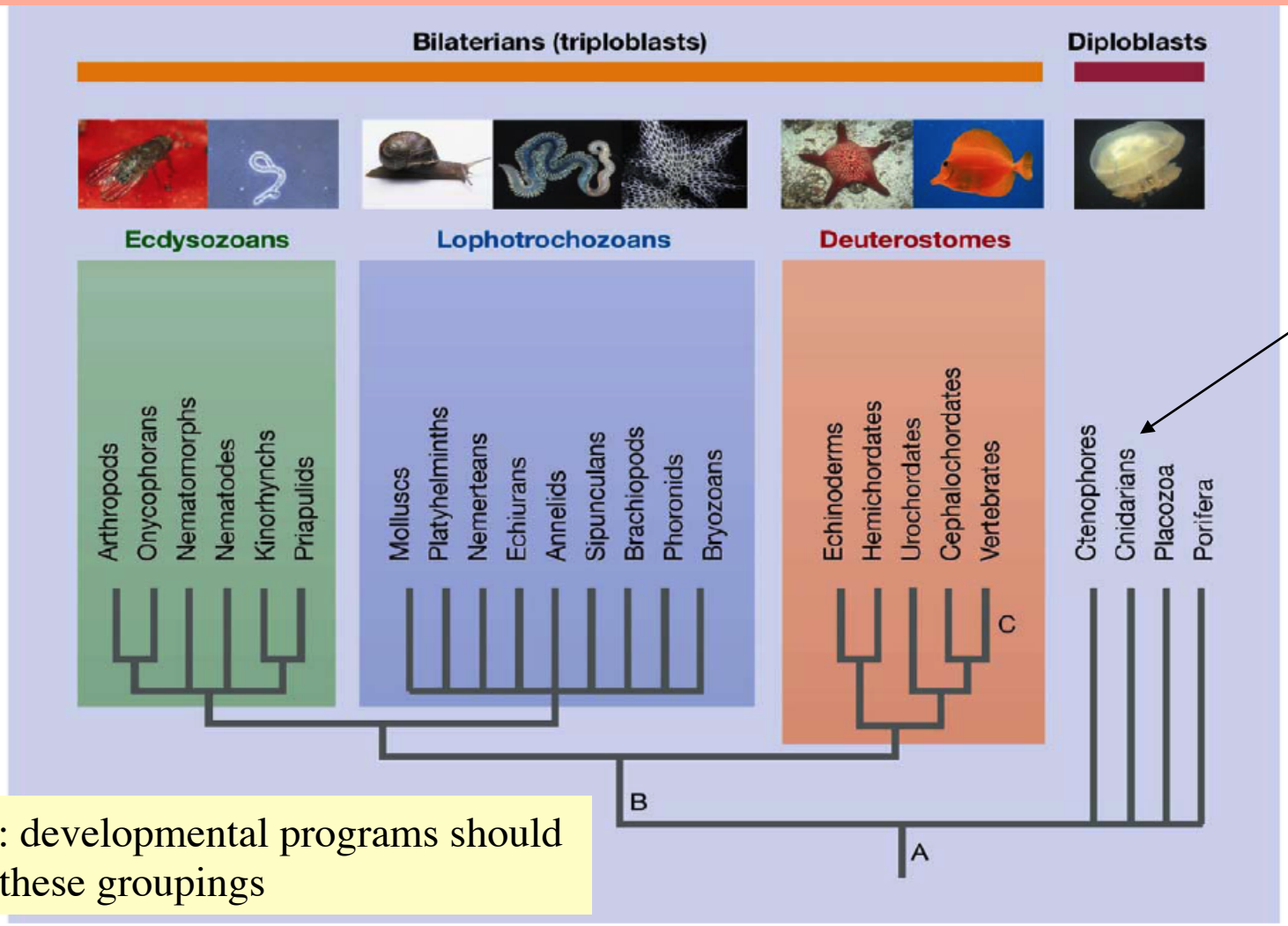


Protostome vs Deuterostome

There does not appear to be a major difference in developmental program between these groups

"Germ layer" concept has also not held up well

Current cladistic phylogeny of animalian metazoa



Predict: developmental programs should follow these groupings

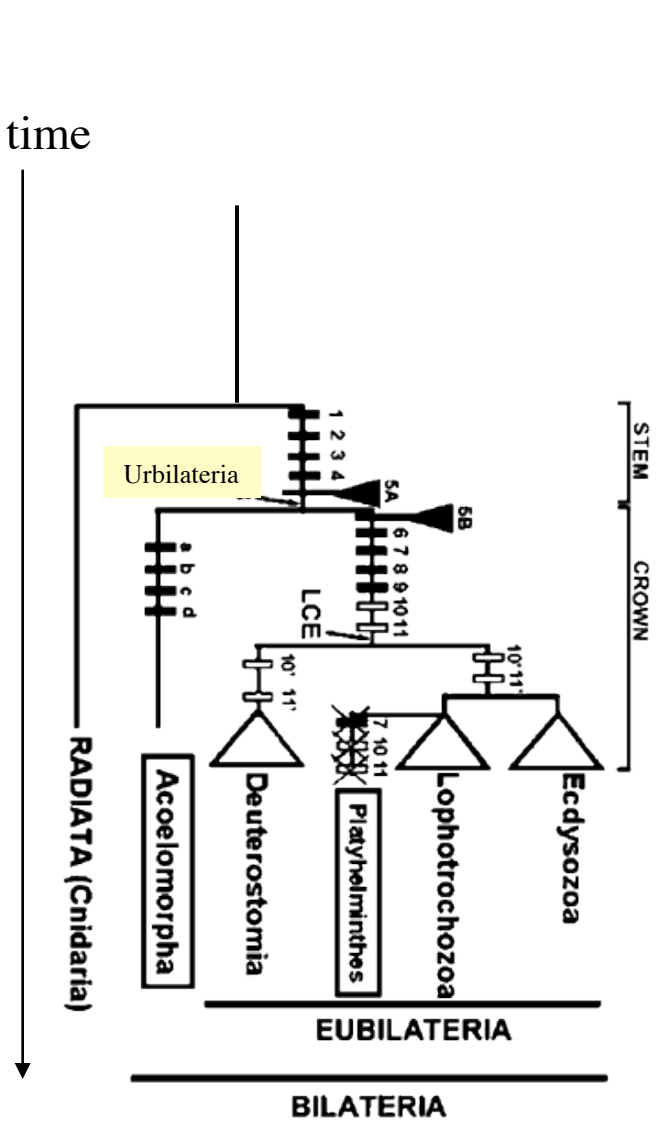
Holland, P.W.H. (1999) The future of evolutionary developmental biology. **Nature** 402, C41-C44. *('Impacts of foreseeable science' Supplement)*

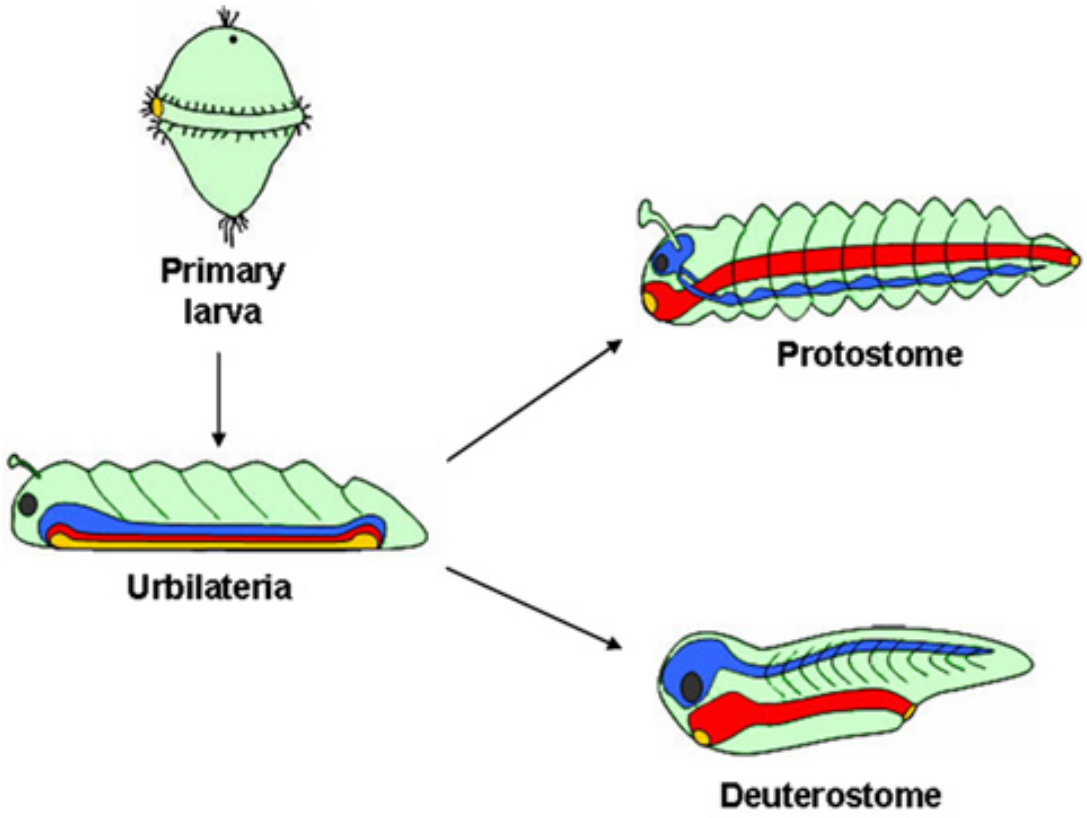
Identifying conserved components of developental programming

What portions of the program are found throughout all major metazoan animal phyla? (This would imply there was common ancestor of all these phyla.)

Such an animal would have lived before Cambrian explosion

The last common Precambrian precursor of bilateral metazoans- Urbilateria



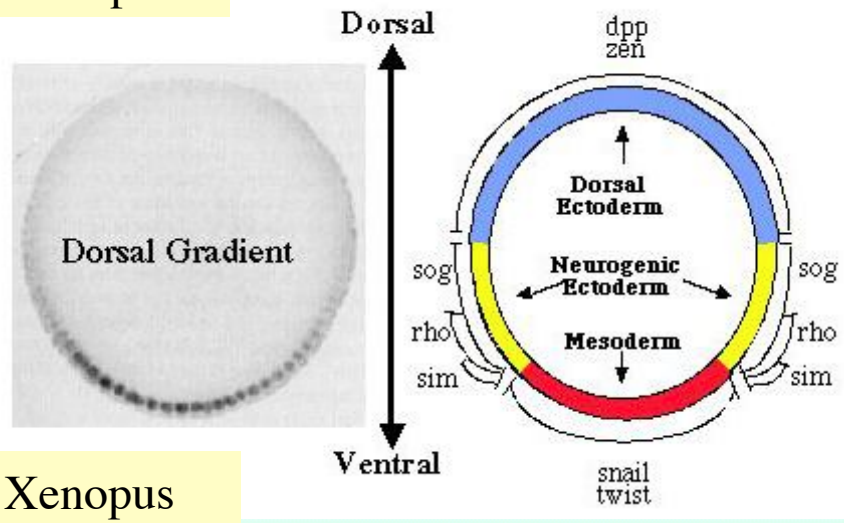


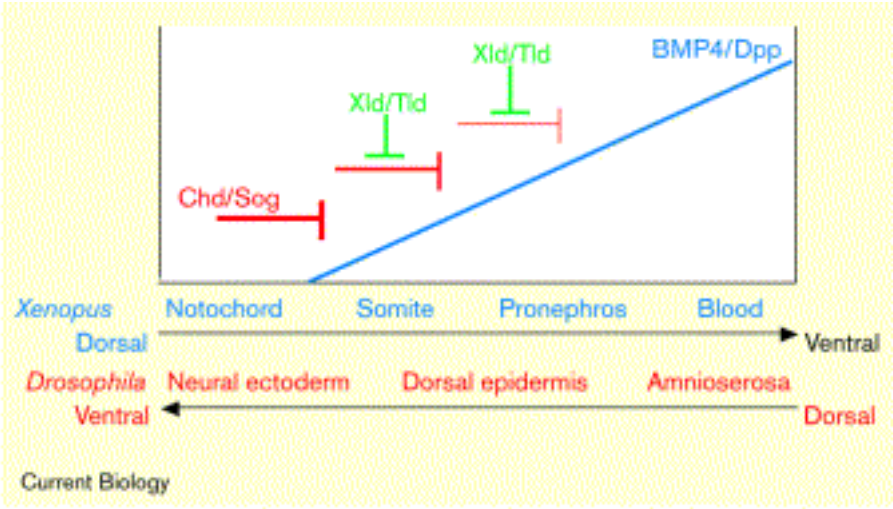
Candidate features: A/P patterning; Dorsal ventral pattern (shown); germ cell specification/function; major somatic organ systems, others?

Major patterning systems are conserved

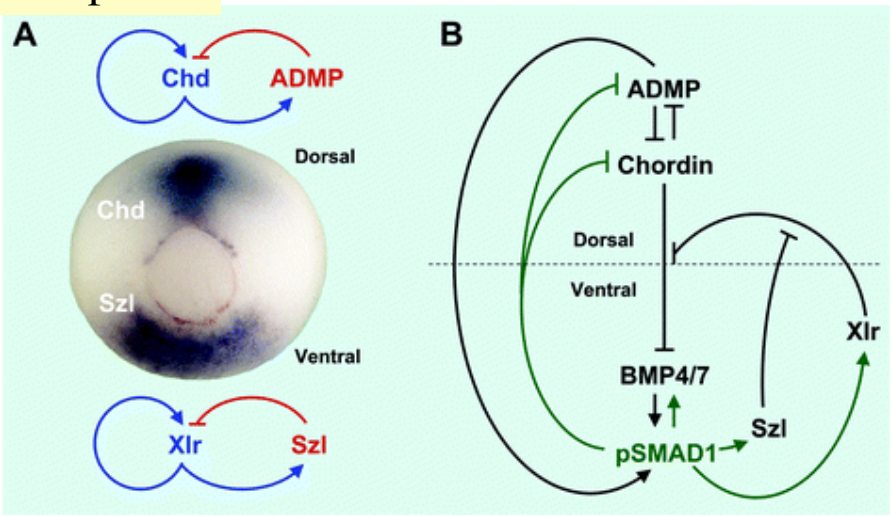
D/V axis patterning

Drosophila





Xenopus

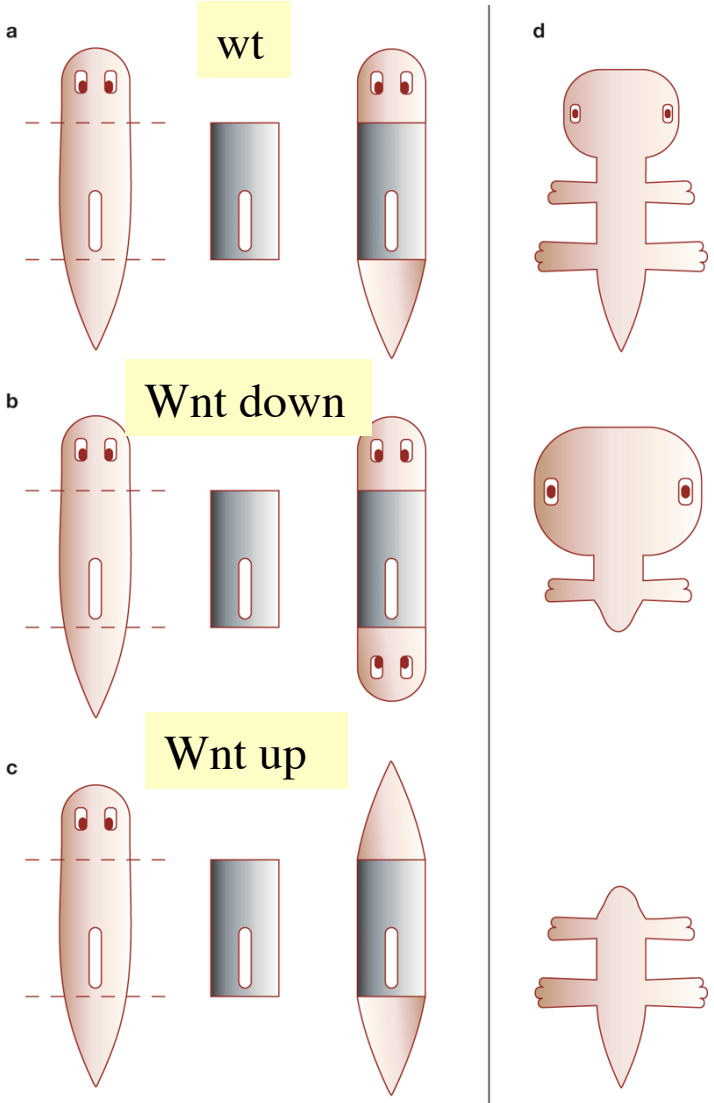


d/v axis in invertebrates and vertebrates controlled by BMP4/dpp signaling

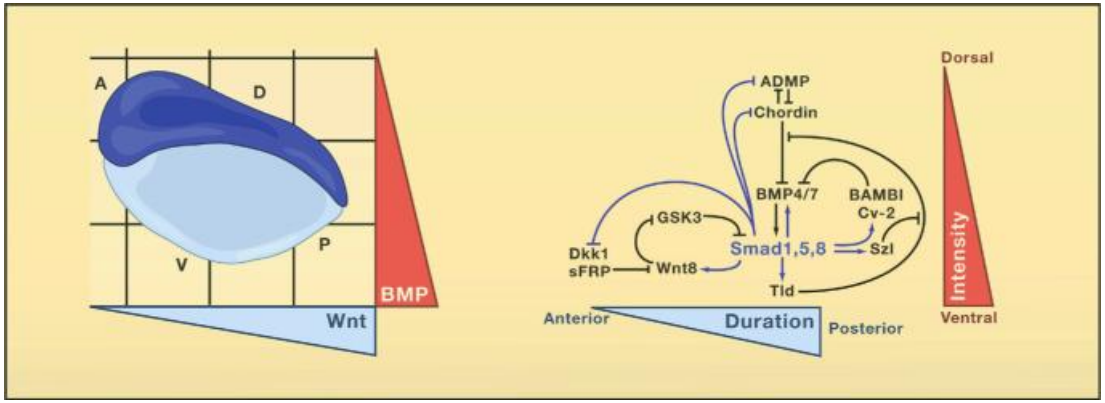
Wnt and conservation of a/p patterning

Planaria

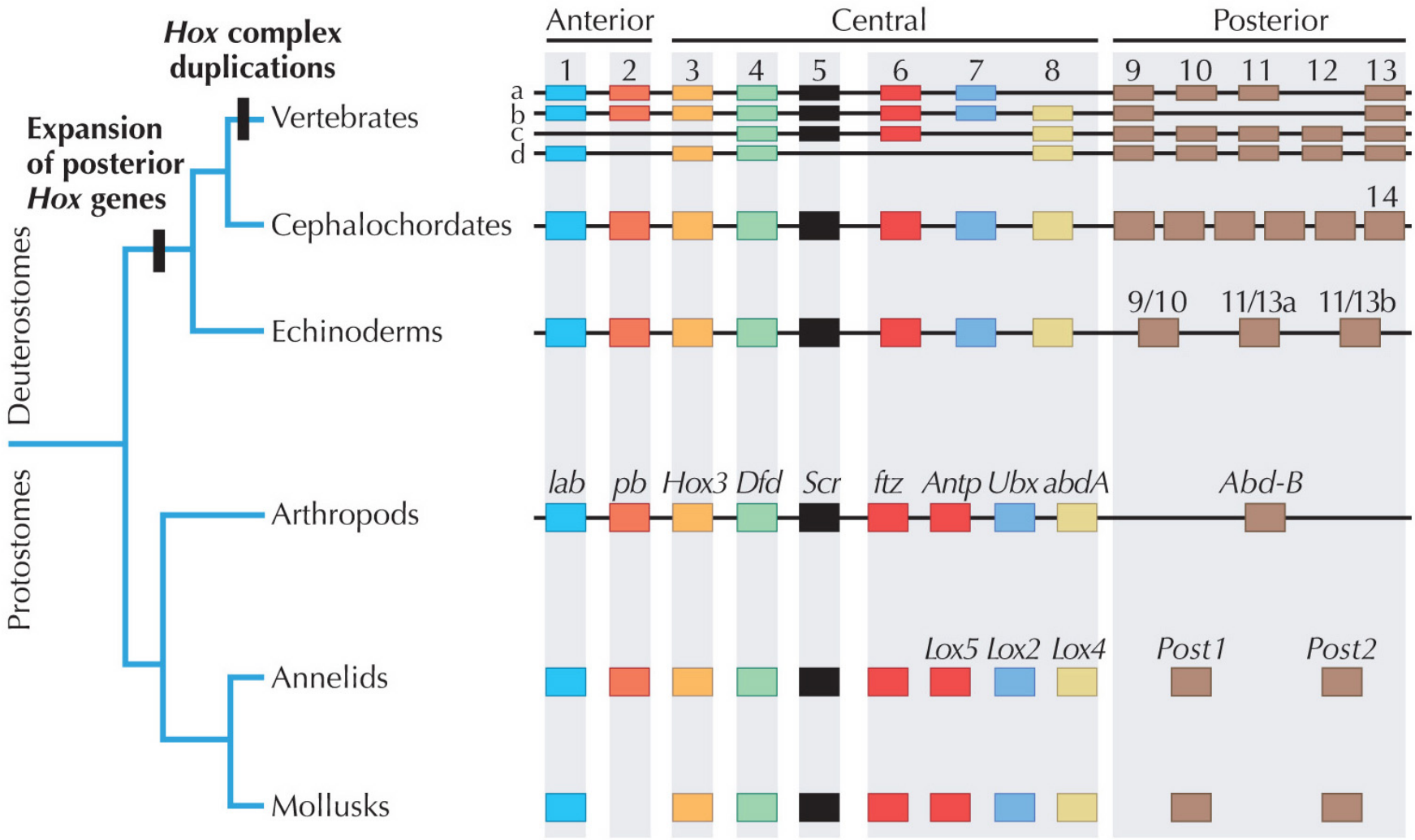
Vertebrate



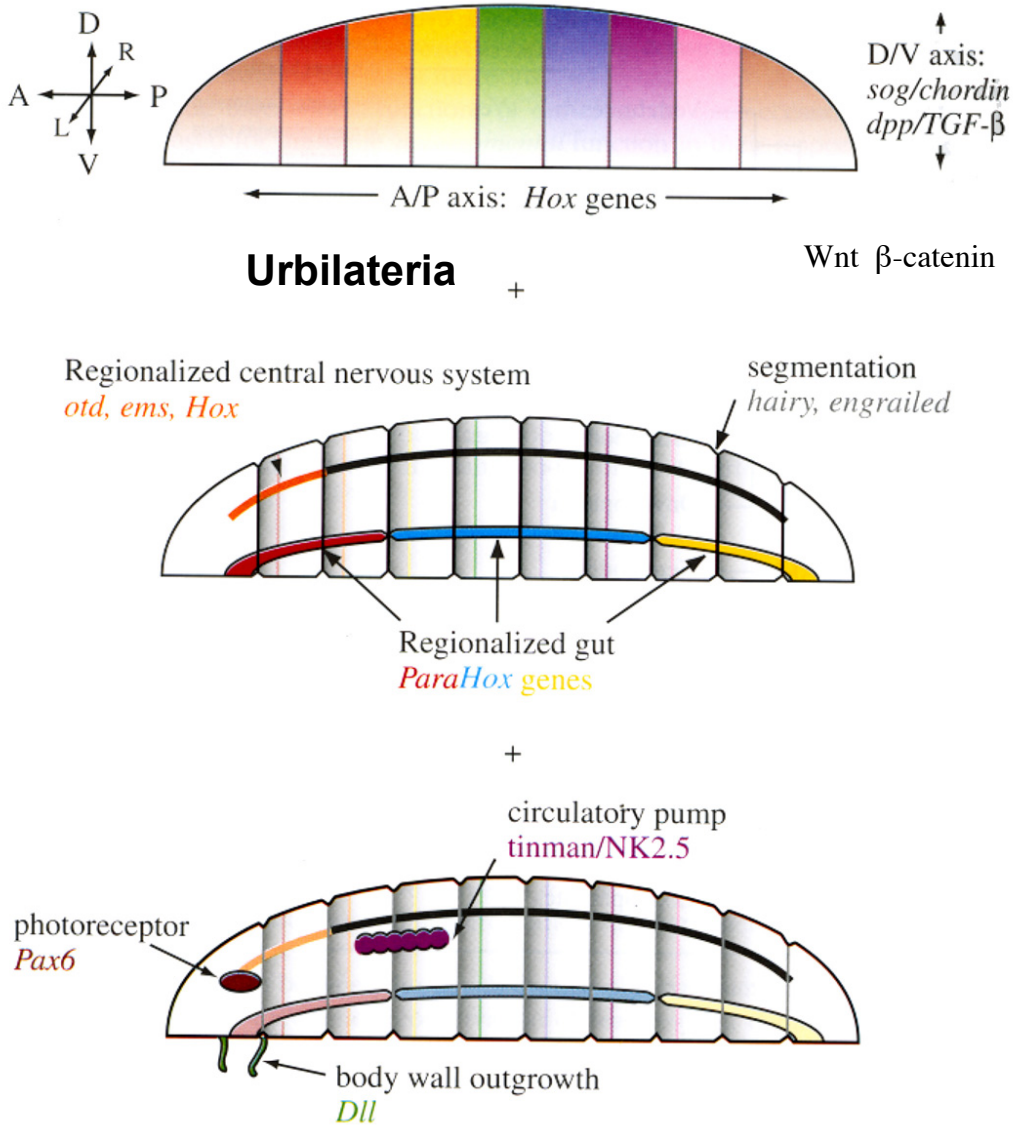
11 of 12 families of vertebrate wnt proteins are present in sponges



Evolution of Metazoan Hox genes



Developmental features of Urbilateria



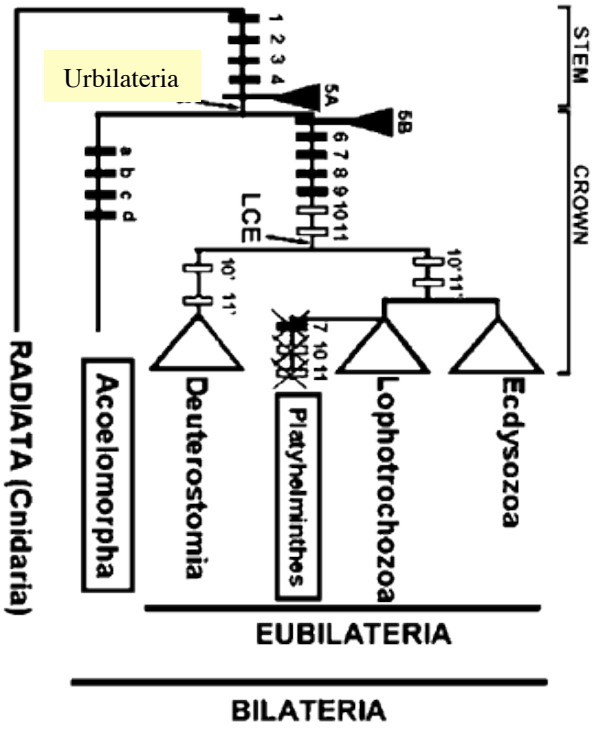
The basic nervous system, sensory inputs, motor nerves, neurosecretion, channels, etc.

All other critical organ systems

All the cell types and genes required to support these systems

The basic epigenetic program to support development; including all chromosomal machinery

How complex was Urbilateria?



Arthropod/annelid-like

Planarian-like

complex simple

(c)

character	genes		
AP patterning	*HOX*		
DV patterning	*TGFβ/BMP 2/4 sog/dpp*		
posterior patterning	*evx, cdx*		
central nervous system	*otx, emx, six3/6, HOX1*		
photoreception 'eyes'	*PAX6, RX, opsin*		
heart	*tinman*		
segmentation, segmentation clock	*hairy, engrailed, notch/delta*		
regionalized through gut	*HNFβ 3, GATA factor goosecoid, brachyury*		
appendages	*Distal-less/DLX*		

Change in blastopore location?

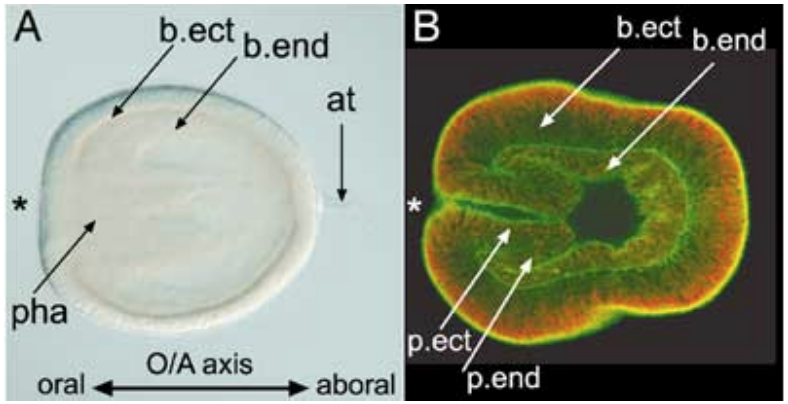
D/v axis is reversed in protostome and deuterostomes

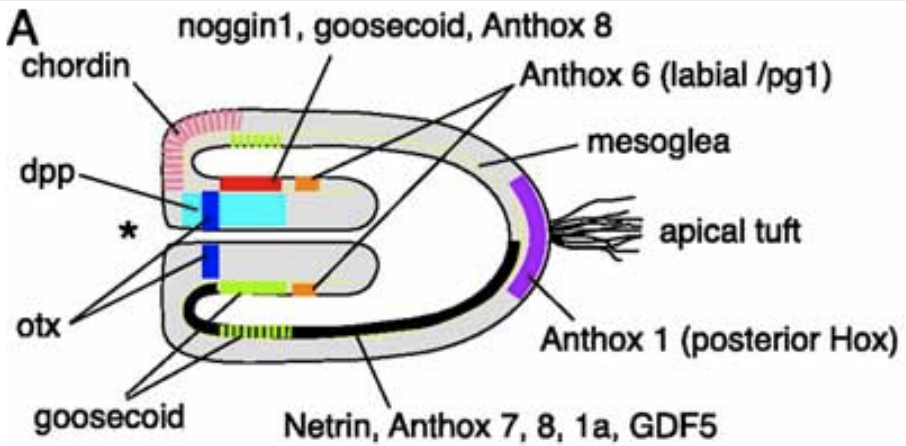
Fate of blastopore is reversed in protostome and deuterostomes

Did migration of the site of gastrulation 180^{o} relative to embryonic axes lead to these differences?

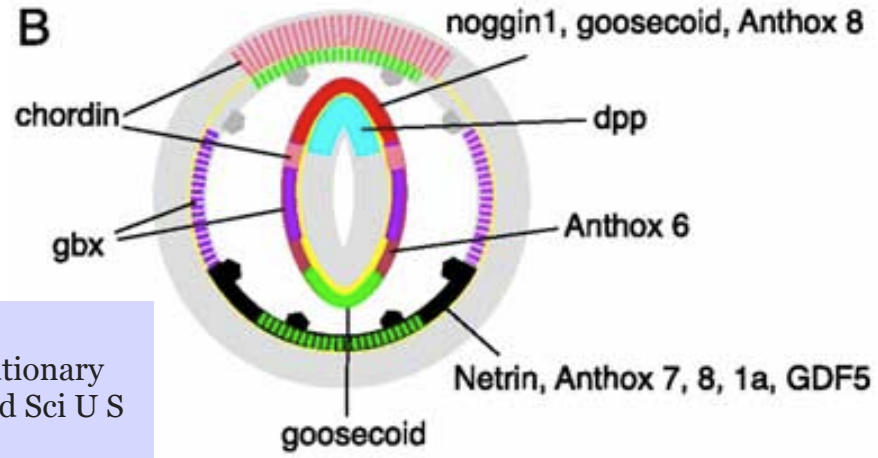
Common mechanisms in Radiata and Bilateria

Nematostella vectensis





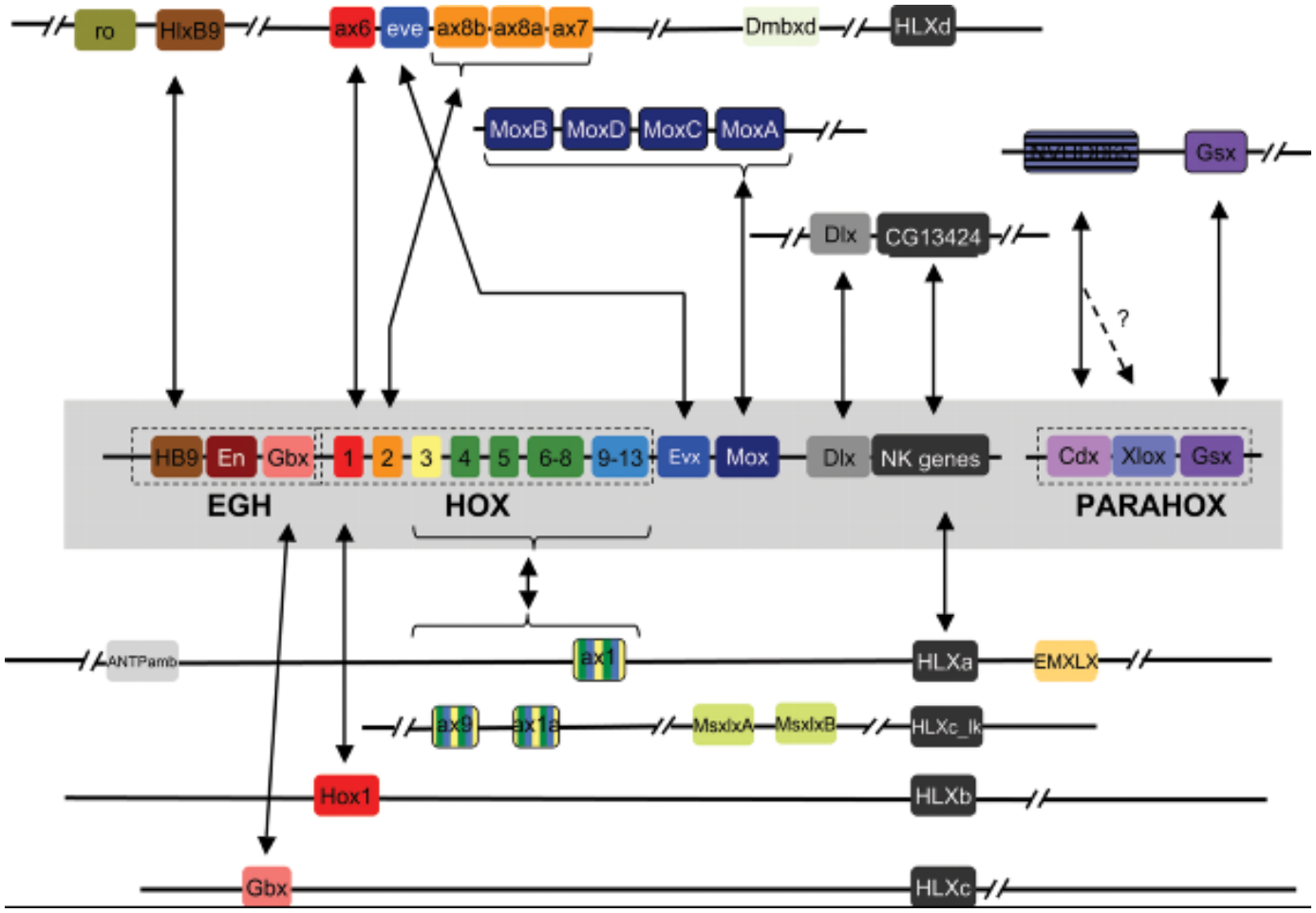
Sea anenome



Matus DQ, Pang K, Marlow H, Dunn CW, Thomsen GH, Martindale MQ (2006) Molecular evidence for deep evolutionary roots of bilaterality in animal development. Proc Natl Acad Sci U S A. 103(30):11195-200.

Radiata have bilateral features and share many patterning mechanisms with Bilateria

Sea anenome: 30+ Hox and ParaHox genes



Cnidarian; related to jellyfish, corals

Have anterior, p Hox genes, paraHox genes, and probably posterior Hox genes;

Nematostella vectensis

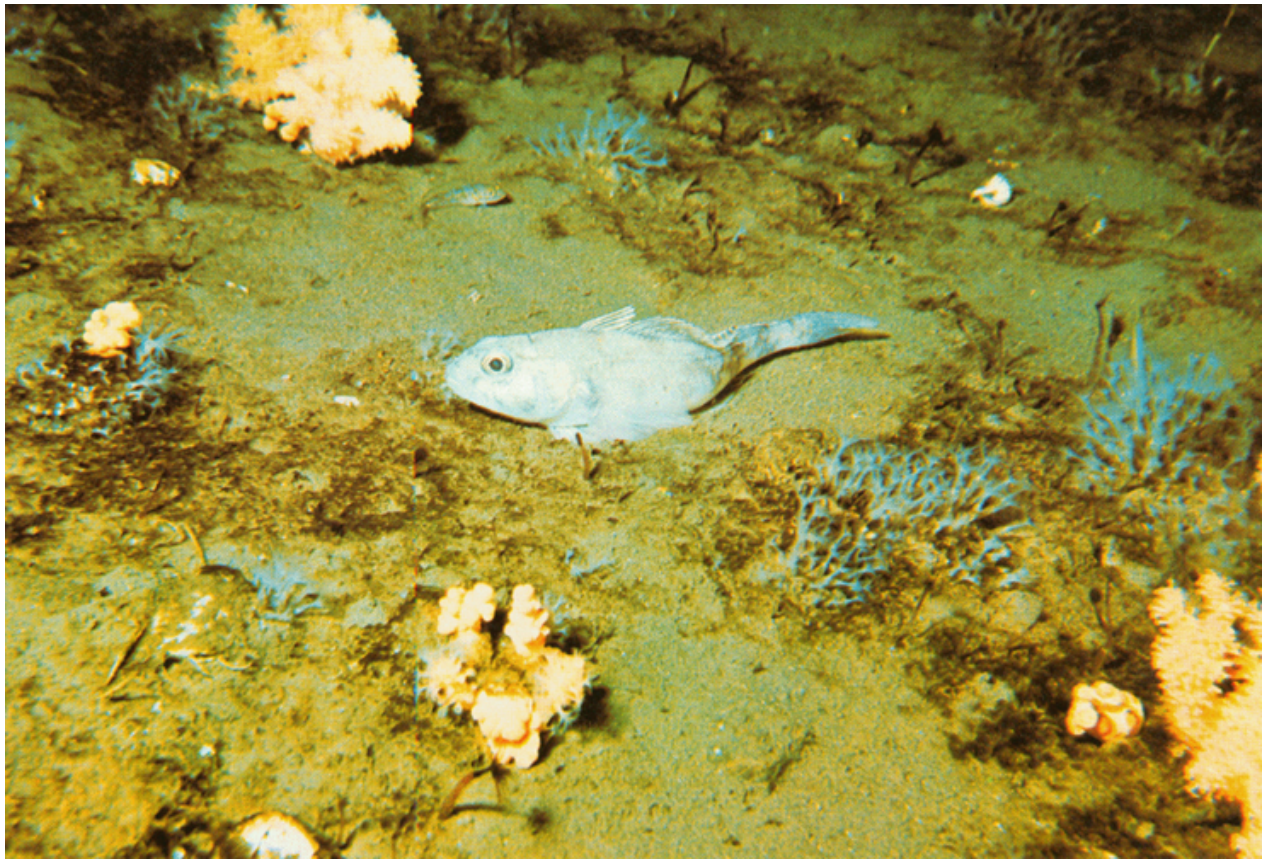
Gene loss model

Unused characteristics are quickly lost

Astyanax fasciatus, cave-dwelling blind form

Danio rerio, the zebrafish

The icefish



No red cells; breaths through skin

Globin genes mutated

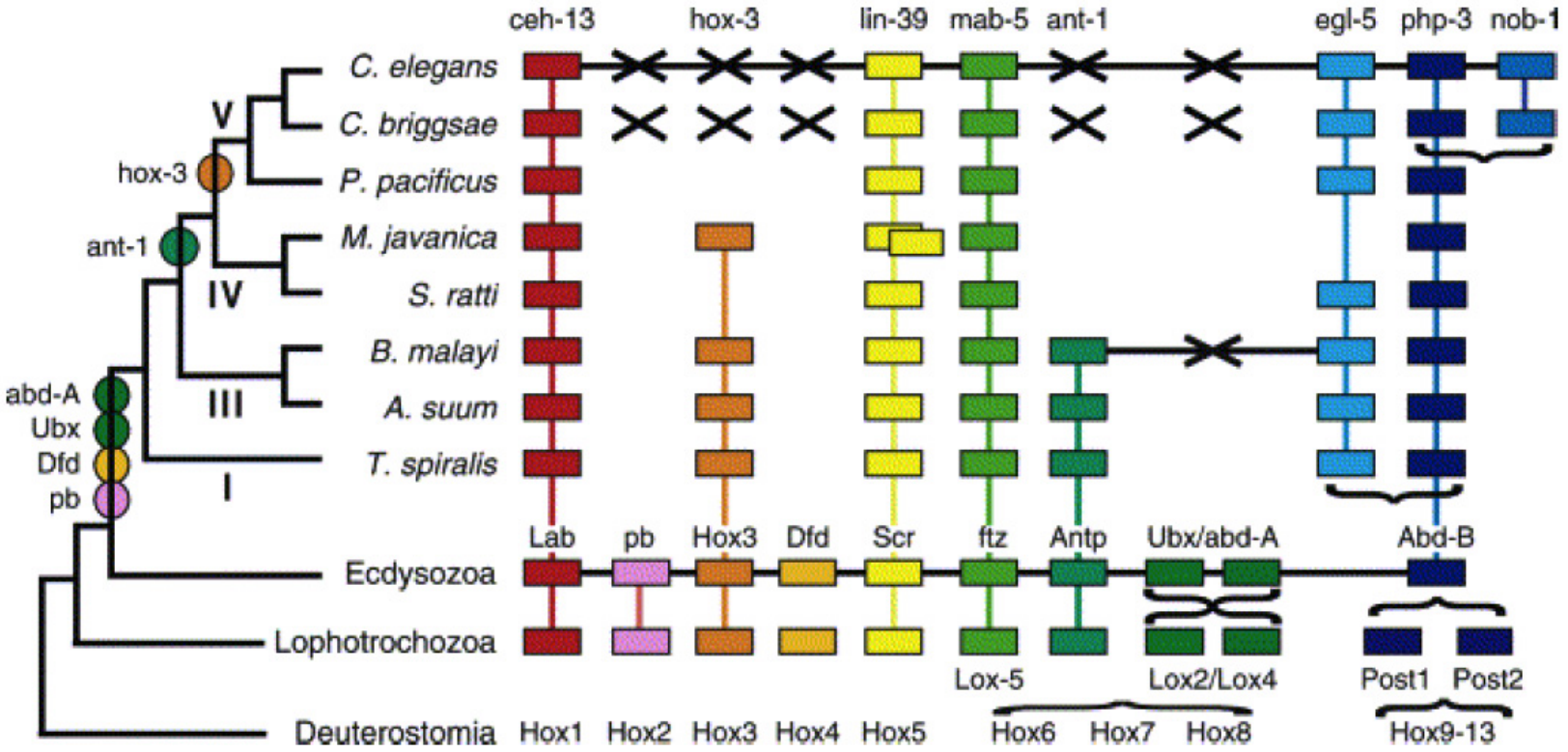
Microtubules cold resistant

These changes are irreversible (short of horizonal gene transfer)

Evolved in last 8 million years as Southern Ocean cooled

Shows the absurdity of the "neutralist" school of evolutionary biology

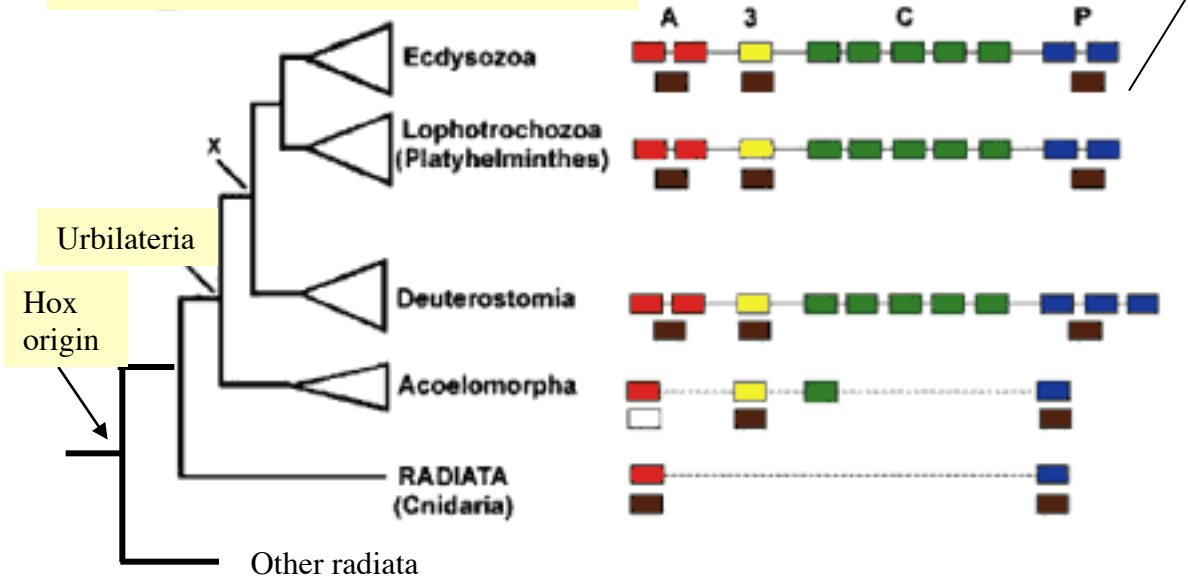
Nematodes have lost many Hox genes



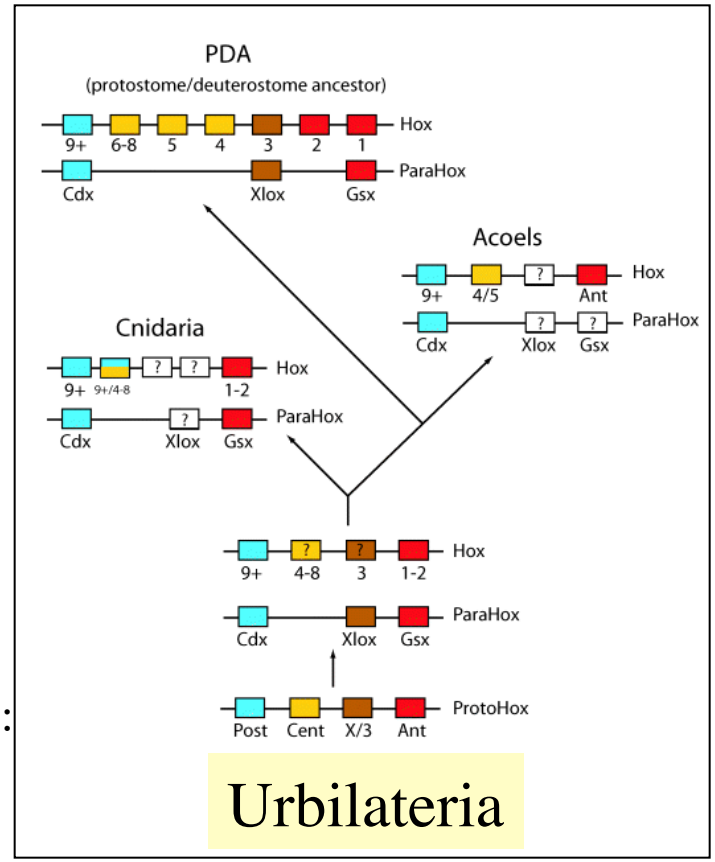
Parasitism appears to be a limiting and may ultimately be a losing strategy in evolution

Relationships of early metazoans

Using homeobox genes to assess early relationships:



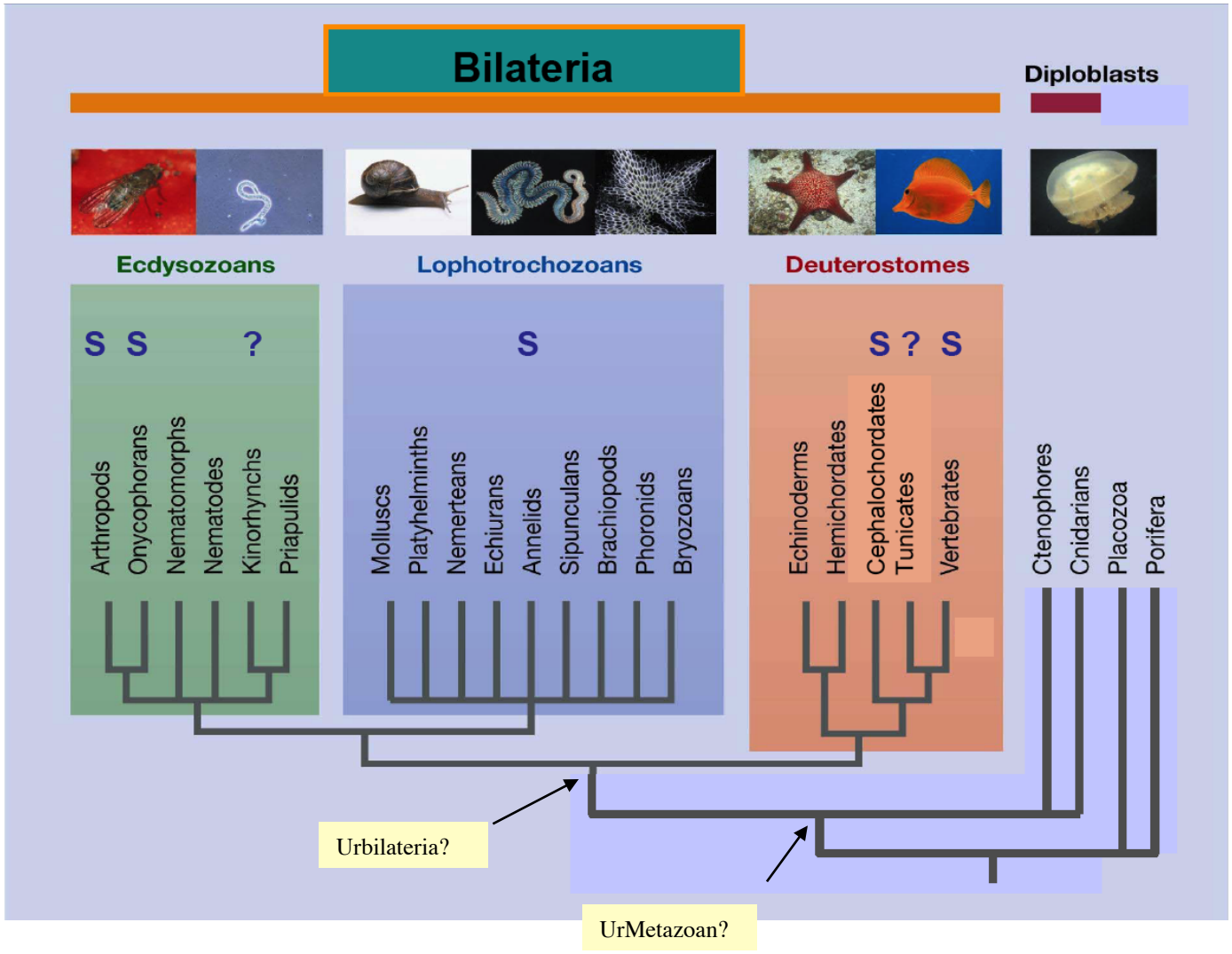
i.e. no evidence supporting the "new" animal phylogeny



True Hox genes absent from sponges and ctenophores.

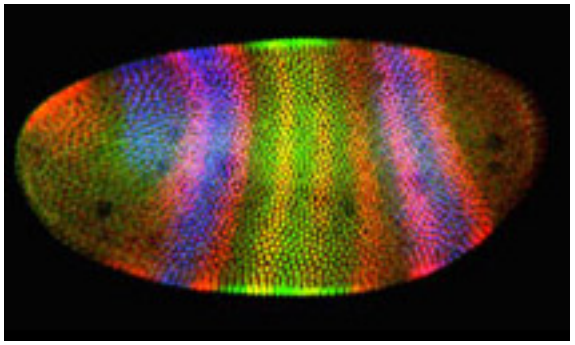
However sponges have 6 of the 7 major signaling pathways:
Notch, BMP, Wnt, Hh, RTK, Jak/STAT, (they lack NRs)
They have nearly every type of cell adhesion gene

Segmentation

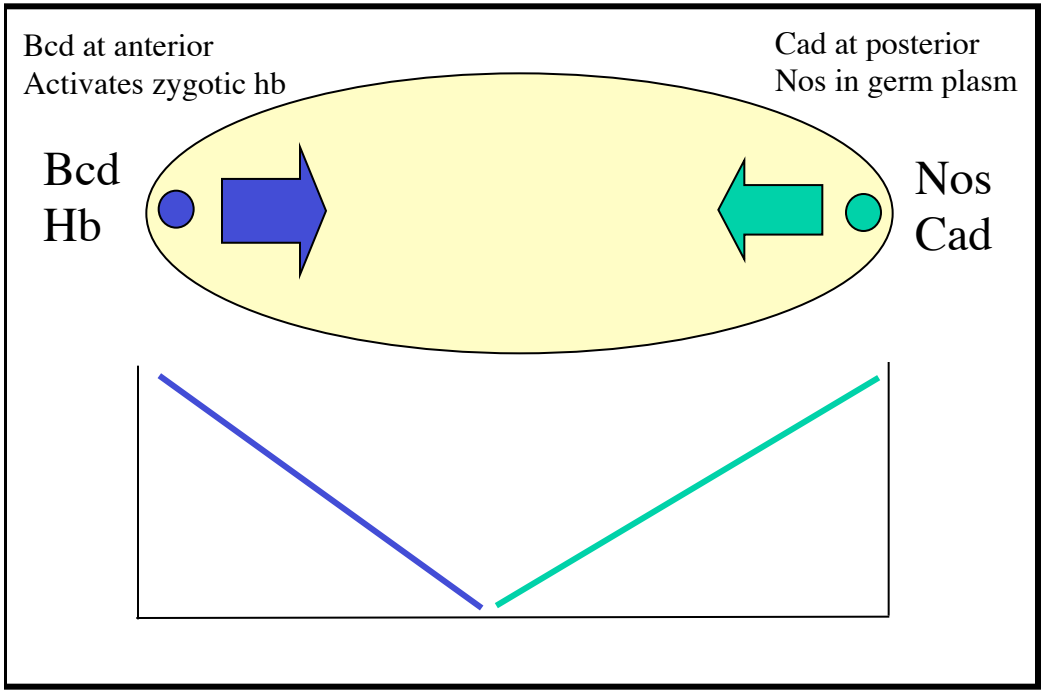


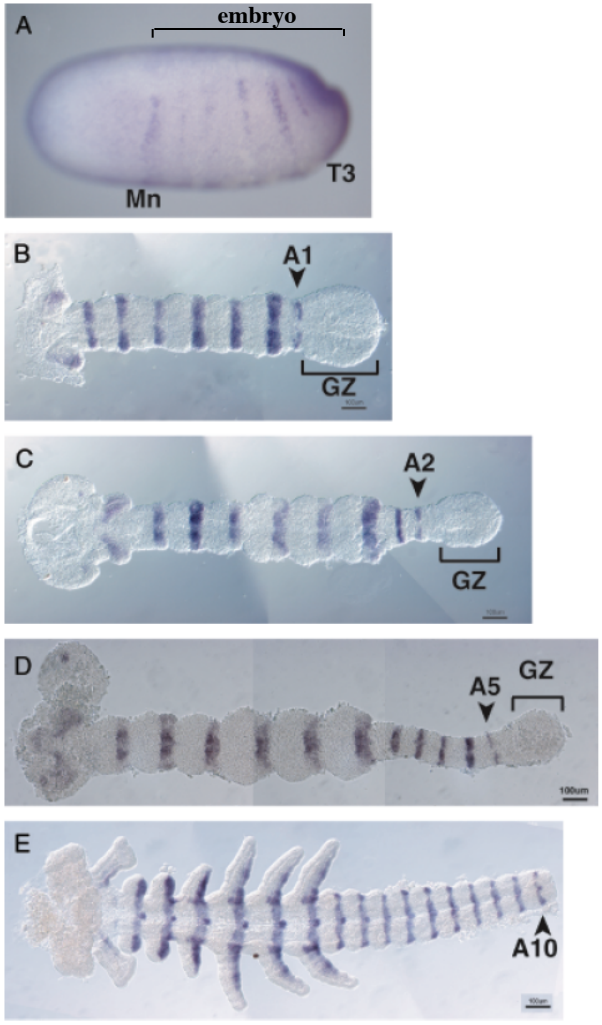
Did most metazoans evolve from a segmented Precambrian ancestor?

Insects become segmented in two ways



All segments ~~form at blastoderm~~
= Long germ band (Drosophila and higher insects)



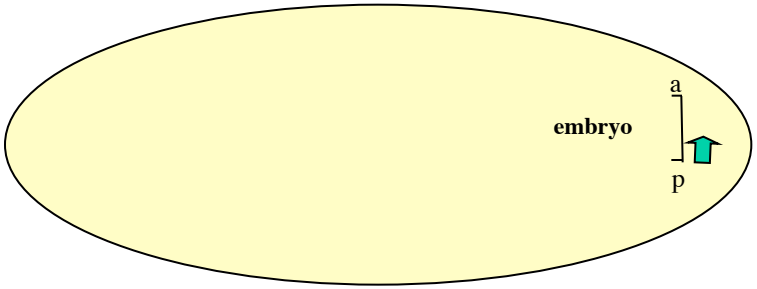


Segments form progressively. Short germ band (Oncopeltus, lower insects, other phyla)

Drosophila-style segmentation: a specialized version of a more ancient system

Bicoid (not conserved)

Hunchback (possibly conserved)



Caudal (Cdx; conserved)

Nanos (conserved)

Schistocerca (Grasshopper)

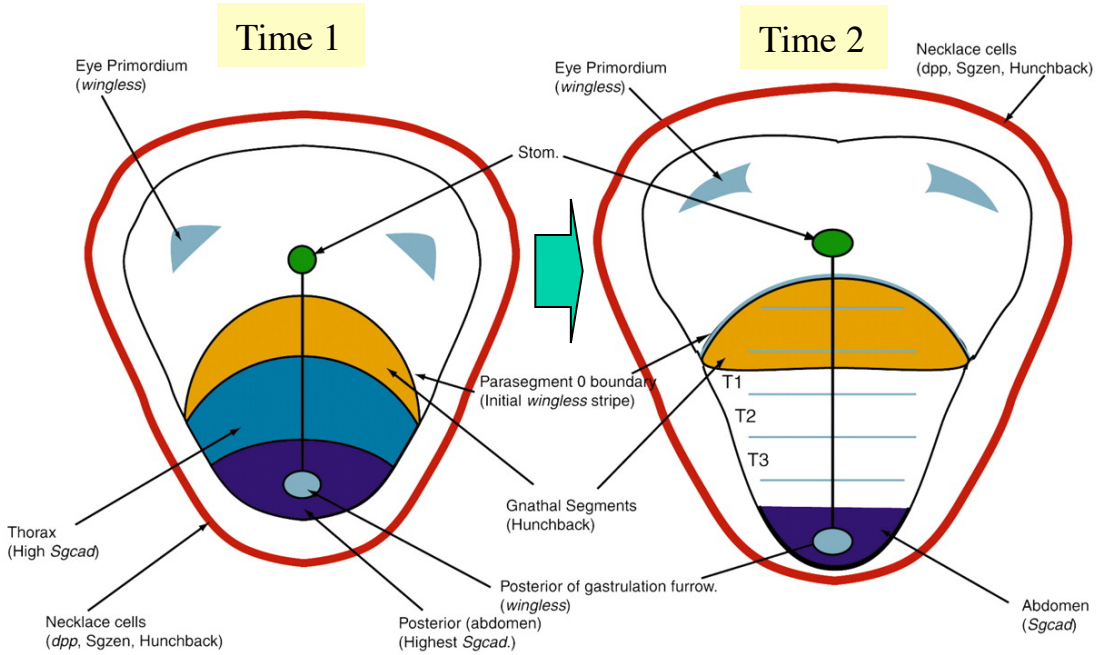
Short germ band segmentation is much more like segmentation in other phyla;
Bcd-style diffusion-based gradients are not involved or required (even in Drosophila)

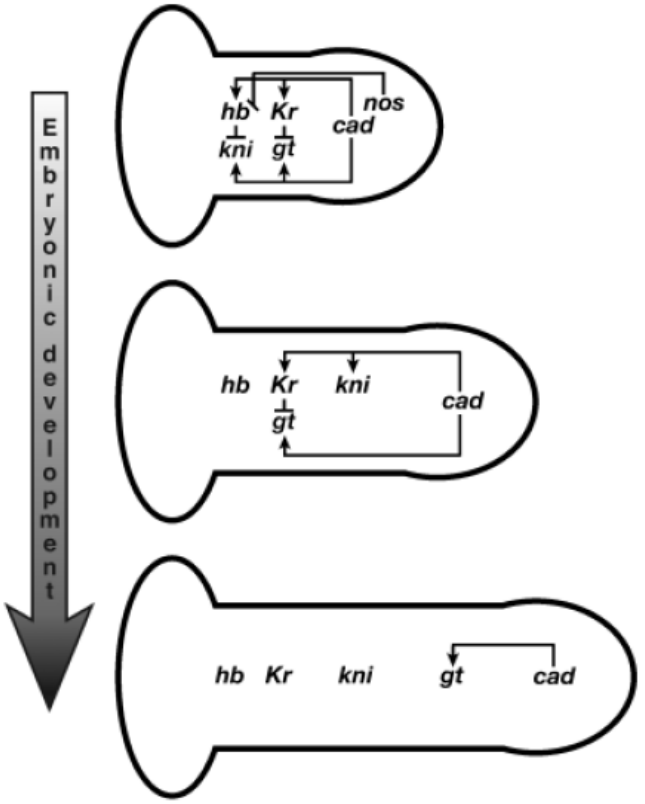
In basal insects the anterior hb gradient may be activated entirely by the posterior genes: caudal activation / nanos repression act within the limited posterior embryonic region of the egg

Schistocerca a/p patterning

Early

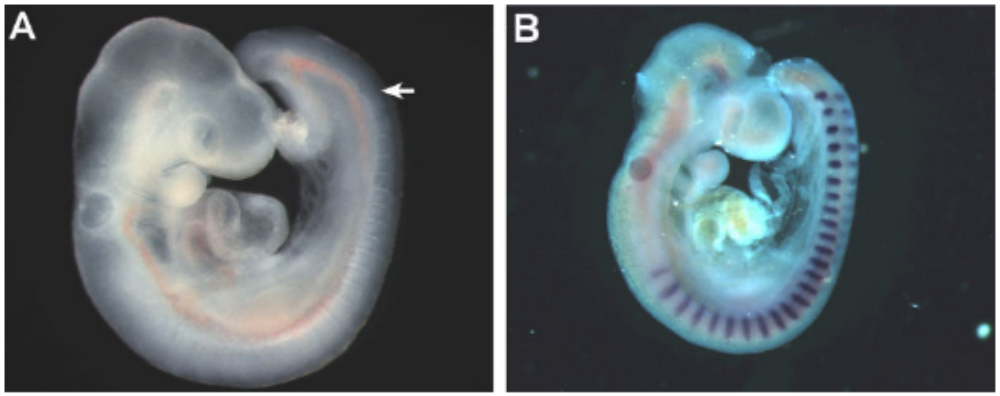
Late

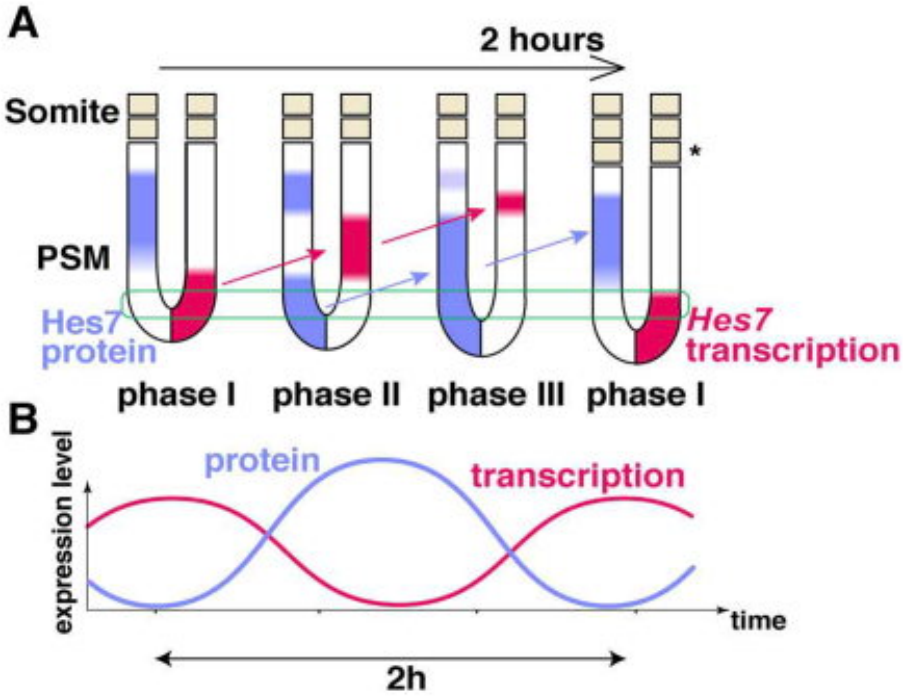


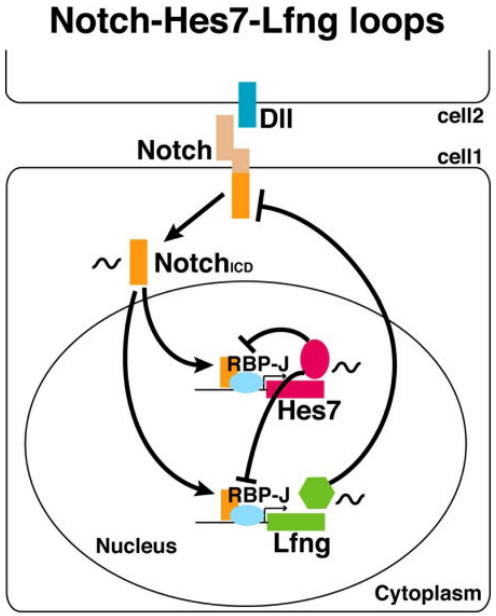


Genetic interactions in segment addition

Vertebrate somites are also added sequentially

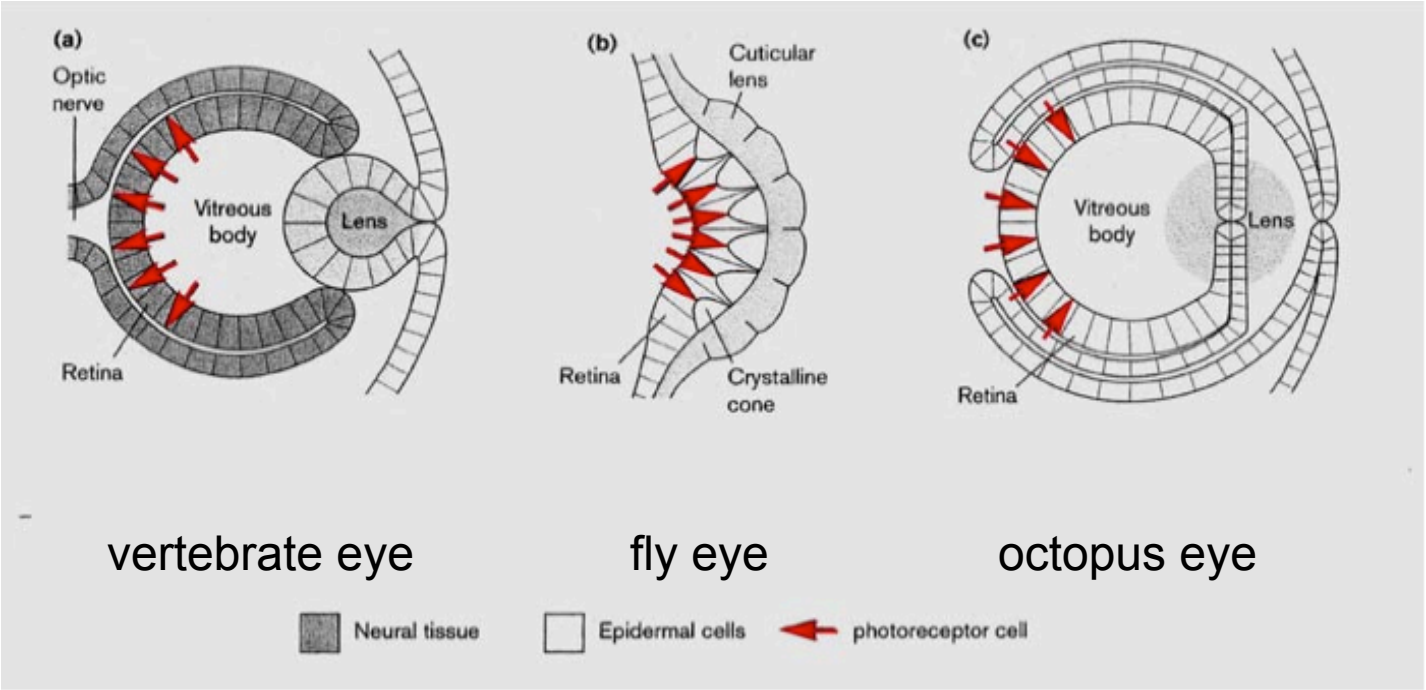






Models of vertebrate and invertebrate segment addition too primitive for comparison

Are major organs and tissues homologous?

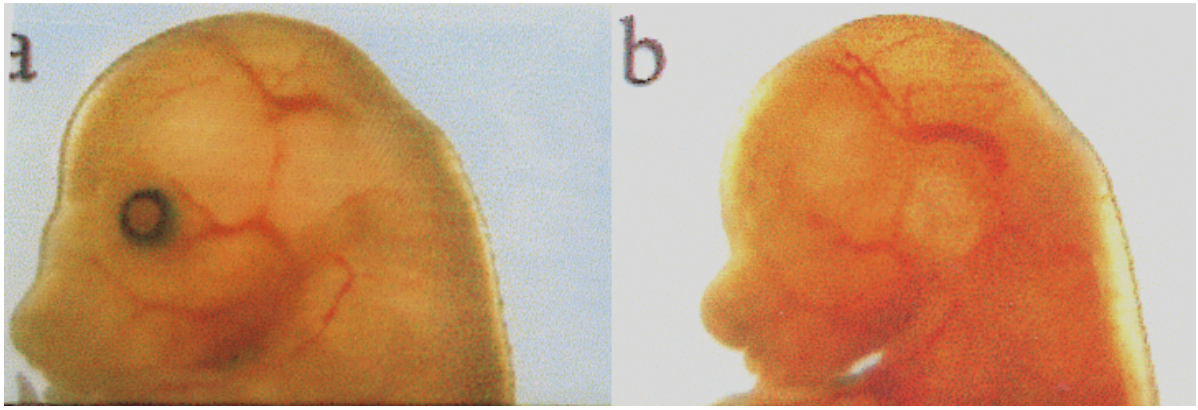


Vertebrate, fly and octopus eyes differ developmentally, structurally and topologically, and were thought to have arisen independently

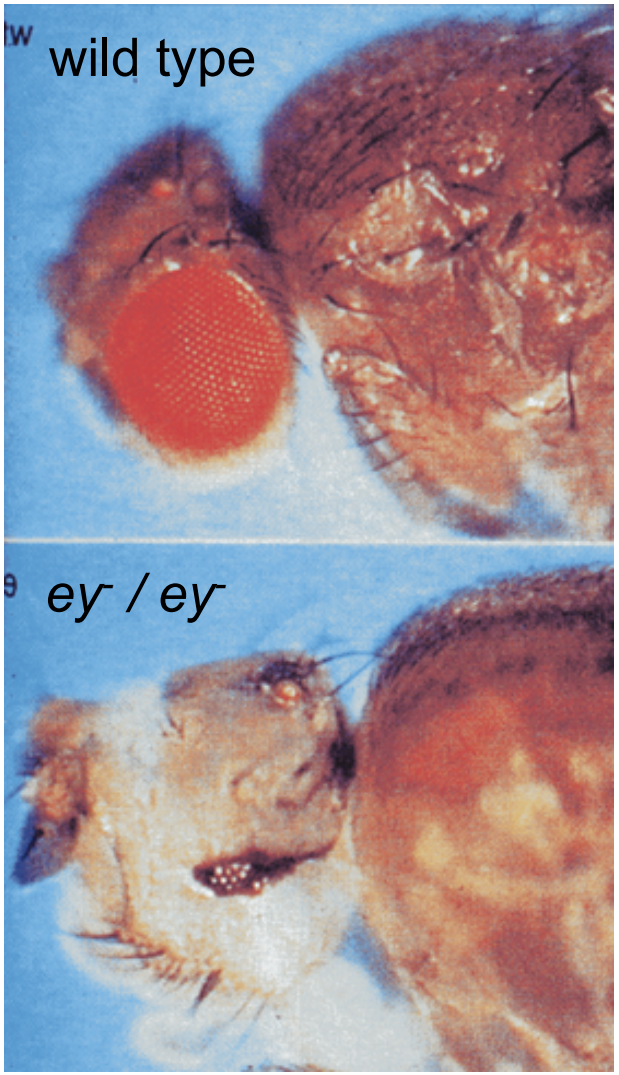
Pax6 : master regulator of eye development

wild type

small eye homozygous

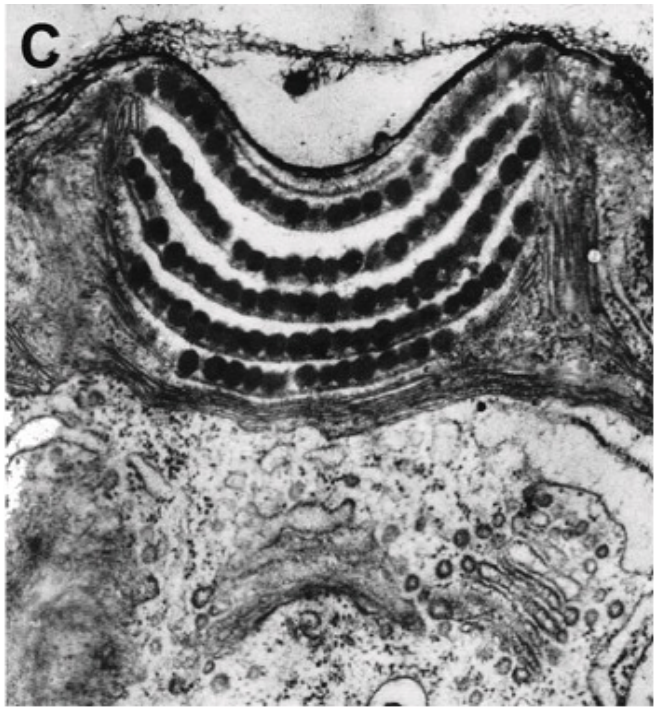


mouse



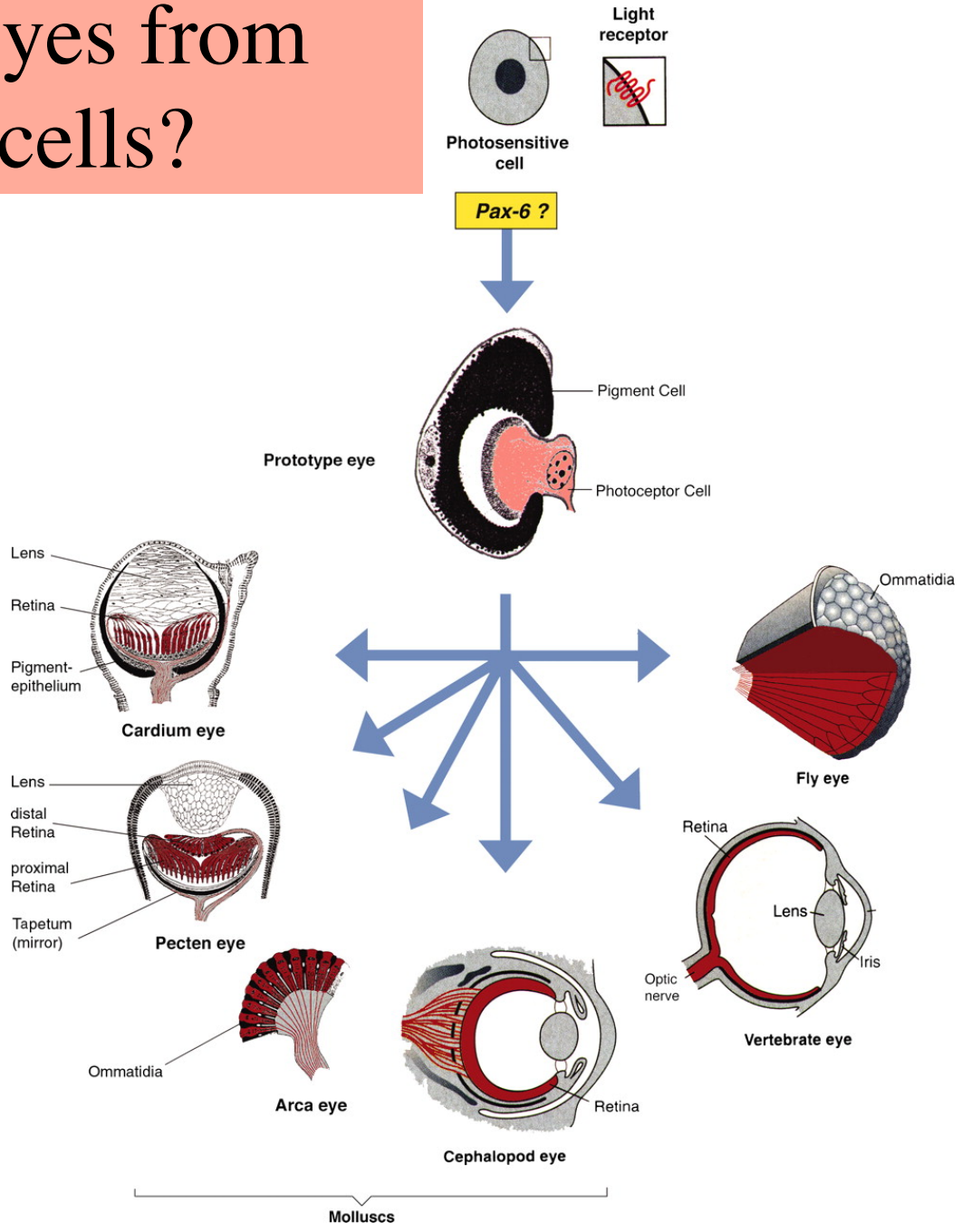
Drosophila

Common origin of eyes from early light sensitive cells?



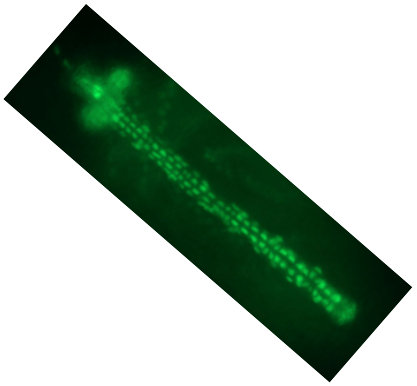
Volvox eyespot (all somatic cells)

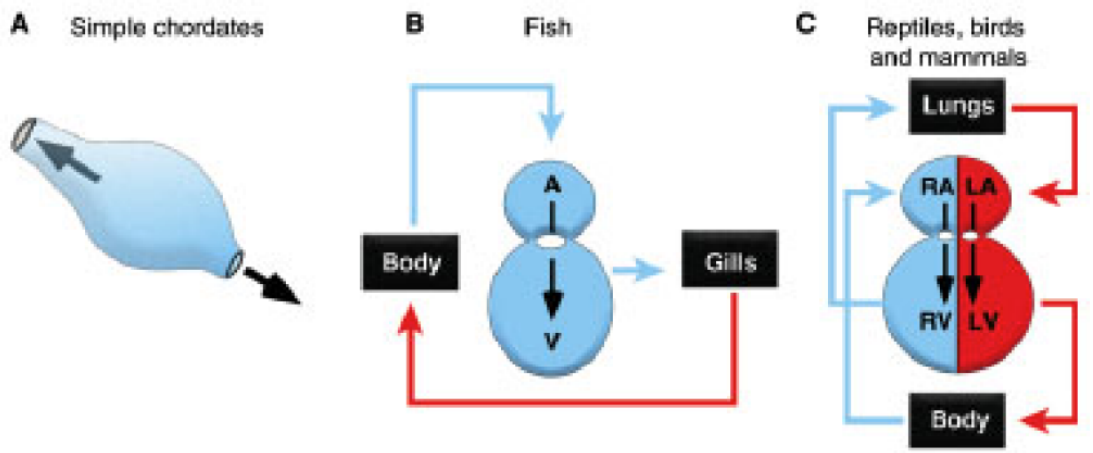
Associated with chloroplast



Heart development

Drosophila heart

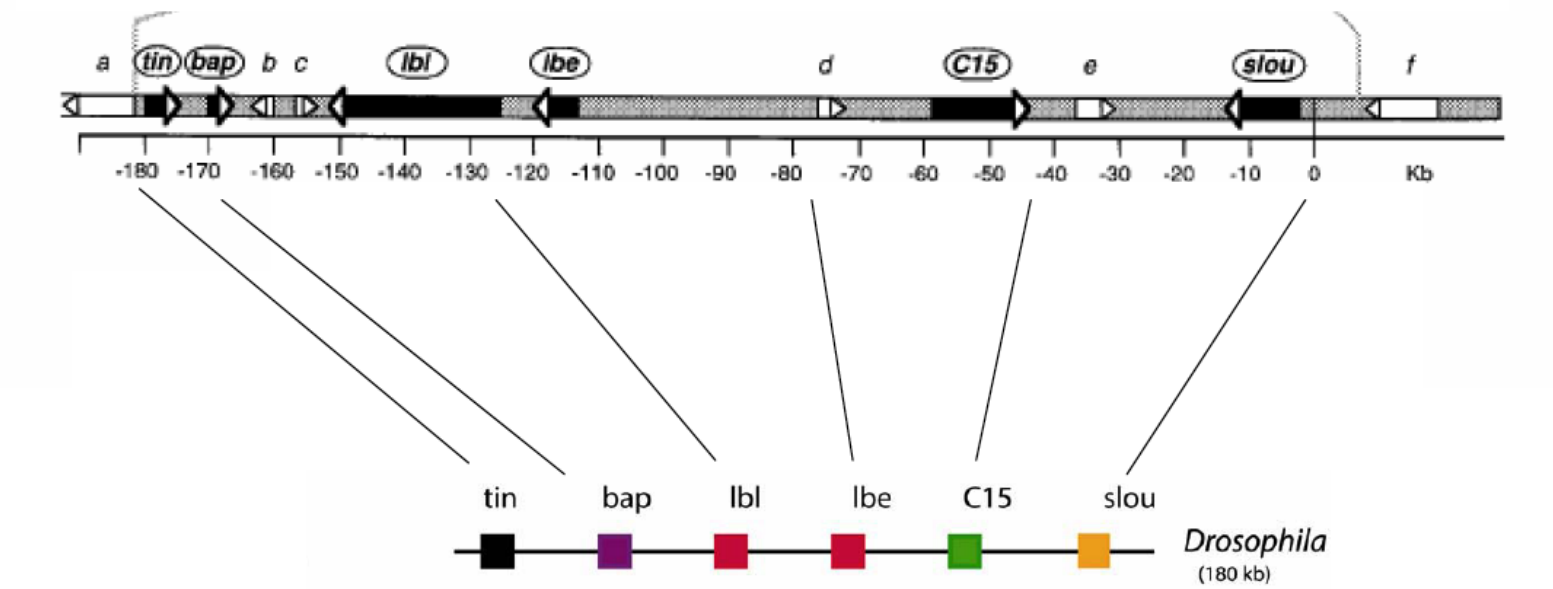




Common transcription factors: NK2, GATA family, HAND proteins

Duplication of HAND protein may be correlated with the evolution of the multichambered heart of reptiles, birds and mammals

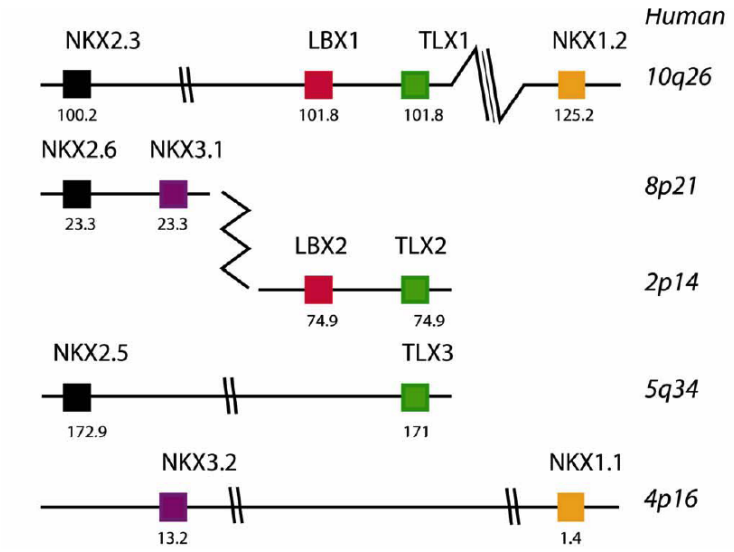
Another homeobox gene cluster: the NK-like genes



Gene name	Gene family	Expression/function
tinman	NK4	all mesoderm; later dorsal muscle (e.g. heart)
bagpipe	NK3	visceral mesoderm (e.g. around midgut)
ladybird	Lbx	heart cell fate; segmental border muscles
C15	Tlx	alary muscles
slouch	NK1	somatic muscle: differentiation of muscle fibres

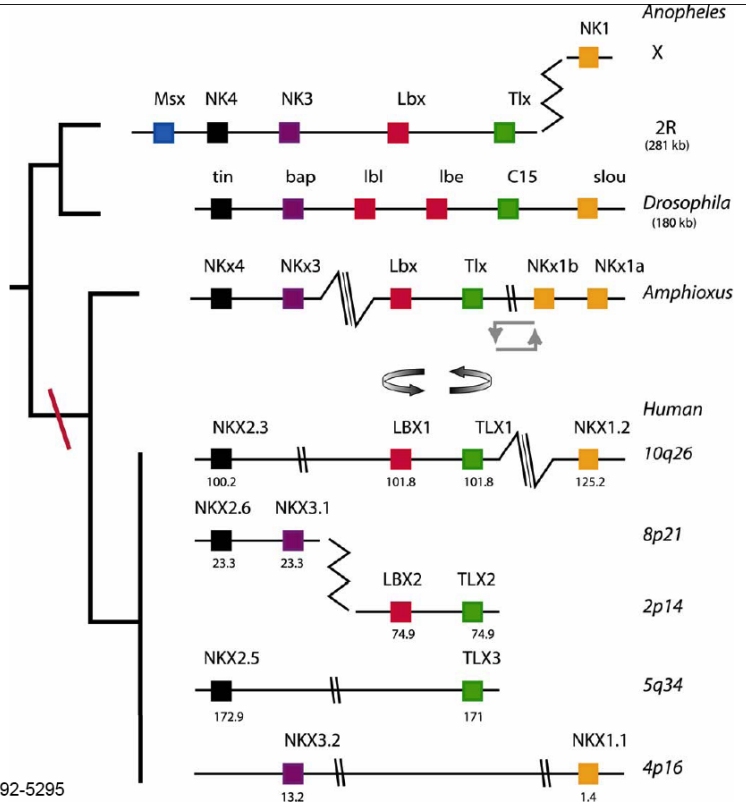
NK-class homeobox genes are conserved

Drosophila homeobox	Human homeobox
NK4 (tinman)	~ NKX-2.5, -2.6, -2.3
NK3 (bagpipe)	NKX-3.1, -3.2
lbe & lbl	LBX-1, -2
C15 (93Bal)	TLX-1, -2, -3
slouch (S59)	NKX-1.1, -1.2



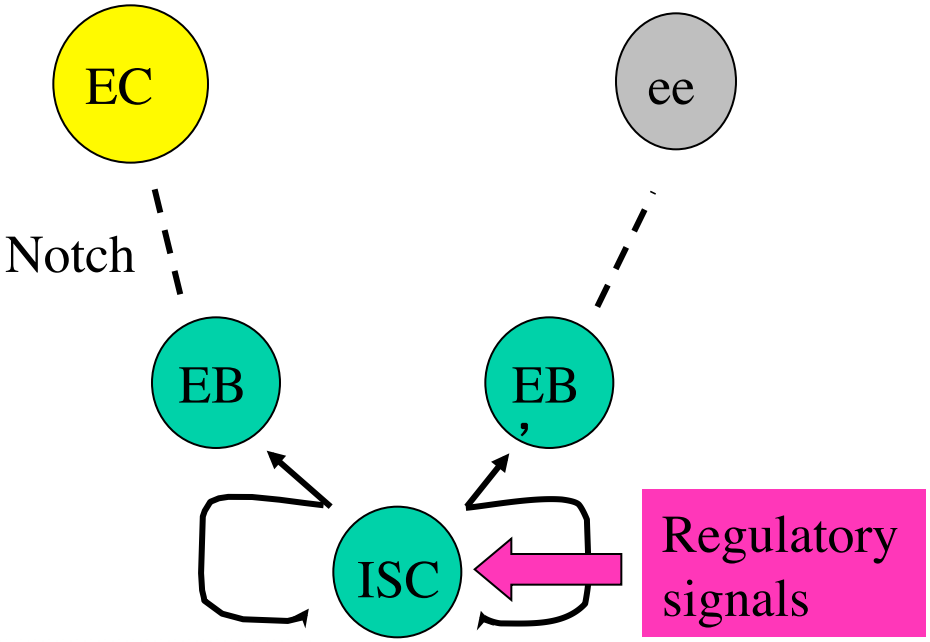
4 clusters that split and dispersed?

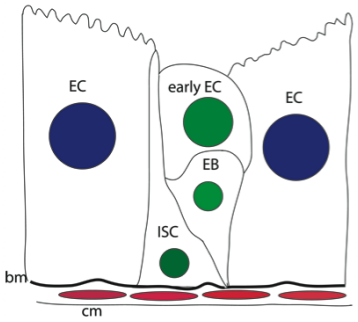
Ancient NK homeobox gene cluster



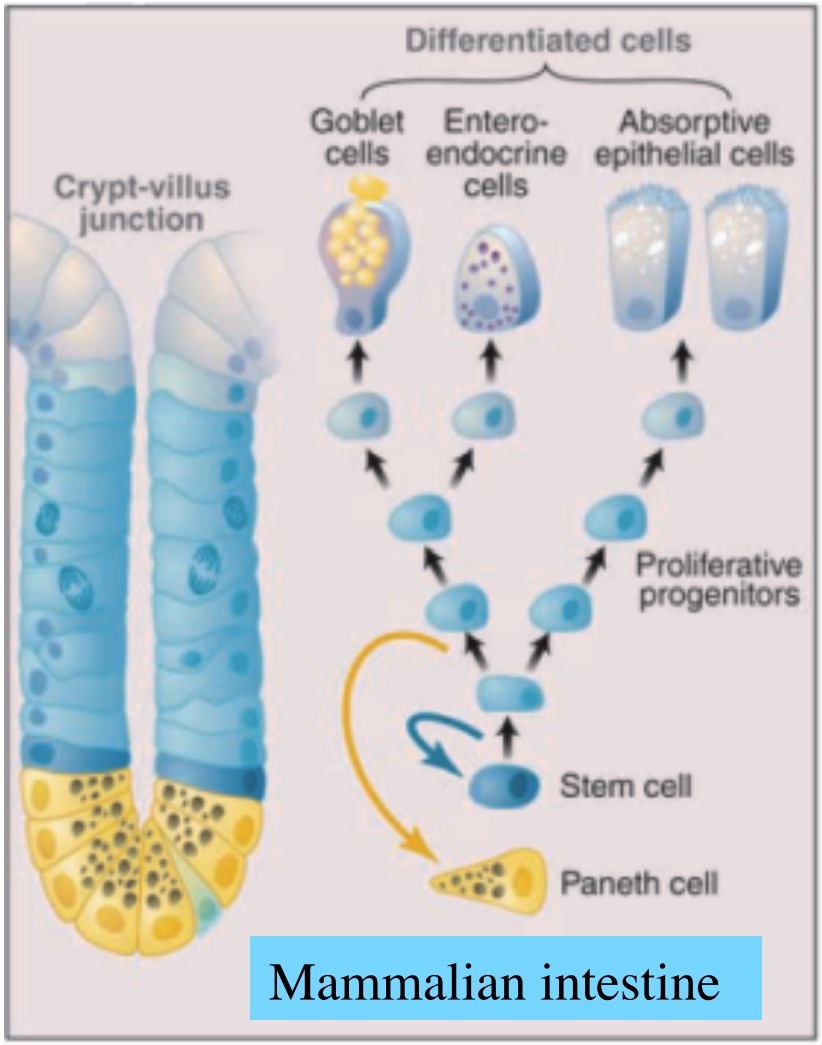
LUKE et al PNAS 100, 5292-5295

Related cellular mechanisms underlie tissue homology- intestinal stem cells





Drosophila midgut



Mammalian intestine

How does novel morphology arise?

1. "Modern Synthesis"

Protein coding mutations drive evolution

Most coding changes are deleterious or neutral, so assumed changes with unmeasurable effects slowly add up

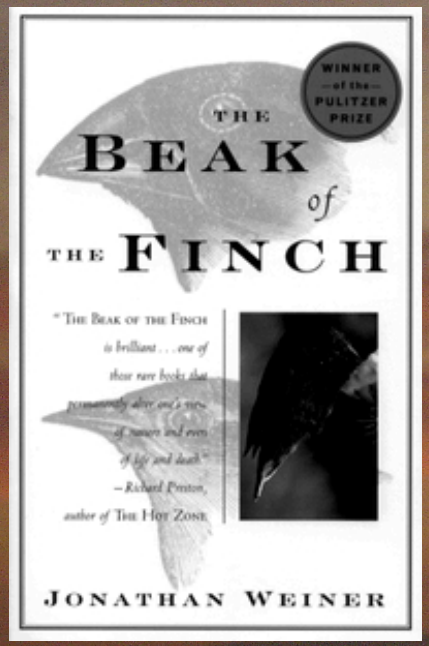
Genes affecting evolution of a trait are different from genes identified by mutation as affecting the trait

2. Evo-Devo:

Regulatory changes in non-coding DNA are most important; enhancers can change with minimal deleterious effects

Genes driving evolution are the same genes involved in development of relevant structures

Sean Carroll review (2008) Cell 134, 25-36.

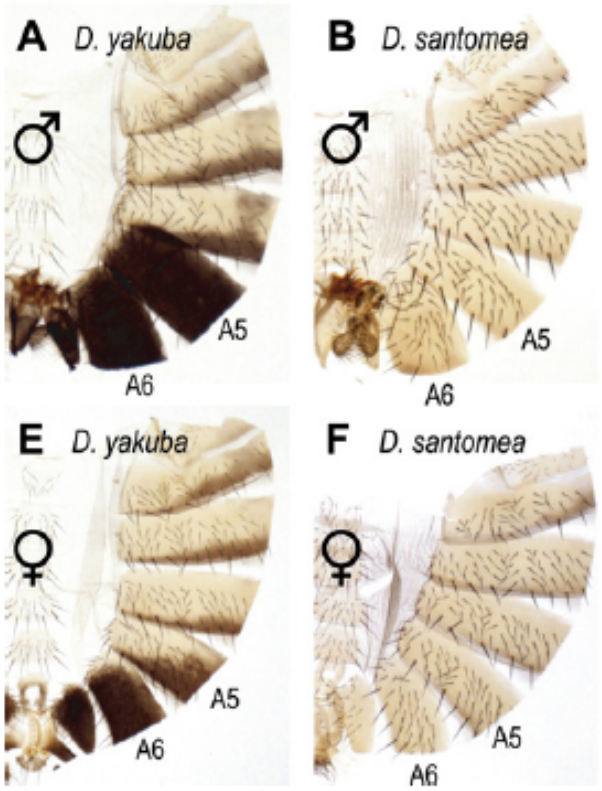


Evolution can be rapid

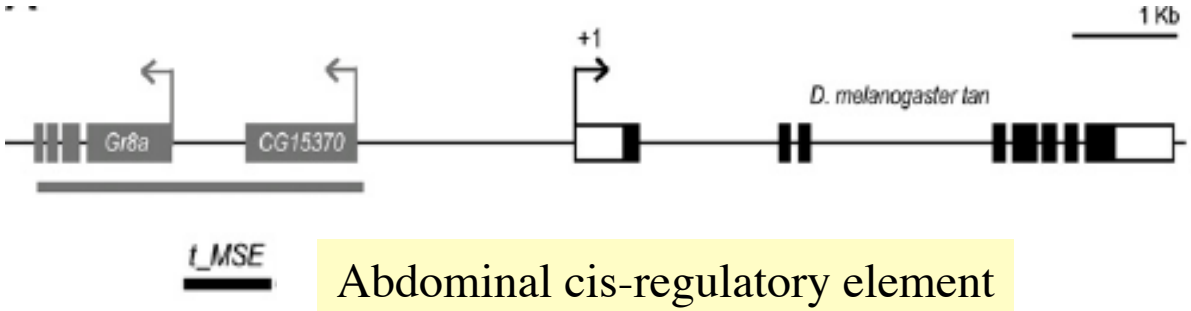
Average beak size changed significantly in 1-2 years due to rainfall-induced changes in seed size

Speciation can also take place rapidly: Cichlids (200 years); sticklebacks (10,000 years); Apple maggot (200 years)

Evolution involves cis-regulatory sequences



Diverged 1.3-5x10^5 yr/ago



Abdominal cis-regulatory element

Specific mutations mapped in D. santomea in t_MSE that account for the downregulation of tan expression

Jeong et al. (2008). Cell 132, 783.

Regulatory changes in stickleback evolution

Ocean stickleback

Regulatory changes in c-kit ligand expression reduce pigmentation

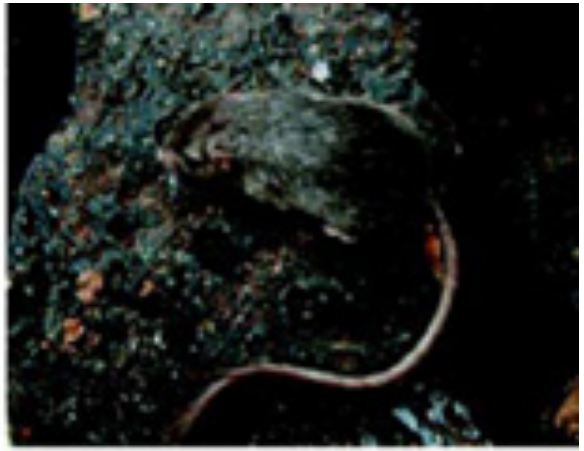
Regulatory changes in secreted signal ectodysplasin reduce coverage by bony plates

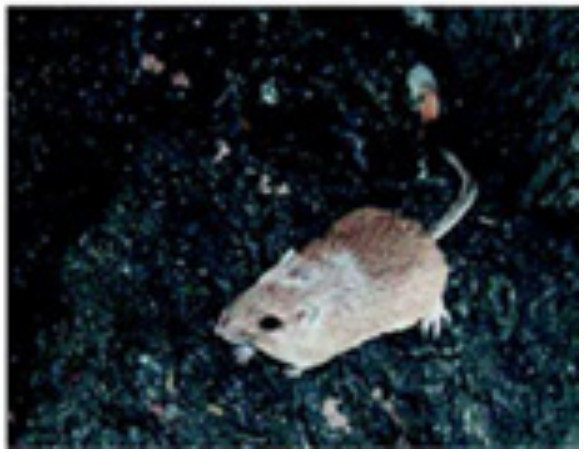
Lake stickleback species

Kinglsey article: Science 327, 302-05 (2010).

Rapid changes can also be selected in specific proteins

Melanism in pocket mice occurs due to mutations at the melanocortin receptor 1 (MC1R) gene





In a typical population of 100,000 mice, new melanotic mutations at MC1R will occur every 100 years

Mutations at the same gene are responsible for many types of coloration in birds, lizards, orange vs black in jaguars, white vs black bears, and coat color in domestic horses, cats and dogs

How do regulatory changes arise

1. Many spontaneous mutations in diverse species are caused directly or indirectly by transposon activity

2. Copy number polymorphisms are frequent in human population and correlate strongly with phenotypic differences; generated by Line activity, replication errors, ?

Evolutionary change is driven by biological mechanisms, not chemical mechanisms

Genomic research has overturned the assumptions of classical evolutionary theory

Evolutionary change is driven by **biological** mechanisms such as transposition, repair, recombination, etc. not **chemical** mechanisms like single base changes

Most of these changes act by influencing **gene regulation** and copy number, not **protein structure**

Rates have not been equal among groups. Evolution cannot be deduced by algorithms.

The Evo-Devo research program can provide a rational understanding of how life evolved on Earth, how organisms are related, and the limits to which organisms could be re-designed.