

# Evolution of Development

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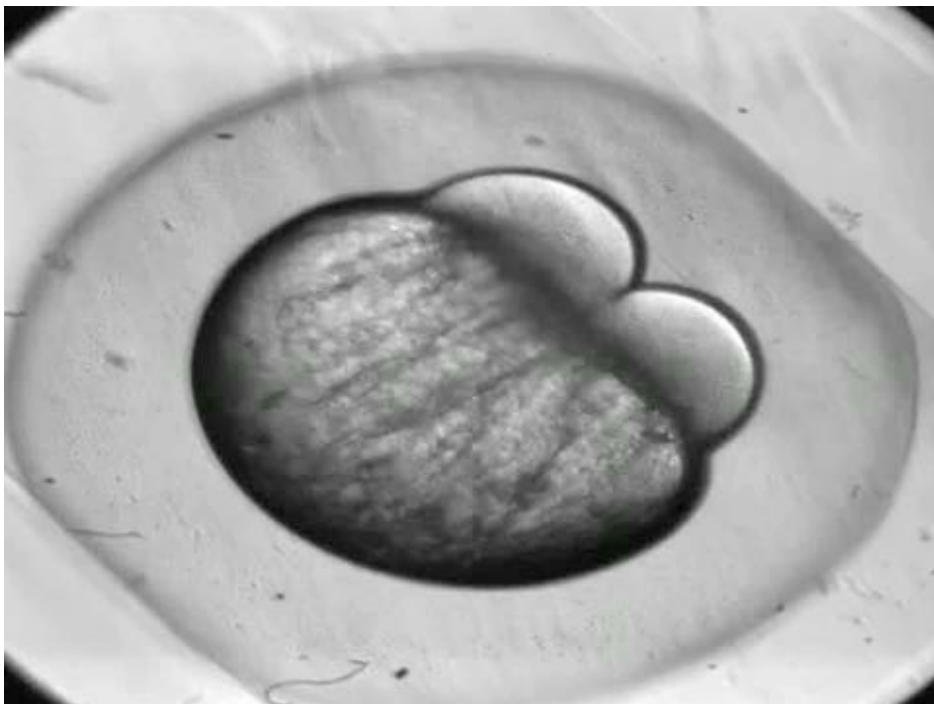
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Advanced-level Evolutionary Biology HS 11

1

## The miracle of development



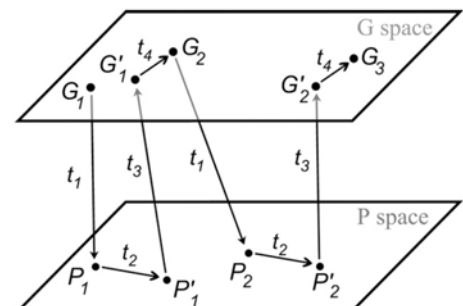
## Summary: Evolution of Development

- development in an evolutionary framework
- developmental processes influence evolution
  - toe loss in frogs and salamanders
  - HOX genes
  - segmentation
- evolutionary processes influence development
  - tissue architecture and cancer
  - self vs. foreign recognition mechanisms
- interplay between development and evolution
  - maternal control and morphological diversity
- home-work: planarian embryogenesis

3

## Development in an evolutionary framework

- the life cycle of an organism is a repeated sequence of three different processes
  - development maps the information in the genotypes of the offspring back to the material phenotypes ( $t_1$ )
    - conversion of information into matter
  - ecology reduces a cohort of newborn organisms to those that have managed to survive and reproduce, producing the variation among individuals in lifetime reproductive success that causes natural selection ( $t_2$  and  $t_3$ )
    - material interaction
  - genetics and mating transforms the genotypes of the surviving and reproducing parents into the genotypes of the offspring ( $t_4$ )
    - transmission of information



from Houle 2010

4

## Developmental processes influence evolution

- insight into developmental processes can help to explain trait evolution because developmental processes can constrain evolution
  - the way a phenotype responds to selection pressures depends on how it is made
- developmental processes can have a strong historical component and understanding this allows to understand (and sometimes predict) evolutionary patterns
  - key innovations (i.e., traits in descendants not present in ancestors) can make prediction difficult
  - key innovations often originate due to gene or genome duplications

5

## Toe loss in frogs and salamanders

- many frog species have lost the first toe and many salamander species have lost the fifth toe
  - the last common ancestor of frogs and salamanders lived about 135 million ago

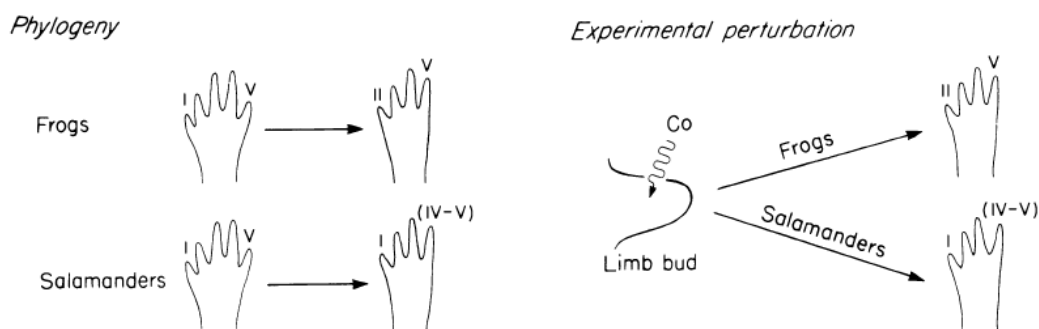


FIG. 8. Summary of trends in digital loss. Phylogenetically, frogs lose the first toe, while salamanders lose their toes postaxially (IV-V). The same pattern is mimicked by experimentally reducing the number of cells in the limb bud using a mitotic inhibitor such as colchicine (Co).

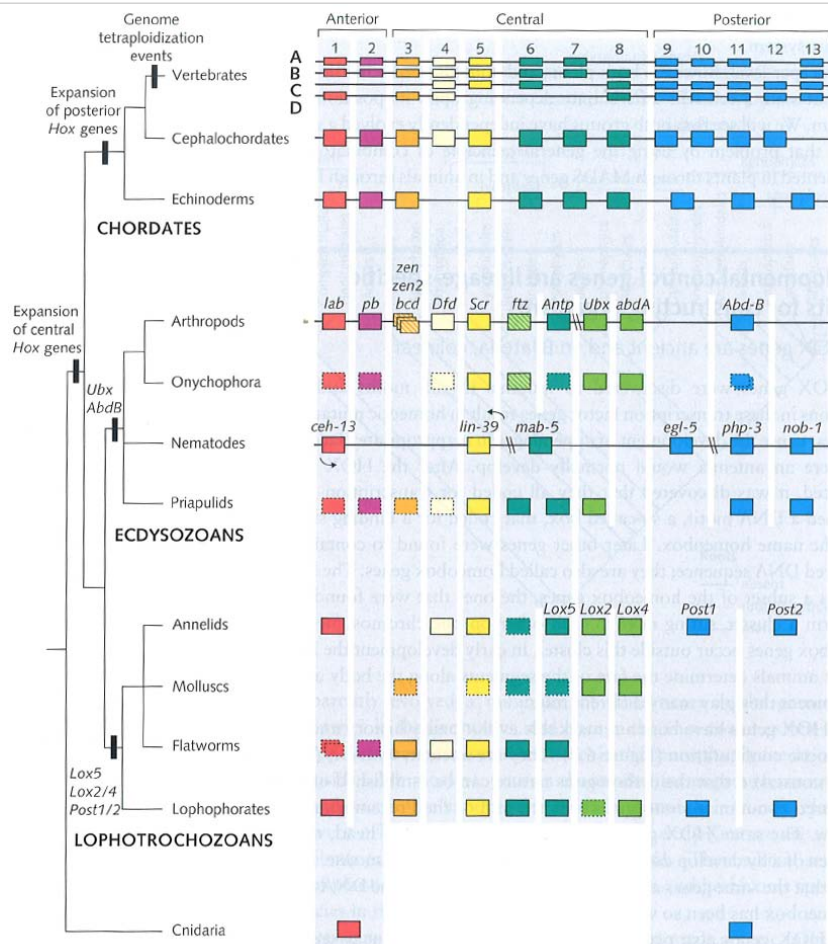
from Alberch & Gale 1985

6

# HOX genes

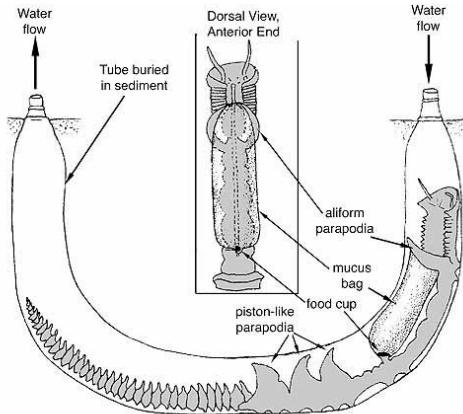
- HOX genes are developmental control genes that influence the formation of patterns along the antero-posterior body axis
  - they are about 600 My old (orthologous genes can usually be clearly identified)
- the same HOX genes determine where the head, thorax and abdomen are formed in both a fly and a mouse
- HOX gene duplication events go along with some of the main diversification events in body plans

**Figure 6.7** The HOX genes have deeply conserved sequence and function. Note both tandem duplication (increase in the number of genes in the cluster) and cluster duplication (increase in the number of copies of the whole cluster). Duplication is associated with increased capacity to control the development of new structures. (Reproduced from Carroll et al. (2001) *From DNA to diversity*, with permission from Blackwell Publishing.)



# Segmentation

- the evolution of segmentation allows to change the function of some body parts with minimal impact on the others
  - different parts of the body can specialise in different functions

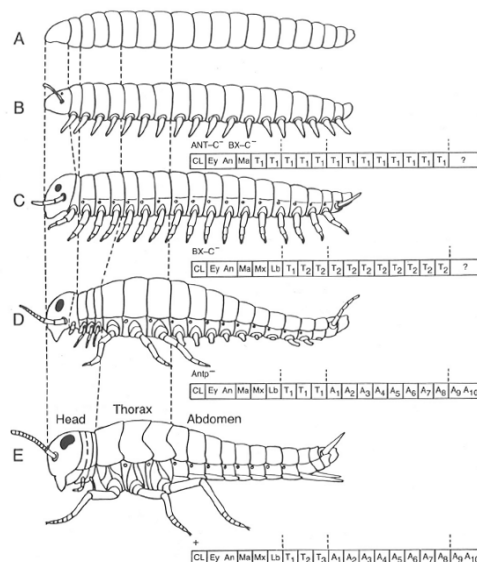


Chaetopterus (Polychaeta)

# Segmentation

- innovations
  - changing segmental arrangements from annelids to flies

FIGURE 3.18 Segment design in an (A) annelid, (B) onychophoran, (C) myriapod, (D) apterygote insect, and (E) pterygote insect. Superimposed on this gross phylogeny are the segment organizations produced by deletion of homeotic genes in the pterygote fly *Drosophila*. (After Raff and Kaufman, 1983.)



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## Developmental processes influence evolution

- these are the type of questions that the very active field of evolutionary developmental biology (Evo-Devo) mainly addresses

11

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## Evolutionary processes influence development

- development evolves
  - development is expected to be influenced by optimality criteria
- development has a strong mechanistic component
  - should allow to understand (and predict) the evolution of developmental patterns in terms of adaptive evolution

12

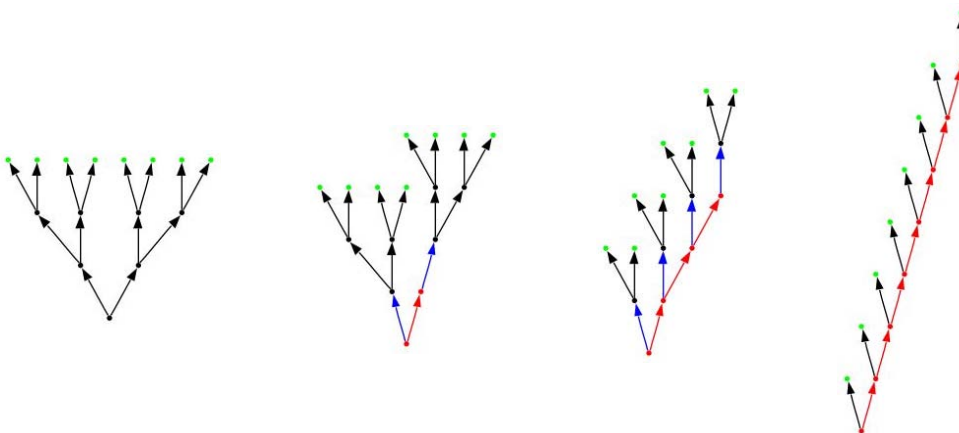
## Tissue architecture and cancer

- cancer is the consequence of an unwanted evolutionary process
  - it arises when several somatic mutations occur in the same cell lineage
  - most mutations occur during DNA replication and cell division
  - constantly renewing tissues have a higher risk to develop cancer because they make many cells
- most tissues are organised into stem cells and transit cells
  - a stem cell division produces a stem cell and a transit cell, and a transit cell division produces two transit cells
  - different numbers of stem cell and transit cell divisions can lead to the same number of cells

13

## Tissue architecture and cancer

- different ways to make 8 differentiated cells



all these topologies result in 8 differentiated cells, and require 7 cell divisions

14

## Tissue architecture and cancer

- Frank et al. (2003) present mathematical models that ask which pattern of stem vs. transit cell divisions minimises the cancer risk if a certain number of cells needs to be produced by a tissue?
  - ‘which developmental process leads to the optimal tissue architecture?’
- selection on the individual level leads to selection on a developmental process
  - individuals with a sub-optimal tissue architecture have a lower fitness

15

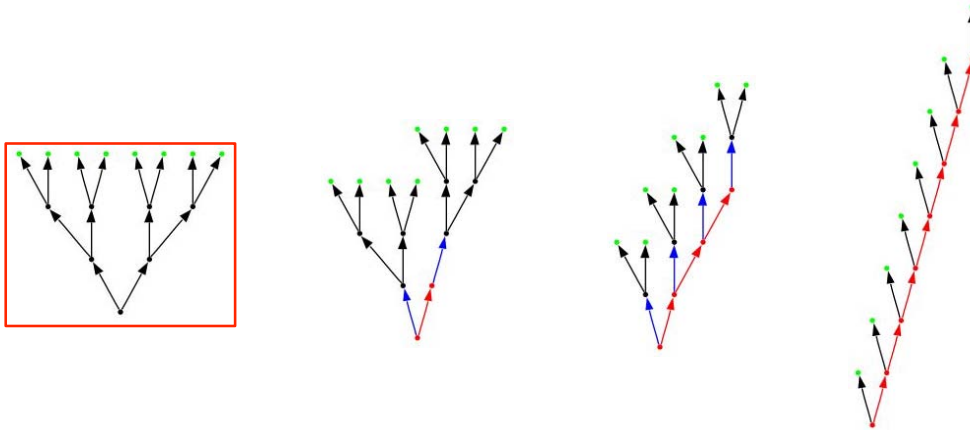
## Tissue architecture and cancer

- Model I
  - assumptions
    - stem and transit cell divisions have the same mutation rate
    - the tissue makes  $k=2^N$  cells
    - no cell death (requires  $k-1$  cell divisions)
    - cancer arises if a cell acquires  $m$  mutations
    - all mutations are dominant
  - if  $m=1$ 
    - the topology is irrelevant, because all topologies require  $k-1$  cell divisions
  - if  $m>1$ 
    - always divide the cell that has so far divided least often (i.e. try to have the tips of the tree as close to progenitor as possible)

16

## Tissue architecture and cancer

- different ways to make  $k$  differentiated cells

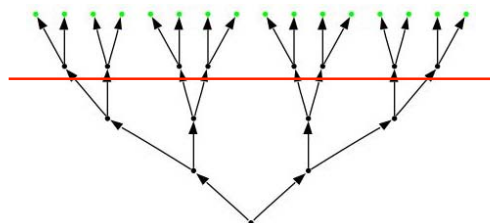


all these topologies result in 8 differentiated cells, and require 7 cell divisions

17

## Tissue architecture and cancer

- in renewing tissues

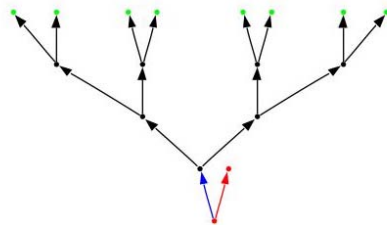


some cells may not be available anymore for division  
constant loss of cells at the surface forces transit lineages to be relatively short

18

## Tissue architecture and cancer

- in renewing tissues



some cells may not be available anymore for division  
constant loss of cells at the surface forces transit lineages to be relatively short  
this creates the need for a basal stem cell that divides more often

19

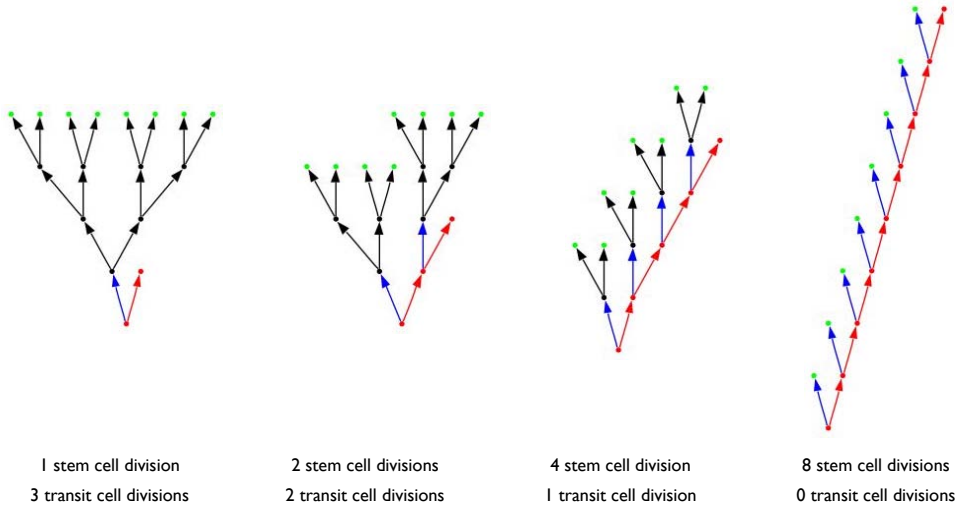
## Tissue architecture and cancer

- Model 2
  - assumptions
    - consider a single stem cell that needs to give rise to  $k=2^N$  cells over its lifetime
    - $m=2$  or  $m=3$  mutations lead to cancer
    - stem cells divide  $n_1$  times
    - transit cells divide  $n_2$  times
    - $n_1=2^{N-n_2}$  ( $n_1$  increases exponentially as  $n_2$  decreases)

20

# Tissue architecture and cancer

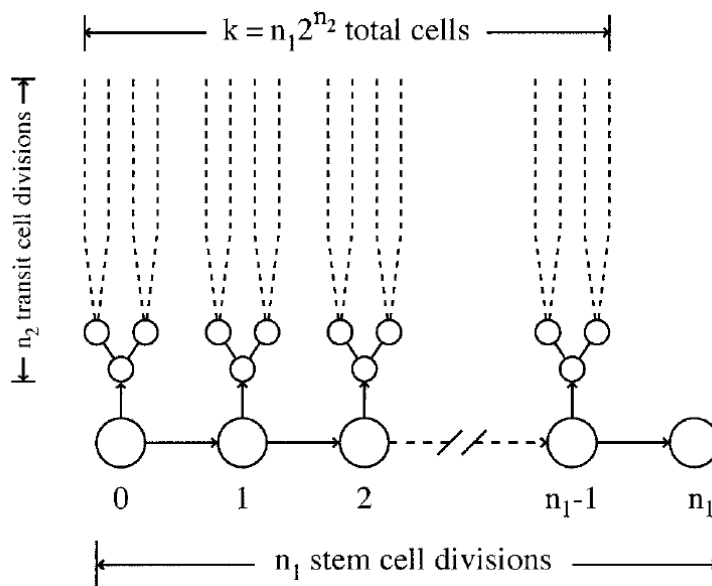
- tissue architecture with a stem cell



all topologies result in 1 stem cell and 8 differentiated cells

# Tissue architecture and cancer

- a generalised topology



# Tissue architecture and cancer

## • Model 2

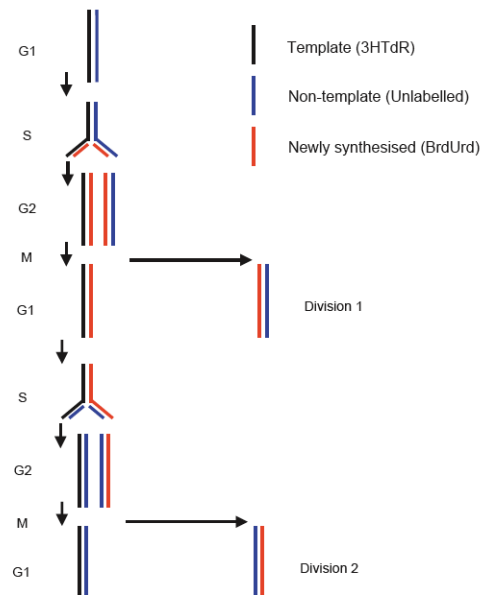
- if all cell divisions have the same mutation rate
  - then minimise lineage length given the constraint of the tissue
    - stem cells are necessary risk imposed by the tissue
- if stem cell divisions have a lower mutation rate than transit cell divisions
  - make longer stem cell lineages
    - the bigger the difference the longer stem cell lineages
- if the number of cells ( $k$ ) that need to be produced changes
  - change the ratio of stem vs. transit cells
    - $n_1$  varies when  $m=2$  and  $n_2$  varies if  $m=3$

23

# Tissue architecture and cancer

## • is there evidence for lower mutation rate in stem cells?

- label retaining cells
- transit cells are more exposed
- stem cells cycle slower and go into apoptosis when damaged
- some stem cell stages are radio-protected



**Fig. 1.** A diagram showing the segregation of template and newly synthesised DNA strands in one chromosome, according to the Cairns' hypothesis (1975), which proposes that all the chromosomes would behave in this way. The template strands are selectively retained by the stem cell daughter of a cell division, whereas the newly synthesised strands are segregated to the daughter cell destined to enter the dividing transit compartment and be shed from the tissue after a few days, thus removing any replication-induced errors. Label introduced into the newly synthesised strands takes two divisions to be removed from the stem cells. Label in the template strand would persist in the stem cell line.

from Potten et al. 2002

24

## Tissue architecture and cancer

- is there evidence for different  $n_1$  and  $n_2$  with varying  $k$ ?
  - an interesting model organ is be the testis because  $k$  can vary greatly due to sperm competition

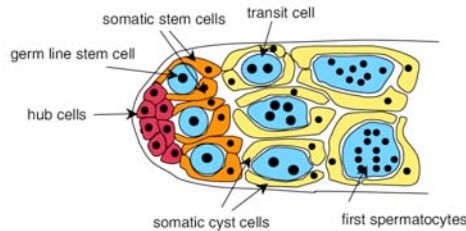


Figure 2  
Organization of the testicular tip of *D. melanogaster* (modified from [30]).

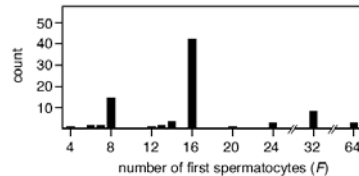


Figure 3  
Frequency distribution of the number of first spermatocytes ( $F$ ) per cyst in 100 species among the Drosophilidae.

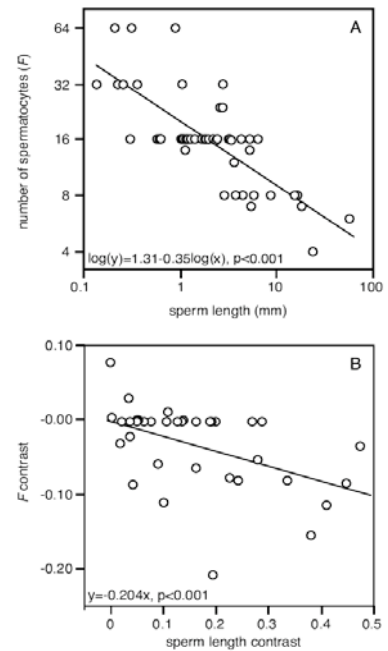


Figure 6  
Relationships between sperm length and the number of first spermatocytes ( $F$ ) per cyst: a) the relationship for the 57 species for which we have values of both sperm length and  $F$  (see Additional file 1 for the data and references) (linear regression,  $F_{1,55} = 86.4$ ,  $p < 0.001$ ), and b) the phylogenetically controlled relationship from the comparative analysis for the 40 species listed in Figure 5 (independent contrasts, linear regression forced through the origin,  $F_{1,34} = 30.2$ ,  $p < 0.001$ ).

from Schärer et al. 2008

25

## Self vs. foreign recognition mechanisms

- a multicellular organism is exposed to cells and particles of different types and origins, which can pose different threats to its integrity
  - normal undifferentiated and differentiated cells
    - many cell types with very different surface compositions
  - benign and malignant cancers
    - cells which may or may not carry signals of their aberrant state on their surface
  - cells of conspecifics (e.g., sperm, saliva, cancer cells, stem cells)
    - may carry more or less similar surface compositions
  - foreign cells (e.g., pollen, parasites)
    - can illicit strong immune response and some are selected to avoid this response
  - foreign particles (e.g., viruses, food, dust)
    - can illicit strong immune response and some are selected to avoid this response

26

## Self vs. foreign recognition mechanisms

- to control such cells and particles a self vs. foreign recognition mechanism needs to evolve and develop
  - needs to recognise a diverse array of epitopes and respond in the appropriate way after recognition
  - achieved through an evolutionarily diversified genetic system (e.g. Fu/HC or MHC) or a genetic system that allows the phenotypic generation of diversity (e.g., via mutation or alternative splicing)
    - generation of somatic mutations needs to be controlled because it carries risks!!!
- if the mechanism is too sensitive
  - it may recognise self-tissues, resulting in auto-immune diseases and allergies
  - it may be too reactive to conspecific tissue, which could lead to sterility
- if the mechanism is not sensitive enough
  - defence against viruses and parasites is compromised
- optimal sensitivity involves a trade-off between these two sides

27

## Evolutionary processes influence development

- these type of questions are rarely asked today, and developmental biology does not really have a strong theoretical arm
  - 'there are books in plenty on experimental embryology but none on theoretical embryology. Why is this?' Woodger 1930 cited in Buss 1987
  - the reason probably is that historical patterns are very important and general patterns difficult to predict
- but there can be very interesting interactions between these different approaches

28

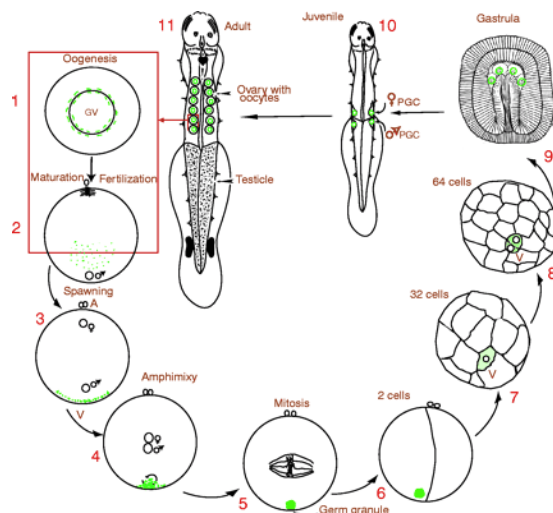
## Interplay between development and evolution

- maternal control and morphological diversity
  - maternal control of development via maternal mRNAs in the egg
    - allows (or leads to?) minimal gene expression by the early embryo
    - can extend to (and exceed) the moment of germ-line sequestration
  - cell lineage diversification from proliferation-induced mutagenesis
    - mutations may lead to new phenotypes (which may or may not become expressed before germ-line sequestration)
    - usually detrimental, but also occasionally beneficial, to the organism
    - mutated cell lines may contribute cells to the germ-line and thereby lead to new morphological adaptations
  - thus the time window between maternal control and germ-line sequestration influences the potential for this kind of adaptation

29

## Interplay between development and evolution

- maternal control and morphological diversity
  - organismal groups with strong maternal control and early germ-line sequestration are expected to be morphologically homogeneous (e.g. Chaetognatha)



from Carré et al. 2002

30

# Interplay between development and evolution

- maternal control and morphological diversity
  - organismal groups with no (or weak) maternal control and somatic determination of germ-line can evolve high morphological diversity (e.g. Platyhelminthes)

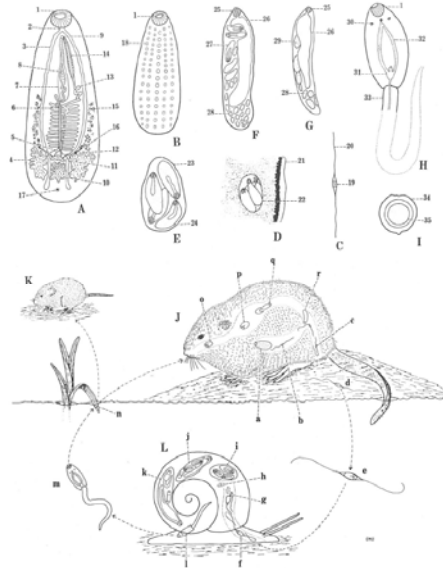


FIGURE 4.5 Life cycle of the digenic trematode *Quinqueserialis quinqueserialis*. Adult worms (A, B, a), parasitic on the muskrat *Ondatra zibethica* (J) or on the meadow vole *Microtus pennsylvanicus* (K), shed eggs (C, b-f) which are eaten by the snail *Gyraulus parvus* (L). The eggs hatch in the snail's mantle (g) and the miracidia penetrate the gut (h) to give rise to sporocysts (D, E, i). The sporocyst gives rise to the rediae (F, i), which migrates to the liver. Mother rediae give rise to daughter rediae (j), which in turn give rise to cercariae (G, k). Cercariae (H) escape from the snail (l-m) to encyst upon vegetation (I). Muskrats eating the vegetation become infected (o-p). (From Olsen, 1974.)

from Buss 1987

31

TABLE 12.1

The modes of development in different groups of living things. In the cellular differentiation column, + means that it is present in all the species that have been studied in the group and +/- means it is present in some species and absent in others. In the developmental mode column, s means new organisms can develop from the "somatic" cells of their parent; e means epigenetic development; p means preformationistic development; and u means unknown. Reprinted, by permission of the publisher, from Buss (1987).

Taxon	Cellular Differentiation	Developmental Mode	Taxon	Cellular Differentiation	Developmental Mode
Protocista			Animalia (continued)		
Phaeophyta	+/-	s	Mesozoa	+	p
Rhodophyta	+/-	s	Platyhelminthes	+	s, e, p
Chlorophyta	+/-	p	Nemertina	+	e
Ciliophora	+/-	s	Gnathostomulida	+	u
Labyrinthulamyxota	+/-	s	Gastrotricha	+	p
Acrasiomycota	+/-	s	Rotifera	+	p
Myxomycota	+/-	s	Kinorhyncha	+	u
Oomycota	+	s	Acanthocephala	+	p
Fungi			Entoprocta	+	s
Zygomycota	+	s	Nematoda	+	p
Ascomycota	+	s	Nematomorpha	+	u
Basidiomycota	+	s	Bryozoa	+	s
Deuteromycota	+	s	Phoronida	+	s
Plantae			Brachiopoda	+	u
Bryophyta	+	s	Mollusca	+	e, p
Lycopodophyta	+	s	Priapulida	+	u
Sphenophyta	+	s	Sipuncula	+	u
Pteridophyta	+	s	Echiura	+	u
Cycadophyta	+	s	Annelida	+	s, e, p
Coniferophyta	+	s	Tardigrada	+	p
Angiospermophyta	+	s	Onychophora	+	p
Animalia			Arthropoda	+	e, p
Placozoa	+	s	Pogonophora	+	u
Porifera	+	s	Echinodermata	+	e
Cnidaria	+	s	Chaetognatha	+	p
Ctenophora	+	p	Hemichordata	+	s, e
			Chordata	+	e, p

s somatic  
e epigenetic  
p preformistic  
u unknown

32

## Summary: Evolution of Development

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- home-work: planarian embryogenesis

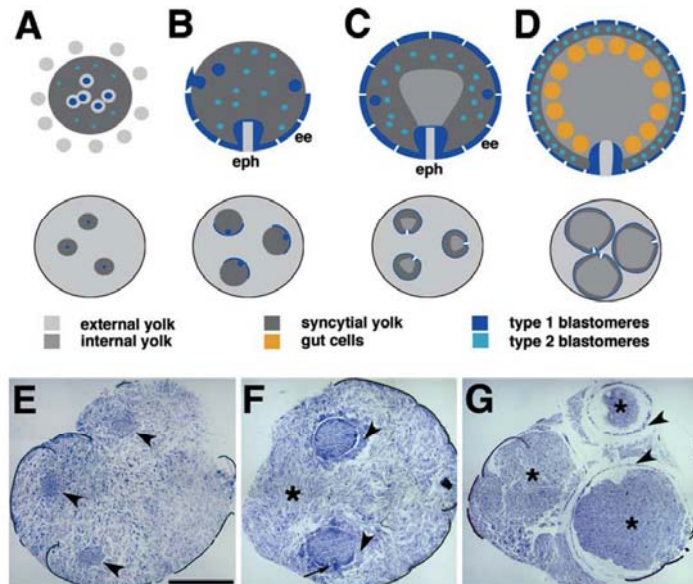
33

## Home work: planarian embryogenesis



- planarians have a highly derived embryology
  - several zygotes develop in a common mass of yolk cells within a cocoon
    - and they cause yolk cells to aggregate around them and to fuse into a syncytium
  - once cell division begins the different blastomeres separate and build two transient structures, the embryonic epidermis and the embryonic pharynx
    - the embryonic epidermis first encloses an certain amount of yolk cells and the embryonic pharynx then pumps in additional yolk cells into the embryo
  - only after most yolk has been taken up by the developing embryos does the actual development of the adult organ systems begin
  - the embryonic epidermis and embryonic pharynx regress and don't contribute in any way to the tissues of the juvenile worm
- planarians have high levels of multiple paternity
  - the number of fathers that contribute sperm to one cocoon can be high
    - more than 80% of all the cocoons have two to five fathers for only three to five hatchlings per cocoon

34



**Fig. 2** Relationship between yolk and embryo in *Schmidtea polychroa*. **a-d** Schematic renderings of embryos at stage 1 (**a**), stage 2 (**b**), stage 3 (**c**) and stage 5 (**d**). In each the *drawing at the bottom* represents the entire egg capsule with three embryos. The *drawing at the top* shows an enlarged view of one embryo. **e-g** Low power photomicrographs of sections of whole egg capsules with embryos at stage 1 (**e**), stage 2 (**f**) and stage 4 (**g**). Sections were stained with MTB. **a, e** During stage 1, yolk cells aggregate around the zygotes contained within the egg capsule and form yolk syncytia (*arrowheads*). Within each syncytium cleavage produces an irregular cloud of blastomeres. **b, f** By the beginning of stage 2, a subpopulation of blastomeres cluster on one side of the syncytium and form the primordium of the embryonic pharynx (*arrow* in **f**) and embryonic epidermis (*ee*). The location of the embryonic pharynx defines the ventral pole of the embryo. Precursors of the embryonic

epidermis spread over the yolk syncytium from a ventral direction. Yolk cells at the dorsal side continue to fuse with the syncytium surface (*asterisk* external yolk cells, *arrowheads* huell membrane). **c, d, g** During stages 3 and 4 the embryonic pharynx becomes functional and starts imbibing external yolk cells into the interior of the embryo, generating a yolk-cell-filled cavity. Thereby external yolk becomes internal yolk (*asterisks* in **g**). The internal yolk compresses the yolk syncytium into a narrow peripheral rind (*arrowheads*) which contains all of the proliferating and differentiating blastomeres (*blue* profiles within); this has historically been known as the germ band. As a result of this process, the embryo grows, the embryonic epidermis flattens, and the syncytium is stretched. A population of cells emerging from within the pool of blastomeres or the internal yolk develop as gut cells (*orange* in **d**). Scale bar: 500  $\mu$ m in **e-g**

from Cardona & al. 2005

35

## Literature

- **Mandatory**
  - think about the home work
- **Suggested Reading for Home Work**
  - Cardona et al. (2005). The embryonic development of the triclad *Schmidtea polychroa*. *Dev Genes Evol* 215: 109-131
  - Pongratz & Michiels (2003). High multiple paternity and low last-male sperm precedence in a hermaphroditic planarian flatworm: consequences for reciprocity patterns. *Mol Ecol* 12: 1425-1433
- **Suggested Reading**
  - Chapter 6 on The Importance of Development in Evolution of Stearns & Hoekstra (2005). *Evolution: An Introduction*. 2nd Edition. Oxford University Press
- **Books**
  - Buss (1987). *The Evolution of Individuality*. Princeton University Press
  - Frank (2007). *Dynamics of Cancer: Incidence, Inheritance, and Evolution*. Princeton University Press, Princeton and Oxford

36