

# Evo-devo

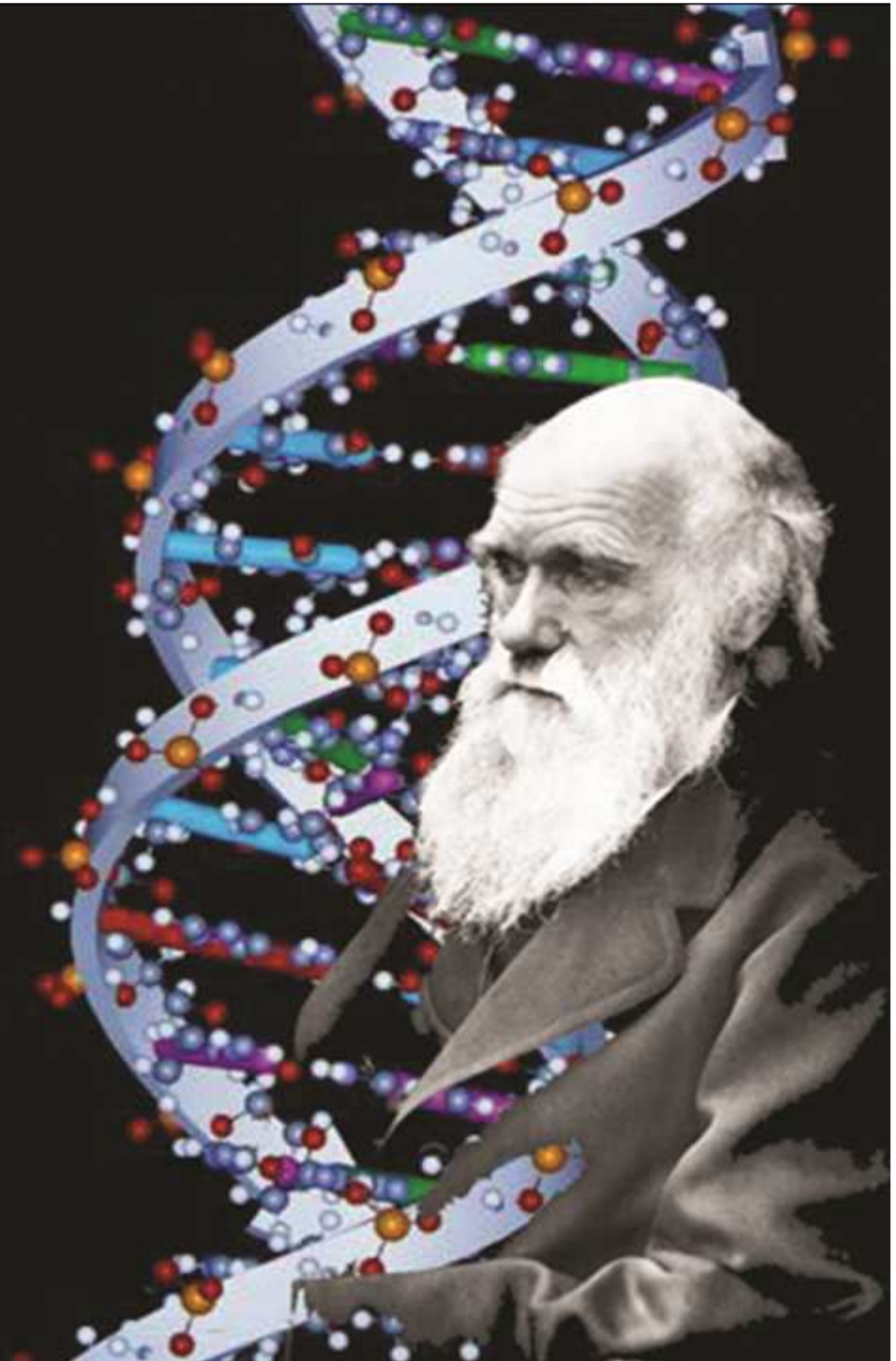
Maurijn van der Zee

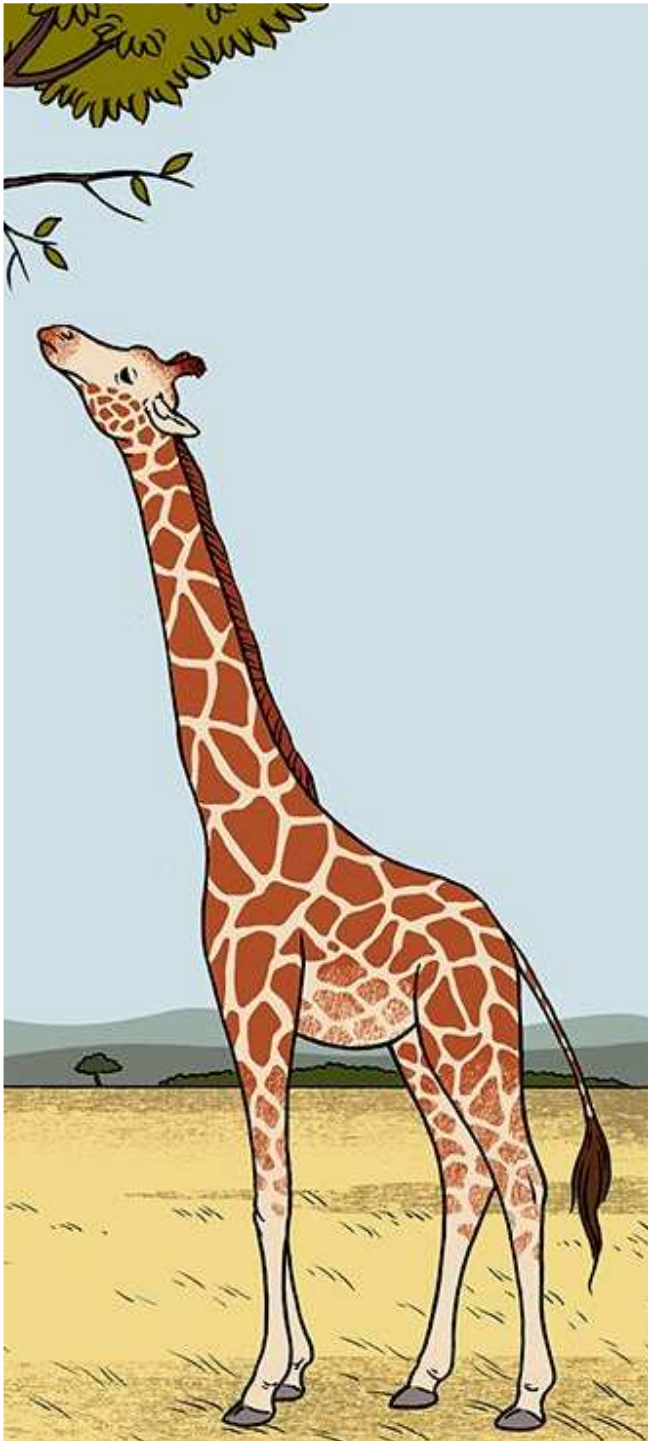
Assistant Professor

Evolutionary Developmental Biology



Universiteit  
Leiden

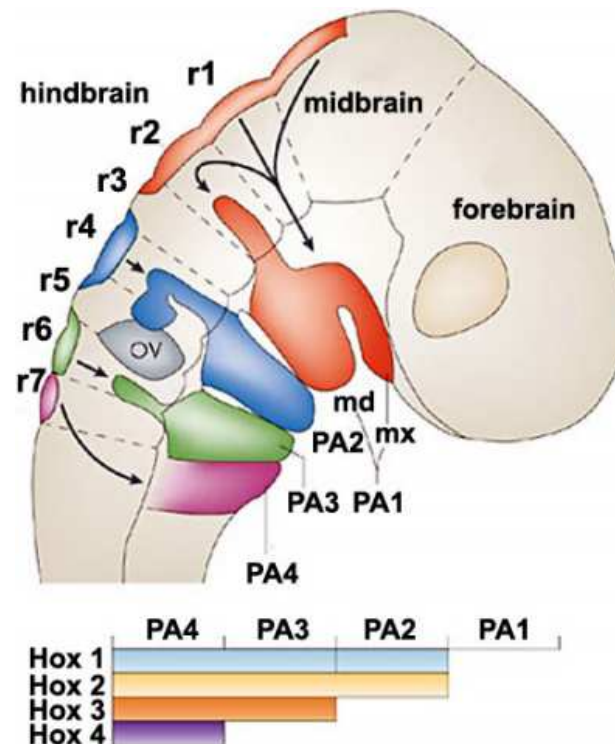




# Evo-devo

## Evolutionary developmental biology

...probeert de genetische en ontwikkelingsbiologische basis van evolutionaire veranderingen te achterhalen

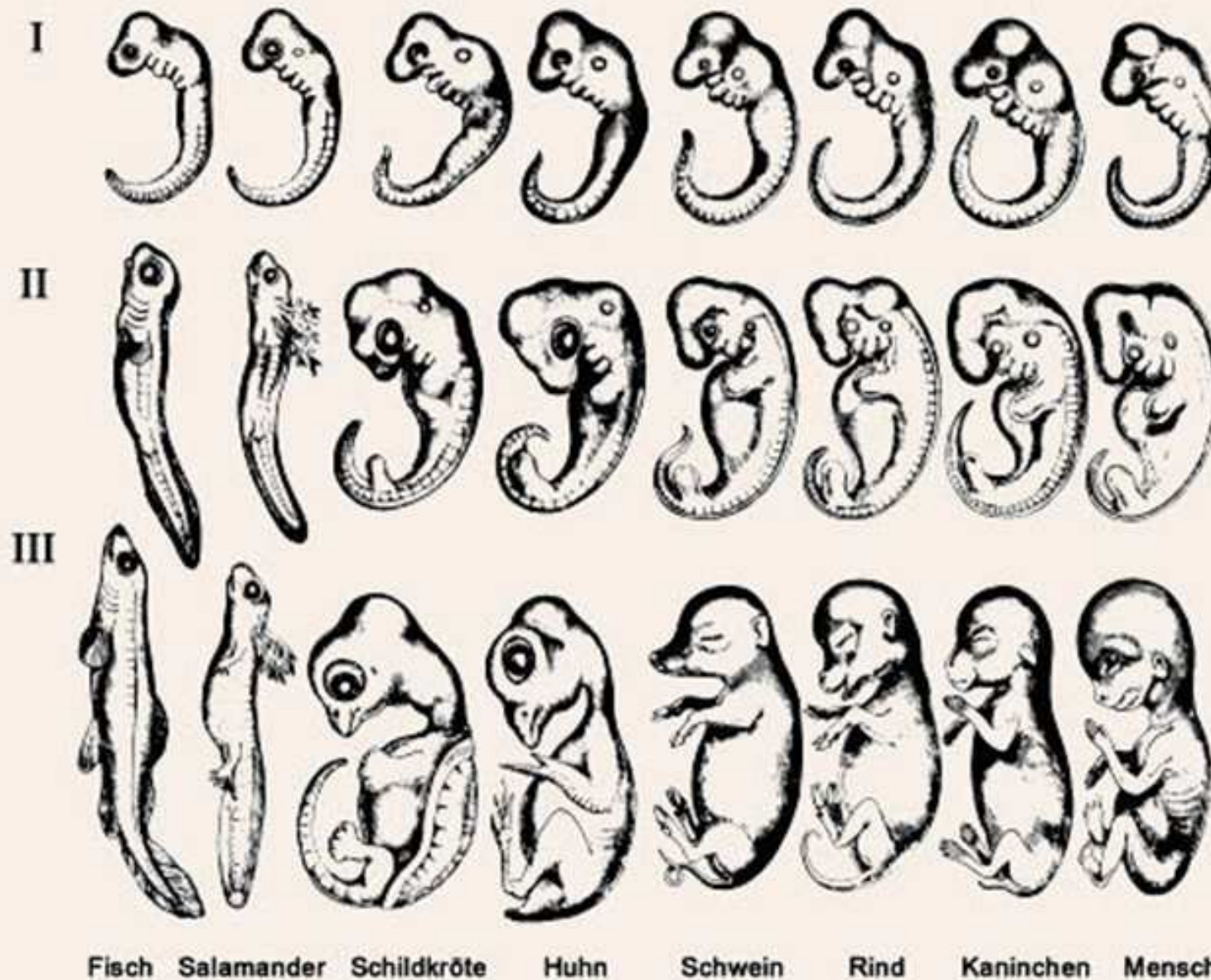


# Evolution and development

1. Embryo's vertellen je iets over evolutie.
2. Evo-devo onthult diepe homologieën.
3. Evo-devo zoekt de genetische en ontwikkelingsbiologische basis van evolutionaire veranderingen.
4. Evo-devo bestudeert de oorsprong van *novelties*
5. Embryonale ontwikkeling kan de evolutie in bepaalde richtingen sturen.

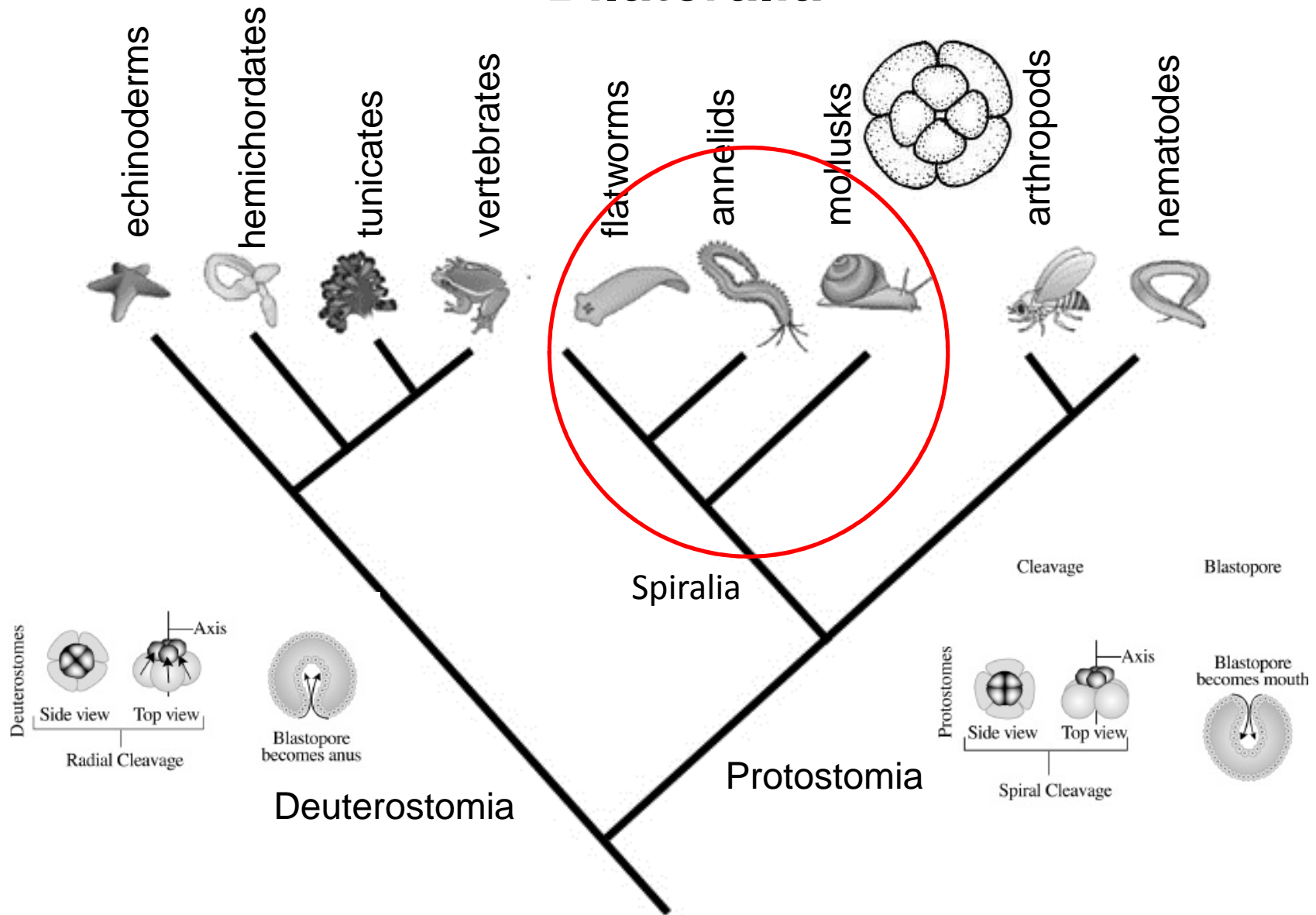


# Ernst Haeckel: 1834-1919: De ontogenie herhaalt de fylogenie





# Bilateria



# Evolution and development

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The search for homologous genes is quite futile  
except in very close relatives.

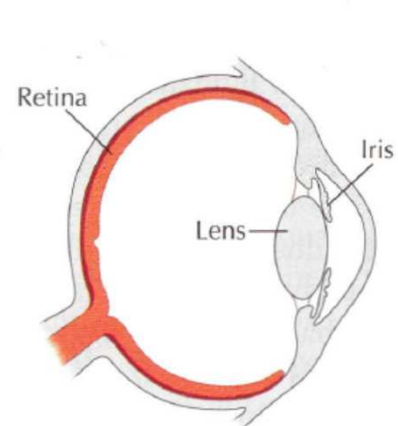
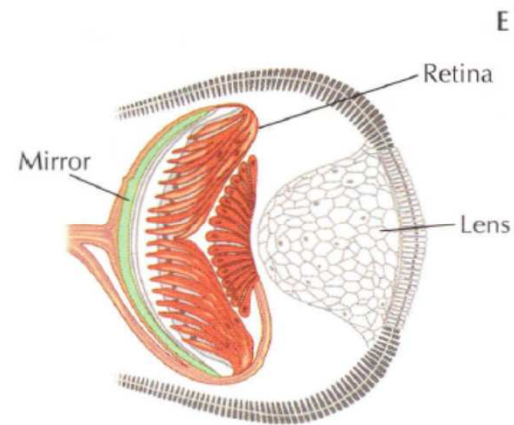
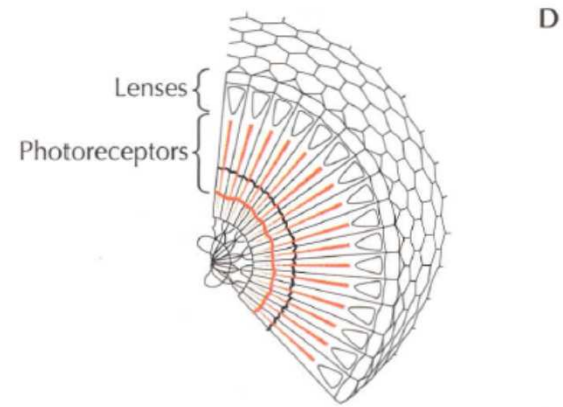
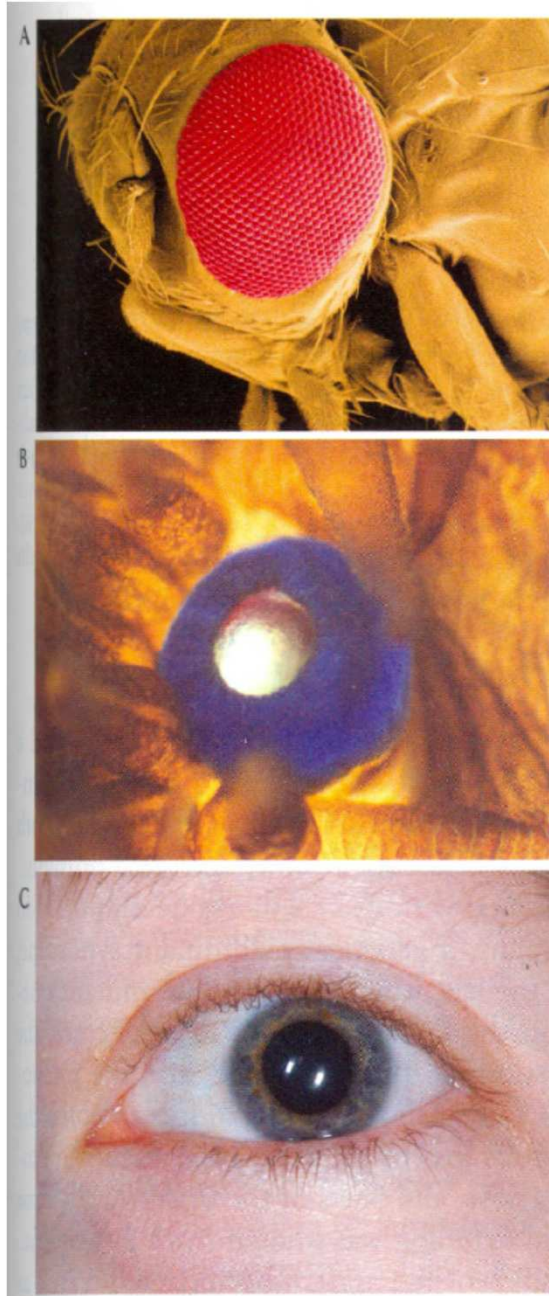
Ernst Mayr, 1963



# Evolution and development

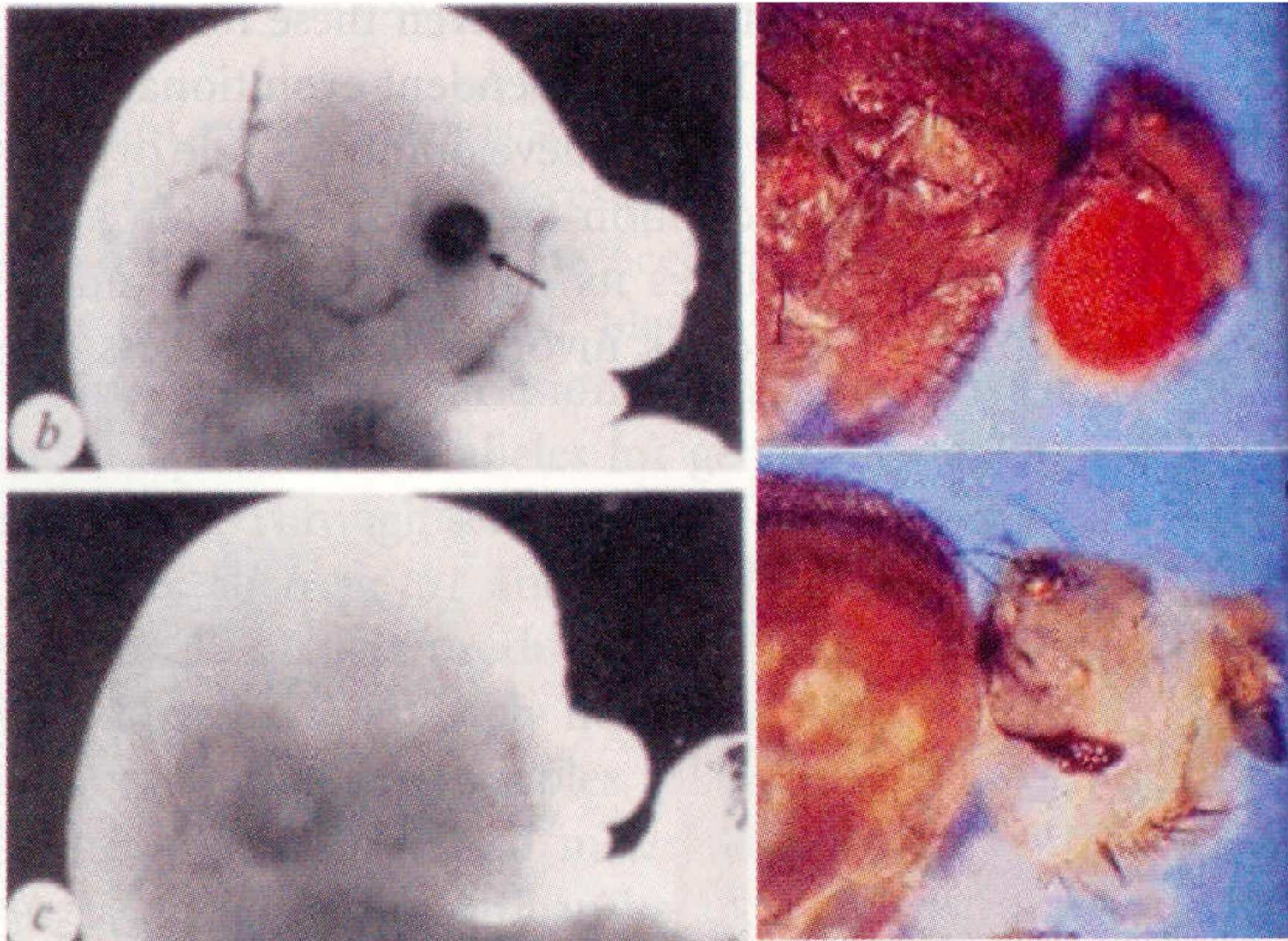
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# Ogen in Arthropoden, Mollusken and gewervelden zijn niet homolog...





**...maar staan allemaal onder controle van Pax6**



Pax6 mutants in mice and flies



## Ectopische expressie van Pax6 leidt tot ectopische ogen



Courtesy of Dr. W. Gehring, University of Basel.  
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# Distalless expressie in protostomen and deuterostomen

Evolution: Panganiban *et al.*

Proc. Natl. Acad. Sci. USA 94 (1997) 5163

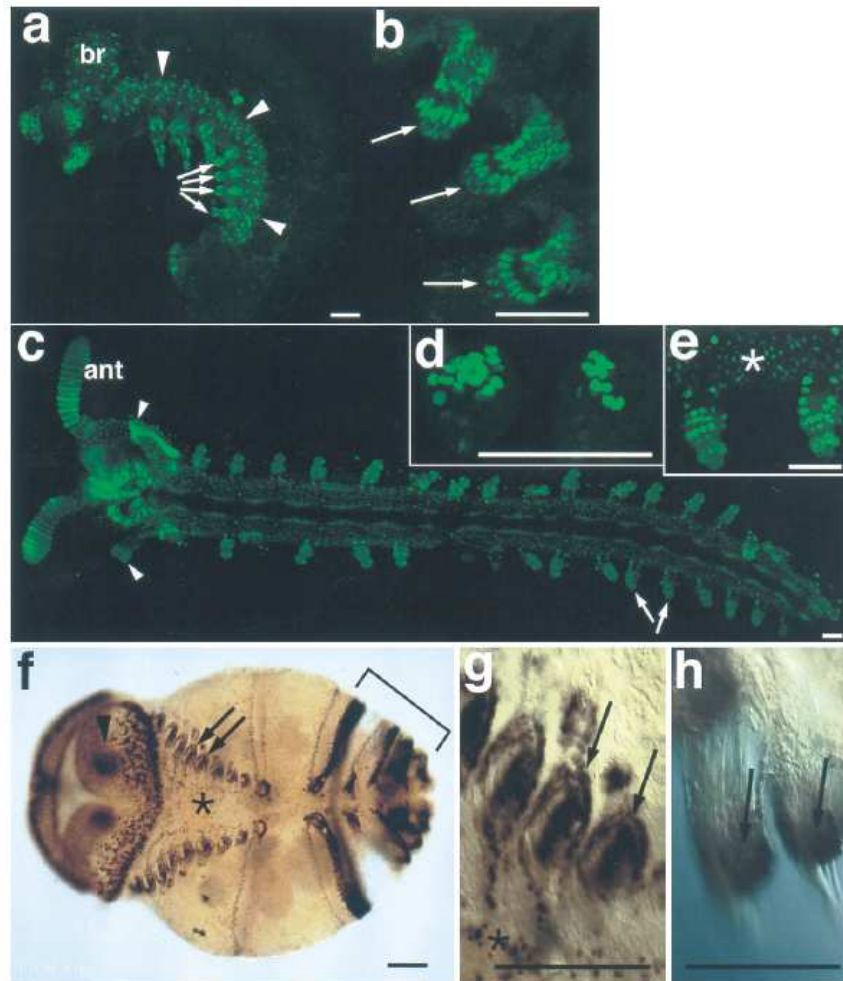


FIG. 1. Dll expression in representative protostomes. (a) Lateral view of a late stage *Precis coenia* butterfly embryo stained with the Dll antibody. Arrows (→) point to the distal tips of the left abdominal prolegs. Dll expression is detected in central nervous system in the brain (br) and in the ventral nerve cord (\*). (b) Higher magnification image of abdominal prolegs (→) from an embryo similar to that shown in a. (c) Ventral view of a late stage *Peripampus capensis* onychophoran embryo stained with the Dll antibody. The antennae (ant), oral papilla (•) and lobopods express Dll. The lobopods shown in higher magnification in e are indicated with →. (d) Right halves of two segments from a young *P. capensis* embryo stained with the Dll antibody. Dll expression is detected in the ectoderm of the presumptive lobopods prior to the formation of visible buds. (e) Higher magnification view of the lobopods indicated in d. (\*) The neurogenic ectoderm, which also expresses Dll. (f) Polychaete annelid *Chaetopterus variopedatus*, ventral view of larva just prior to metamorphosis. Dll expressing cells are visible in parapodial rudiments (→), antennae (out of focus on opposite dorsal surface, (•), prospective feeding organs (r), and in the neurogenic ectoderm (\*). (g) *C. variopedatus*, same specimen at a higher magnification, showing Dll reactive ectodermal nuclei in prospective distal cells of the anterior parapodia (→) and in the neurogenic region (\*). (h) Later stage *C. variopedatus* larva showing staining in distal portions of two anterior parapodia (→). Anterior is to the left in all panels. (Bars = 0.1 mm.)

5164

Evolution: Panganiban *et al.*

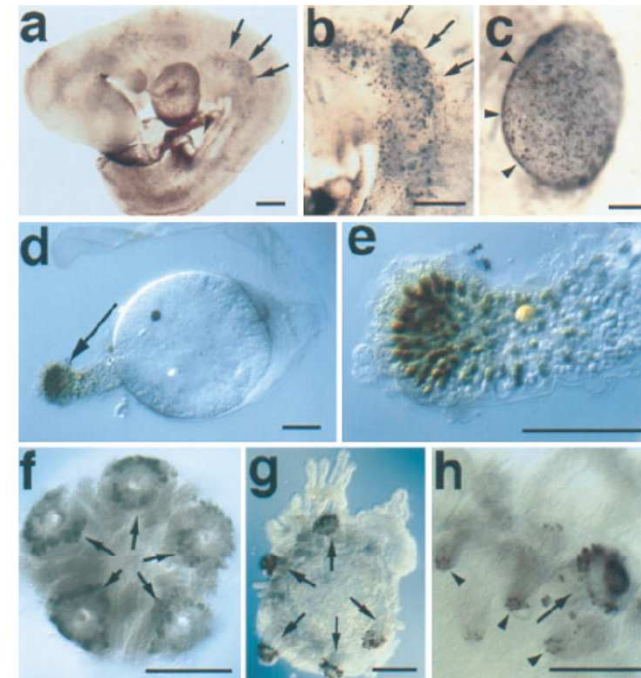


FIG. 2. Dll expression in representative deuterostomes. (a) Nine-day mouse embryo stained with the Dll antibody. Arrows (→) point to medial border of cells expressing one or more *Dlx* genes in the presumptive forelimb. Dlx expression can be detected in developing mouse limbs as the bud forms from the flank, and somewhat earlier than previously reported for mice or other vertebrates (6–11). (b) Higher magnification view of the forelimb indicated in a. (c) Dorsal view of the forelimb of a 10-day mouse embryo stained with the Dll antibody. (▶) The position of the apical ectodermal ridge. (d) Three-day *Molgula occidentalis* ascidian larva from which an ampulla is extending. Cells at the distal tip of the ampulla express Dll (→). (e) Higher magnification view of the ampulla shown in d. (f and g) Metamorphosing *Strongylocentrotus droebachiensis* sea urchin larvae stained with Dll antibody. Cells at the distal tip of the tube feet (→) express Dll prior to (f) and during (g) extension from the body wall. (h) Higher magnification view of a tube foot (→) and spines (▶) from an *S. droebachiensis* larva similar to that shown in g. Cells at the distal tip of the developing spines, as well as the tube feet express Dll. (Bars = 0.1 mm.)

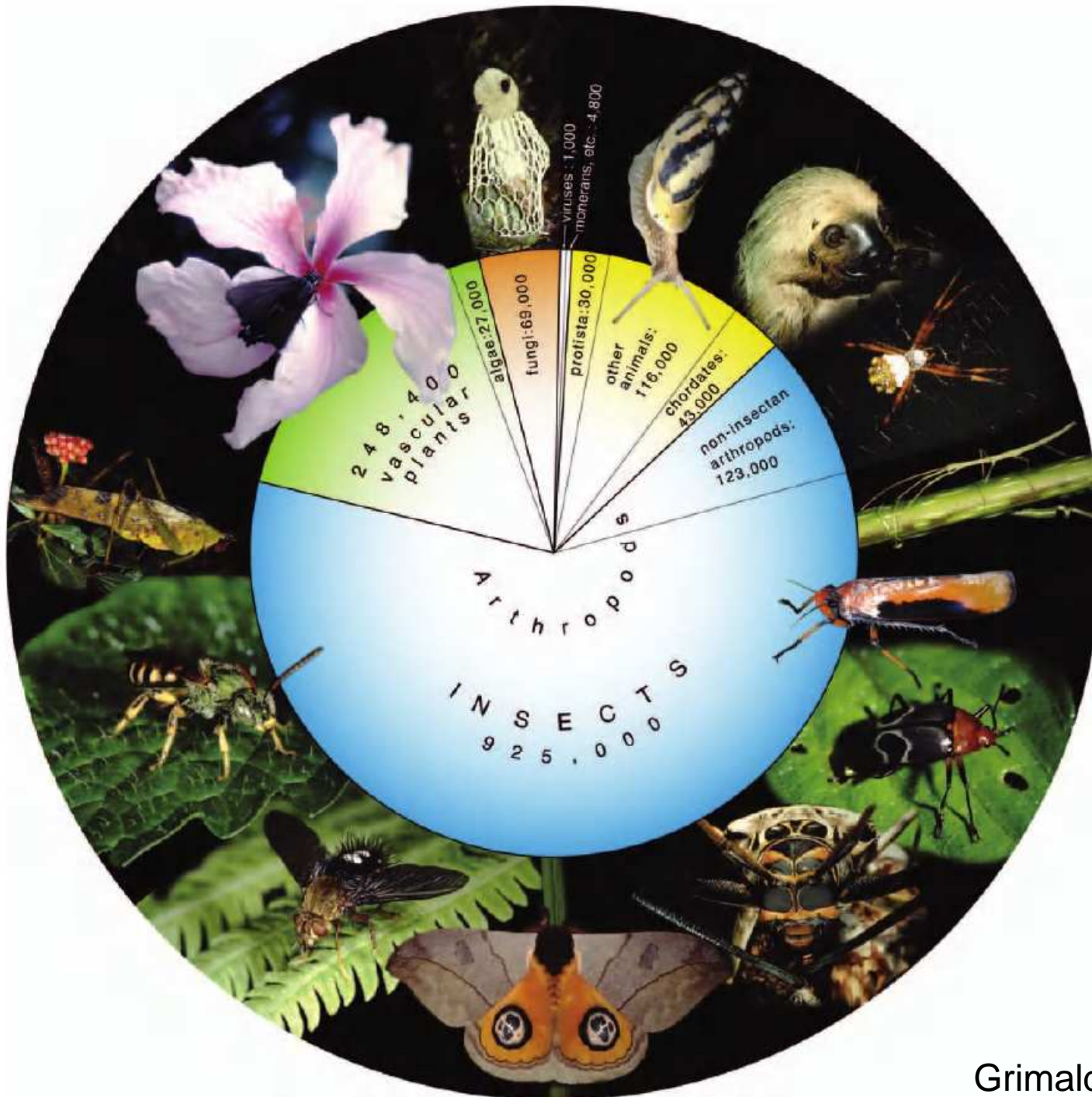
# Evolution and development

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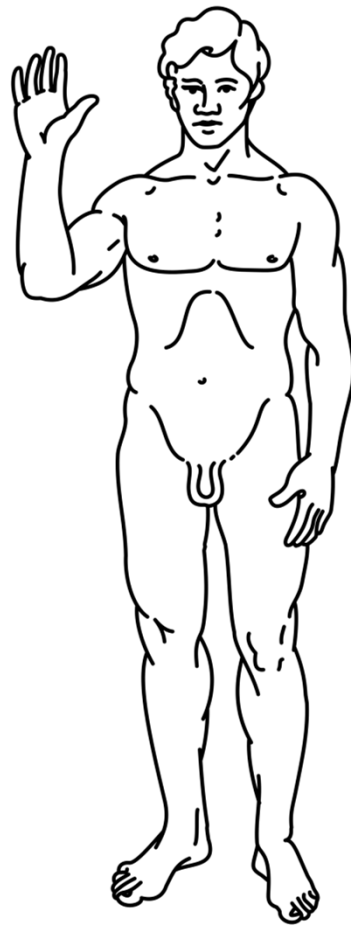


# Evolution and development

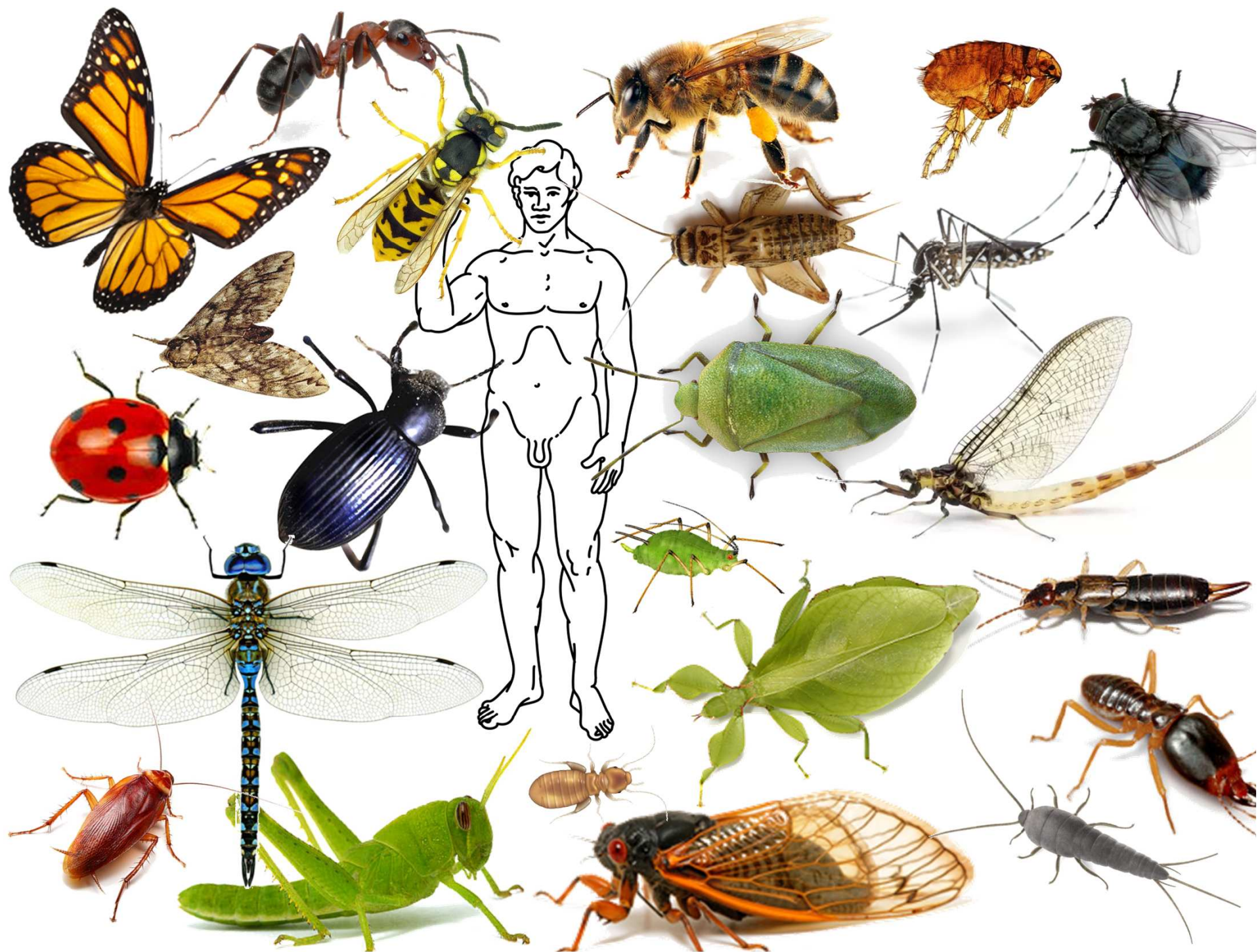
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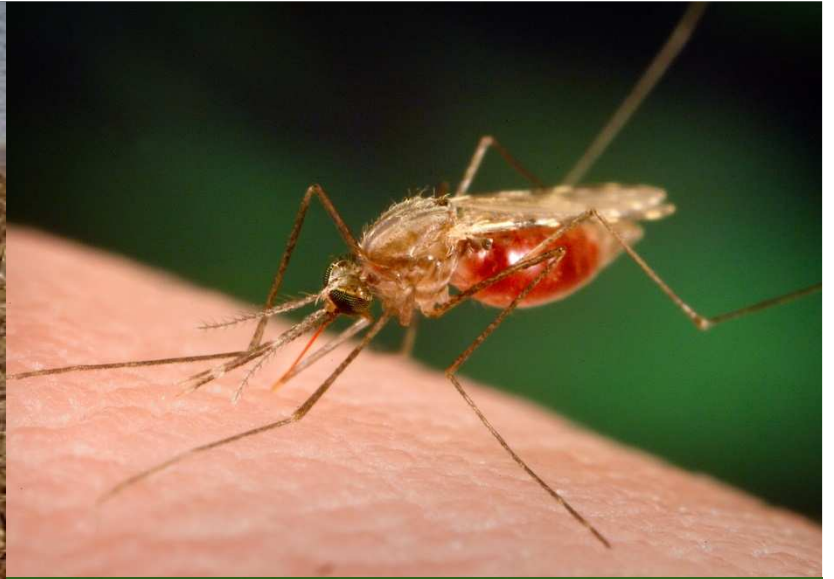
Grimaldi & Engel 2005

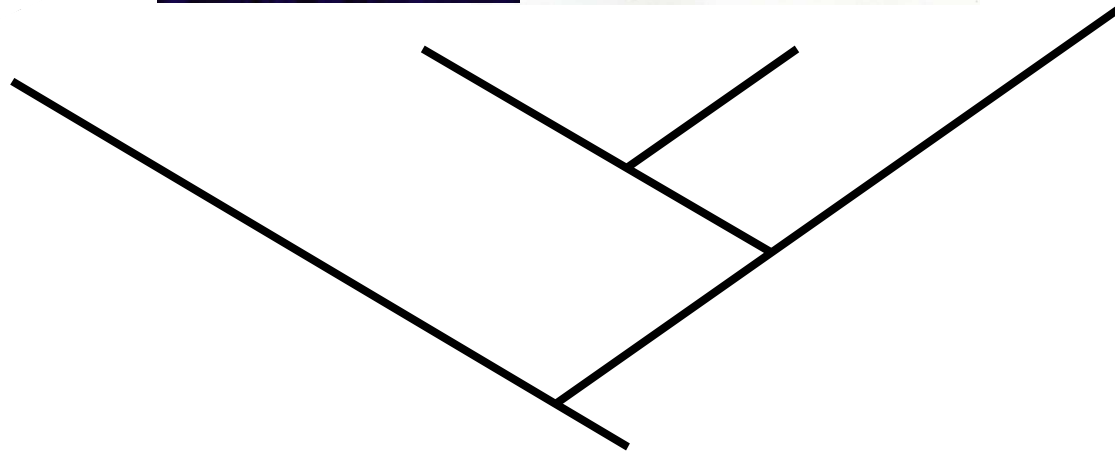








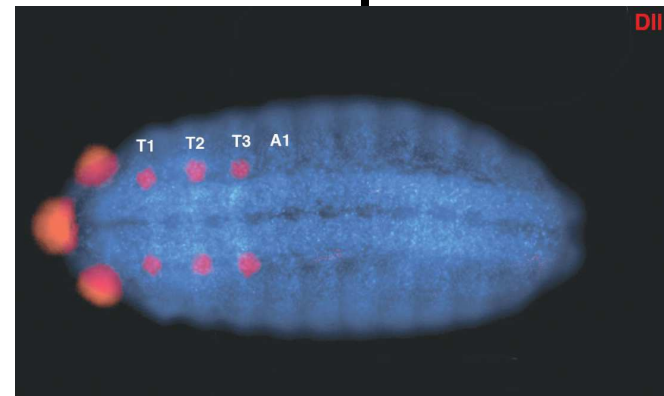
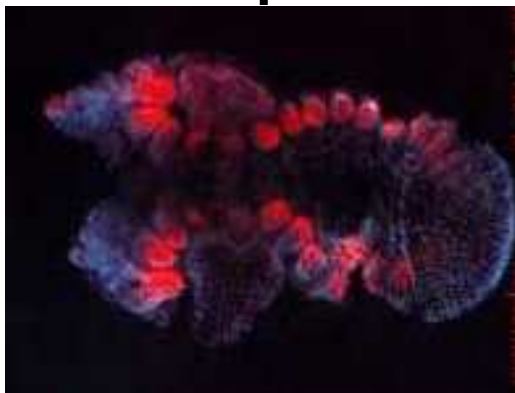




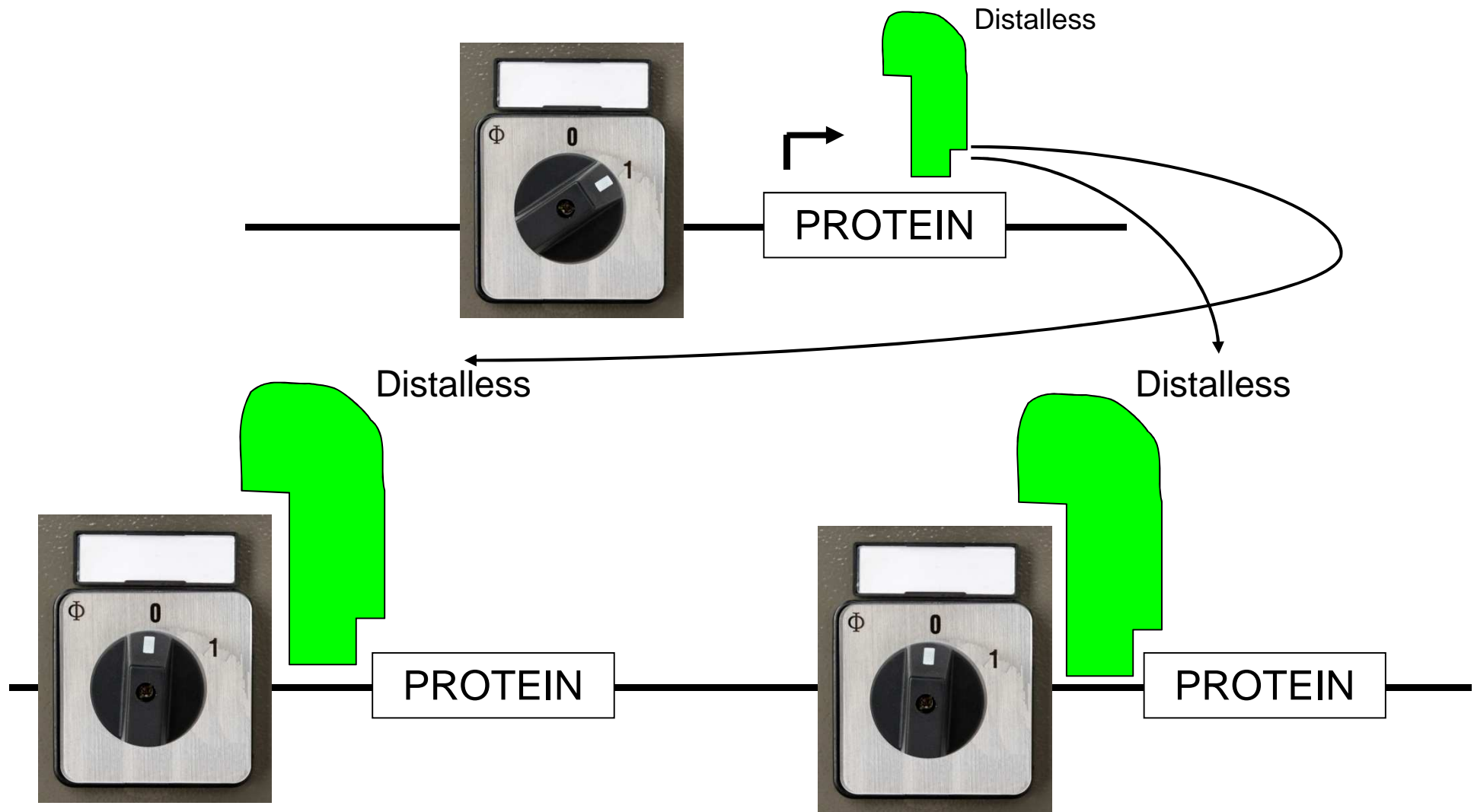


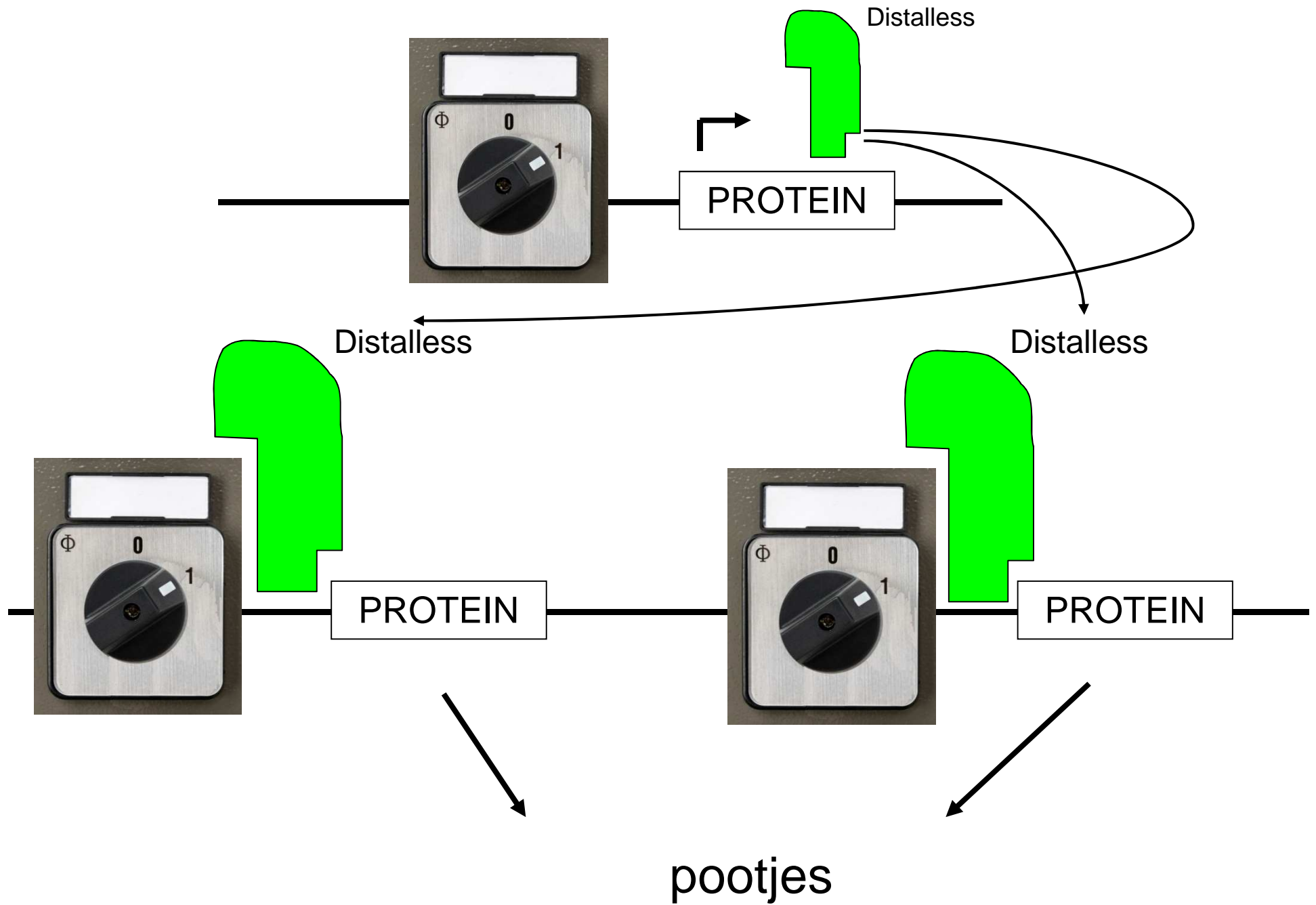


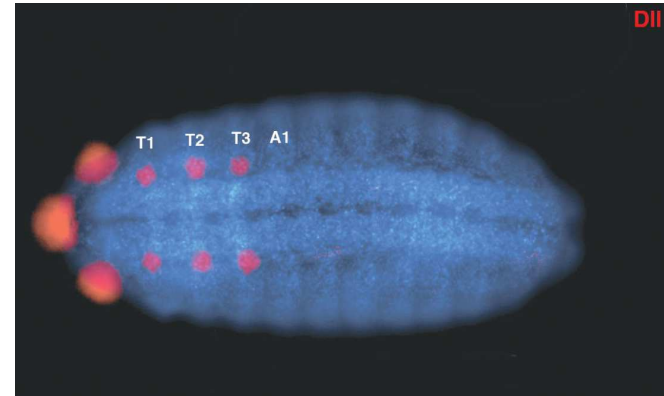
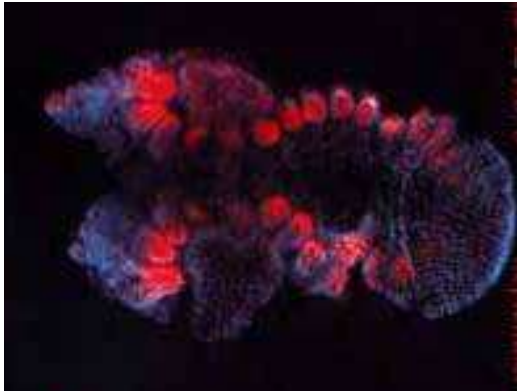
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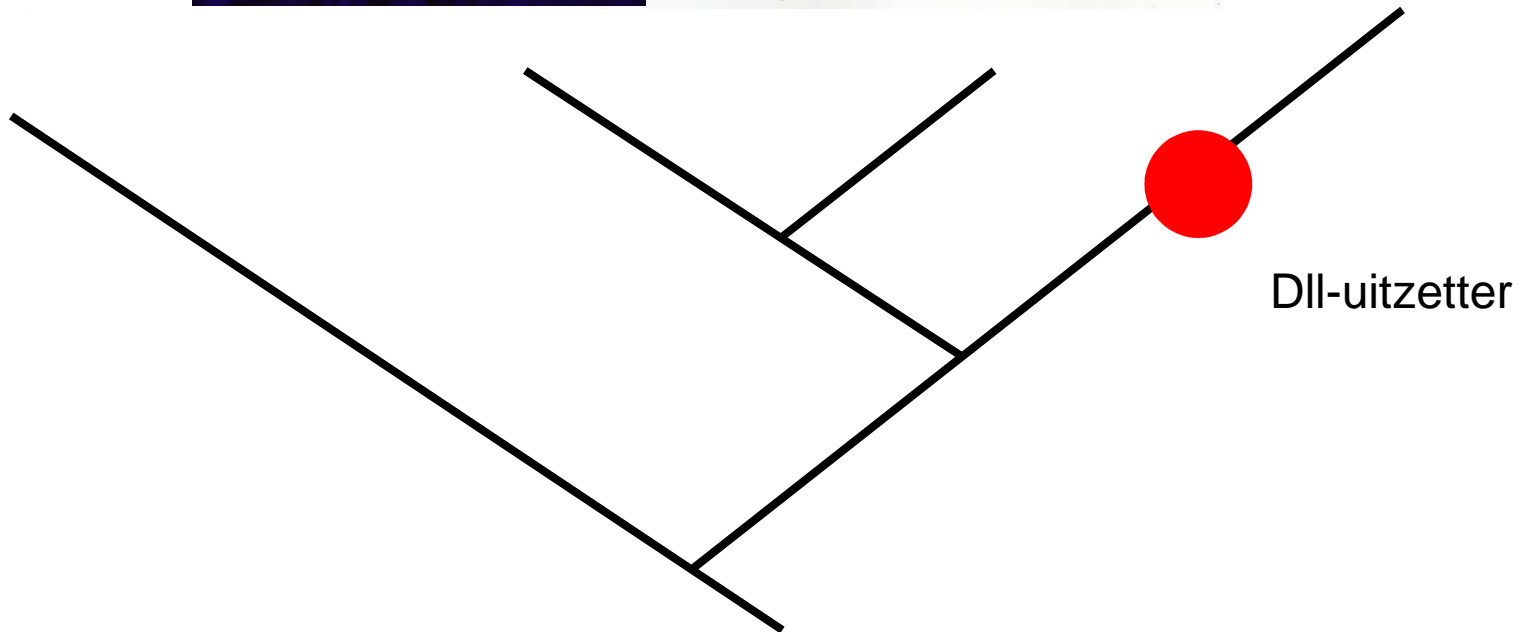
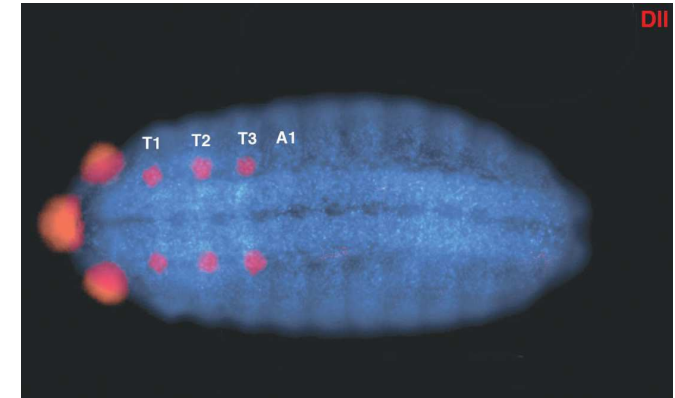






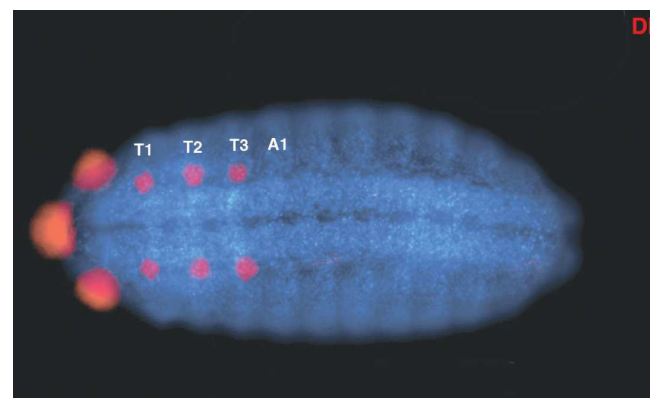
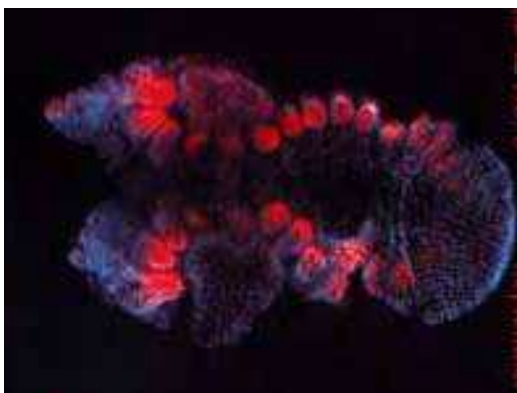
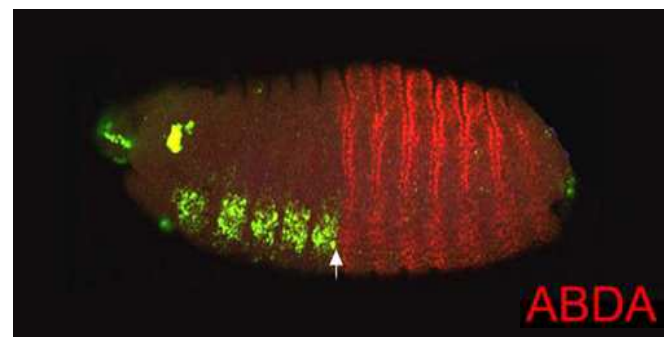


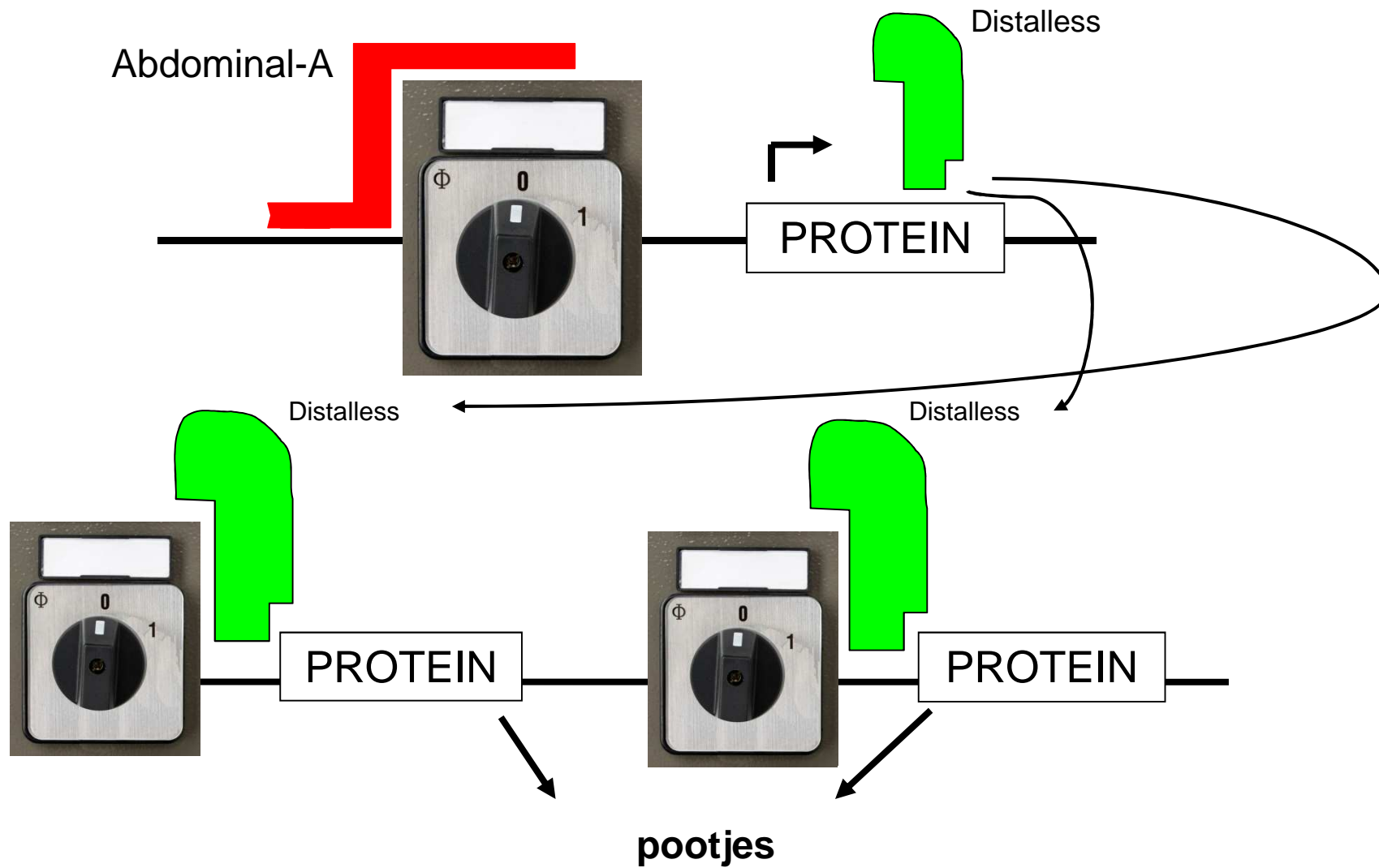


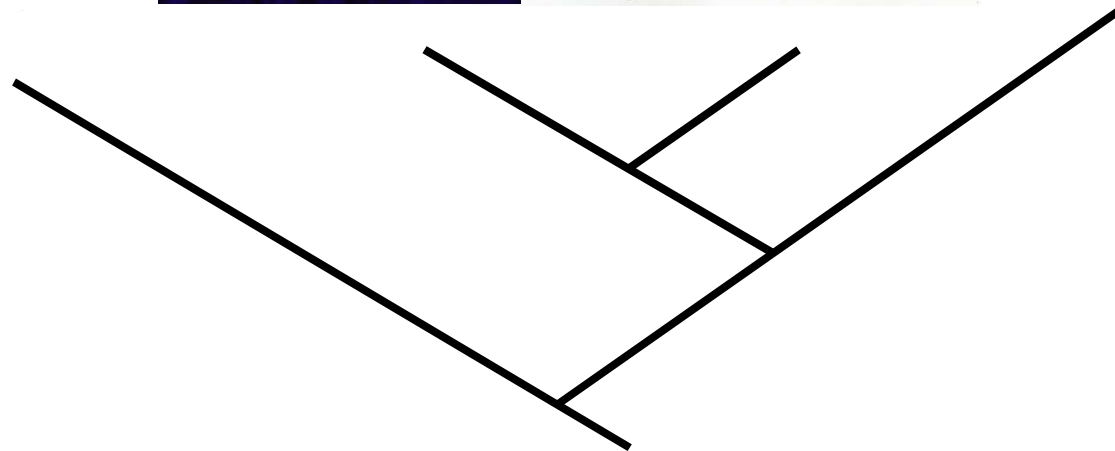
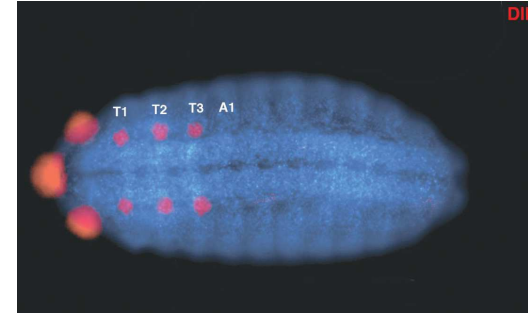
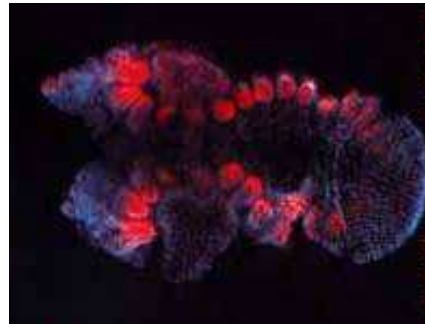
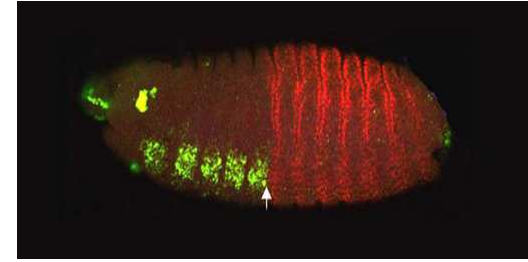
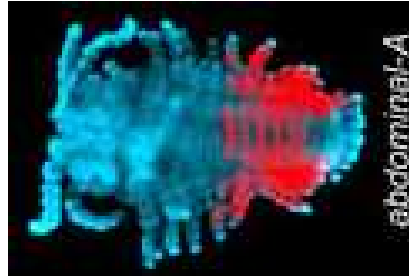


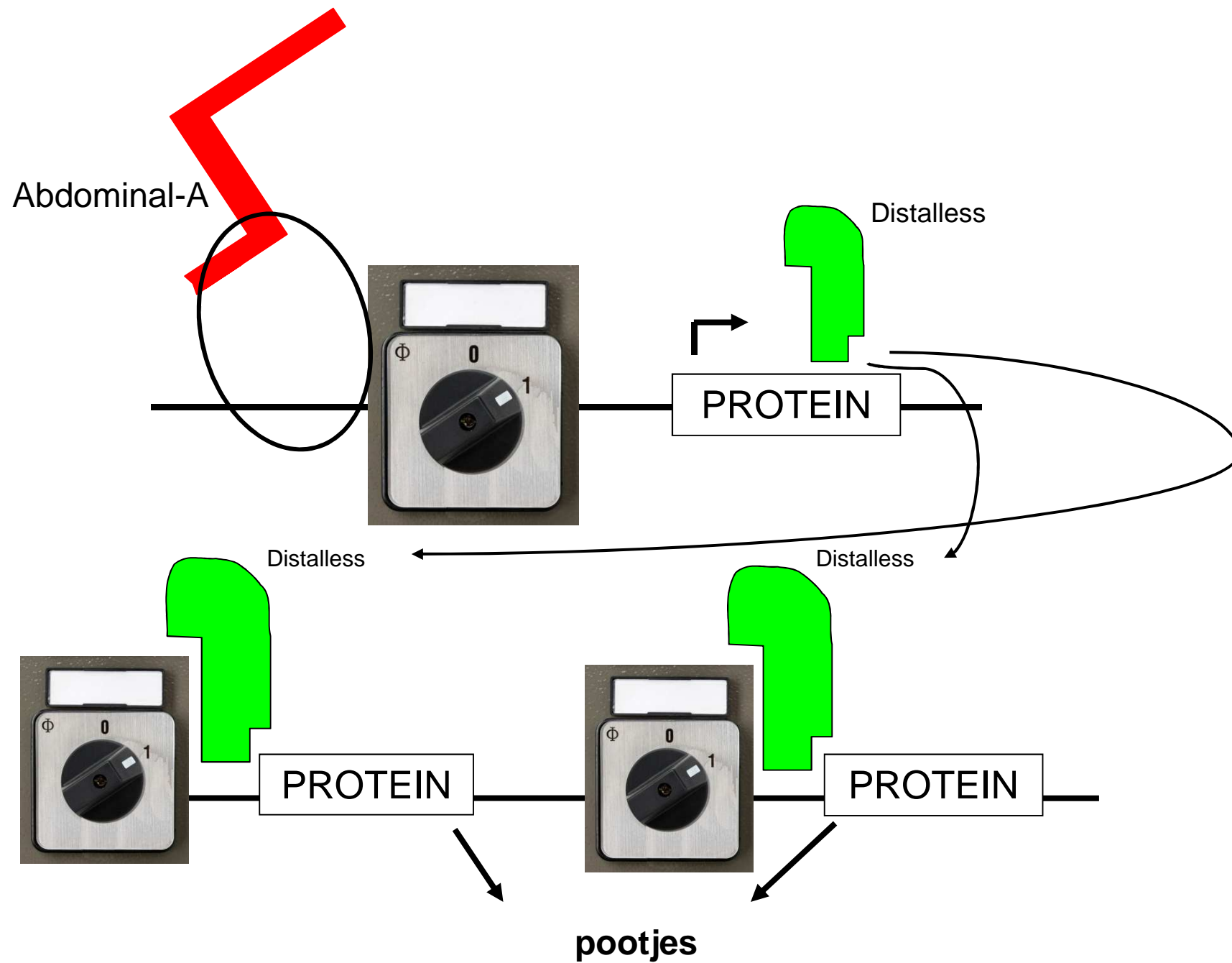


Abdominal-A













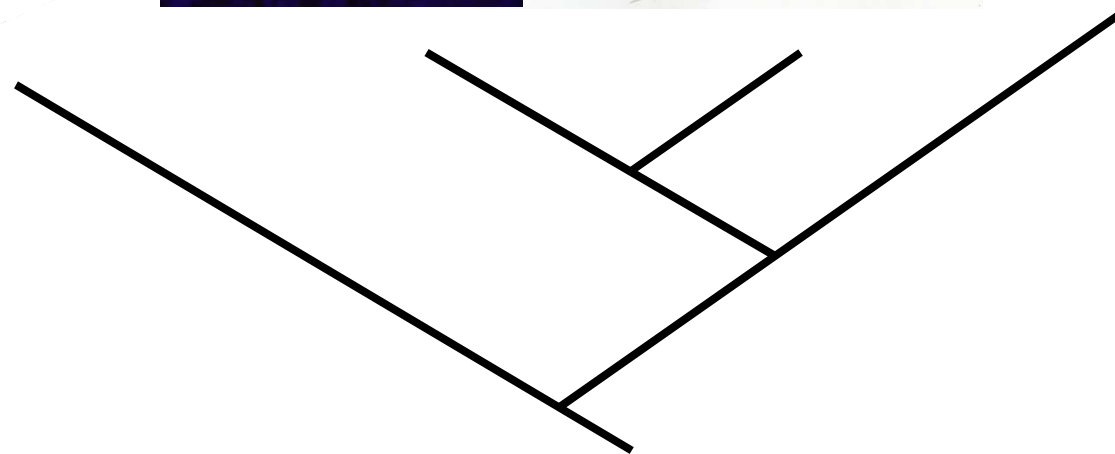
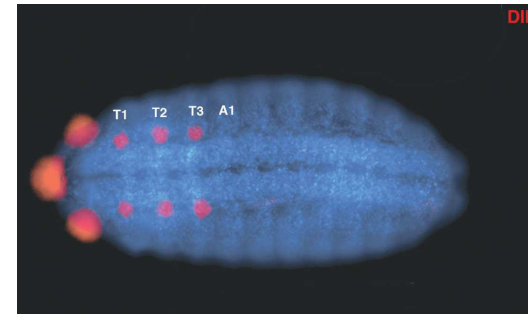
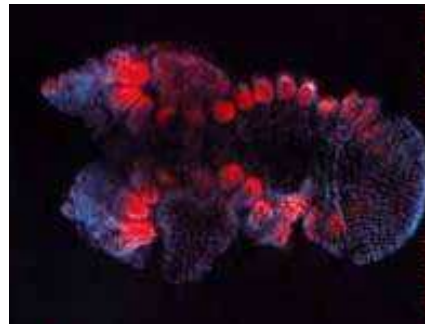
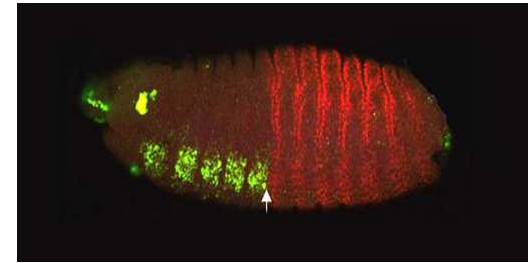
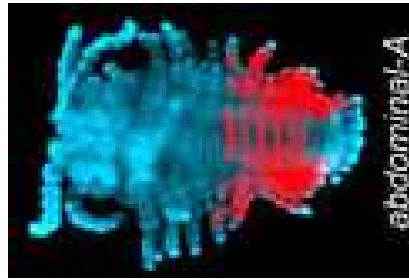


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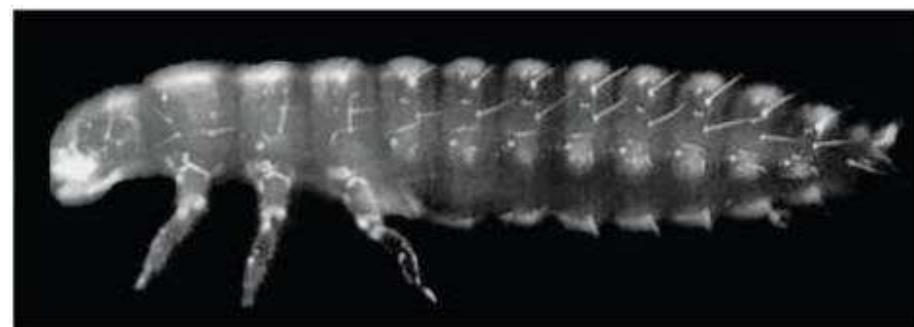




*cis*-regulatory evolution

***Tribolium castaneum***

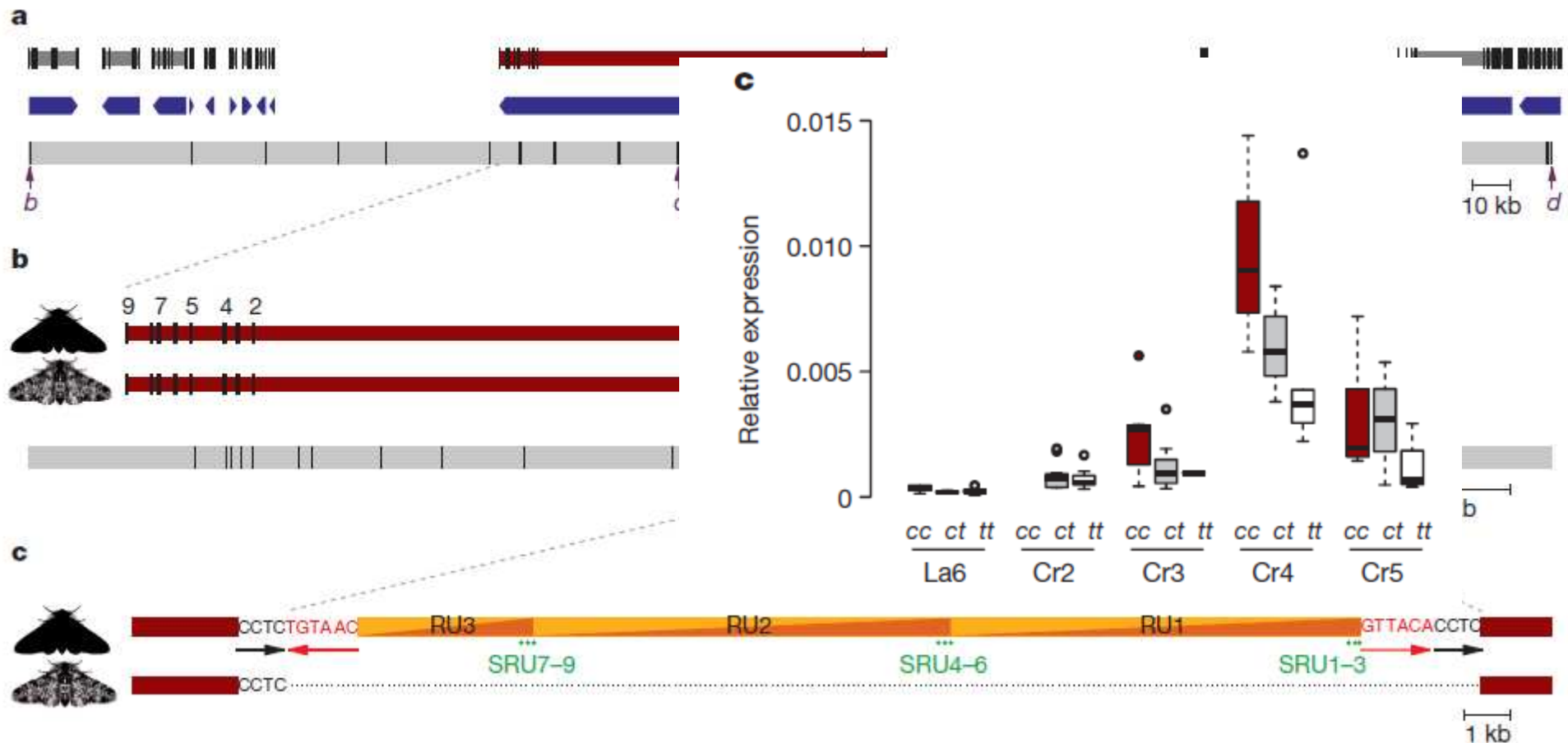




*cis*-regulatory evolution

# The industrial melanism mutation in British peppered moths

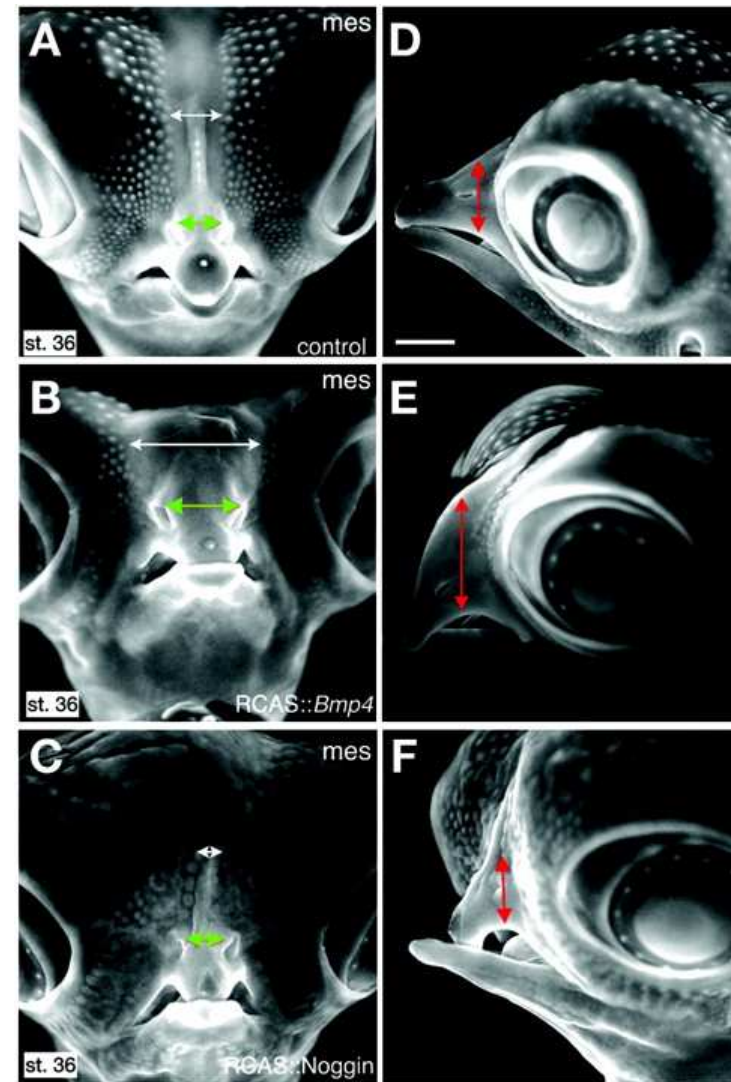
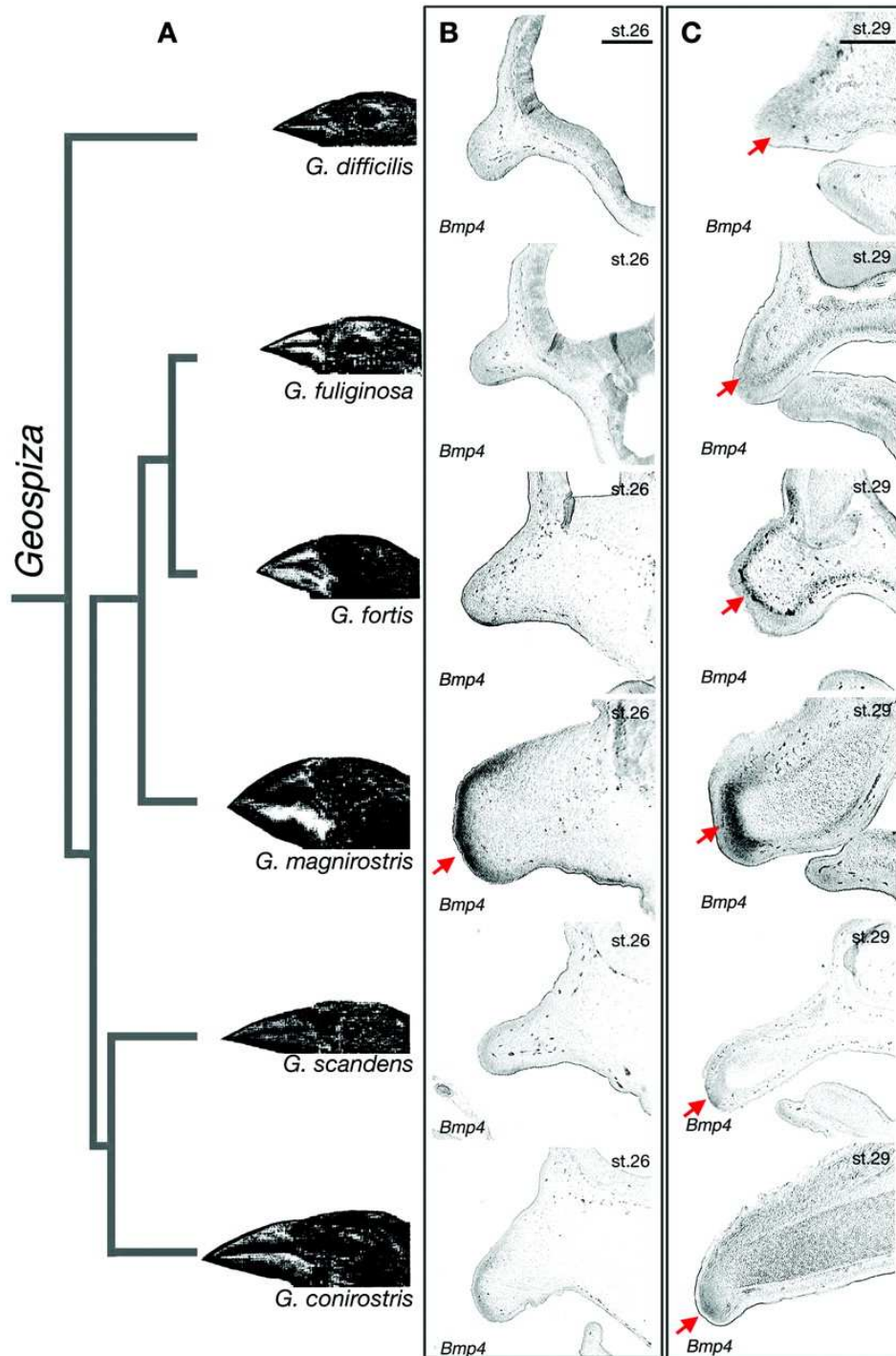
Arjen E. van't Hof<sup>1</sup>\*, Pascal Campagne<sup>1</sup>\*, Daniel J. Rigden<sup>1</sup>, Carl J. Yung<sup>1</sup>, Jessica Lingley<sup>1</sup>, Michael A. Quail<sup>2</sup>, Neil Hall<sup>1</sup>, Alistair C. Darby<sup>1</sup> & Ilik J. Saccheri<sup>1</sup>



<sup>1</sup>Institute of Integrative Biology, University of Liverpool, Biosciences Building, Crown Street, Liverpool L69 7ZB, UK. <sup>2</sup>Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire CB10 1SA, UK.

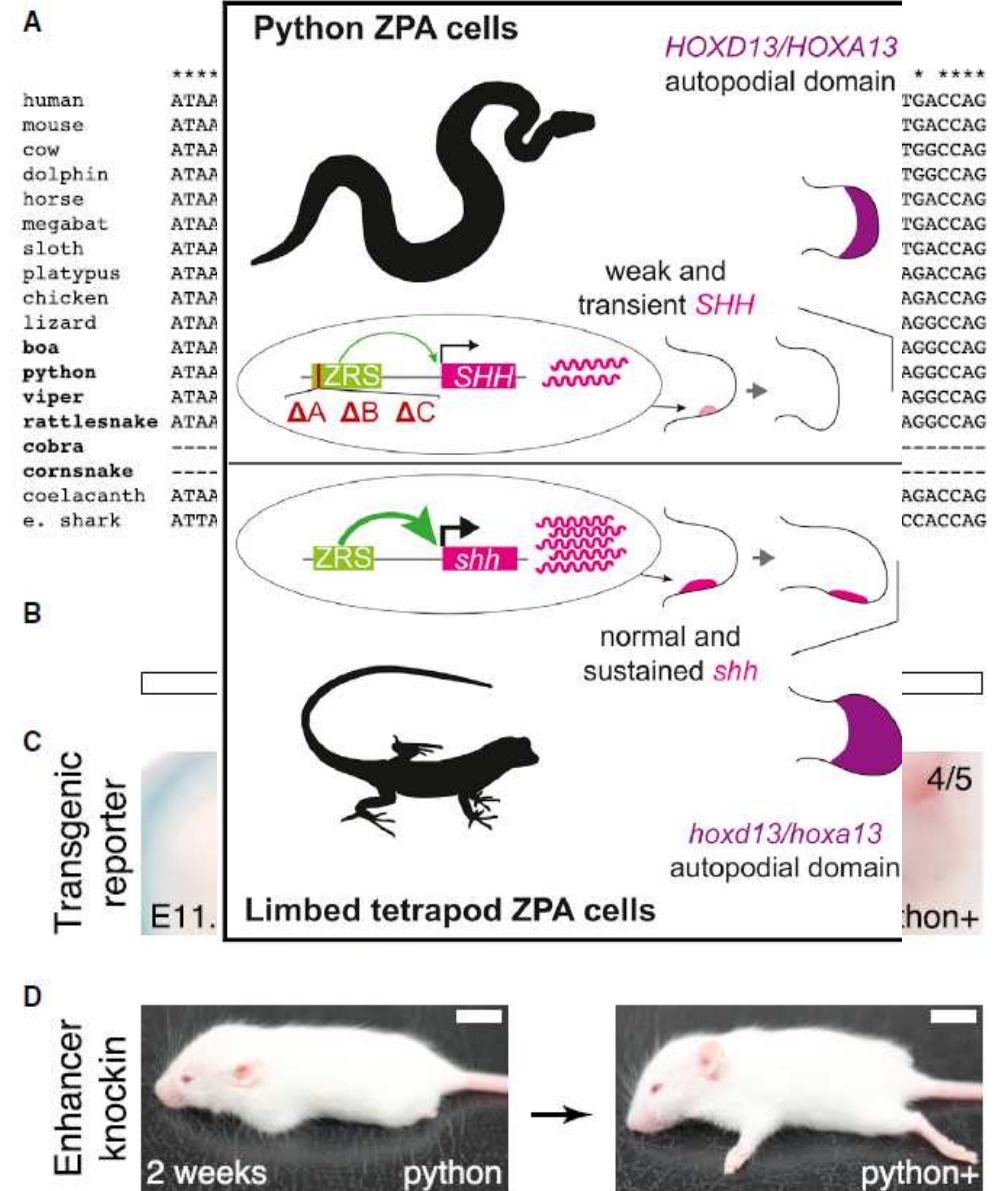
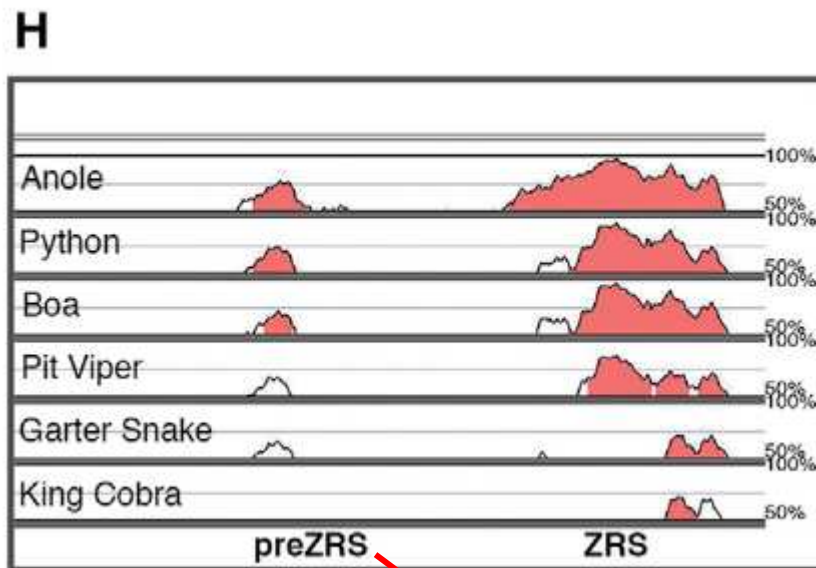
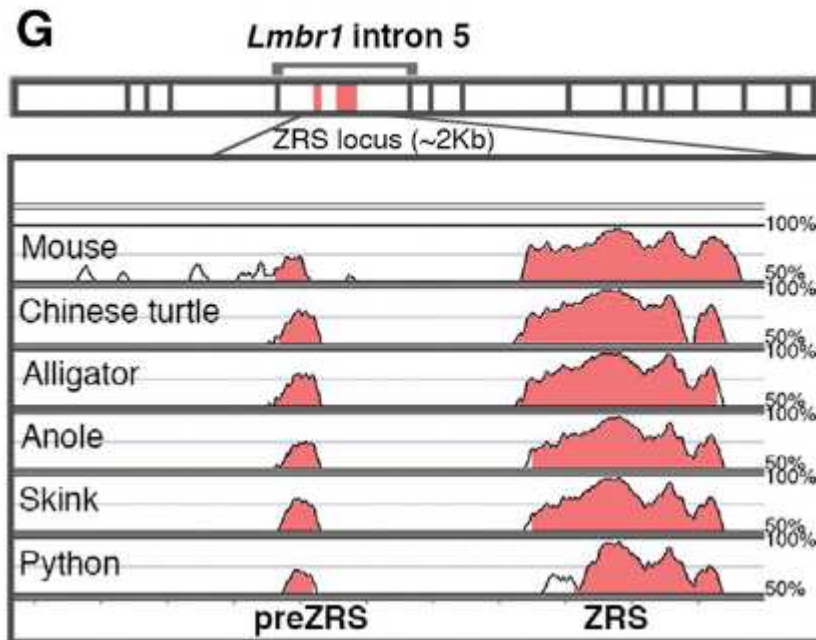
\*These authors contributed equally to this work.





Abzahnov et al. *Science* 2004



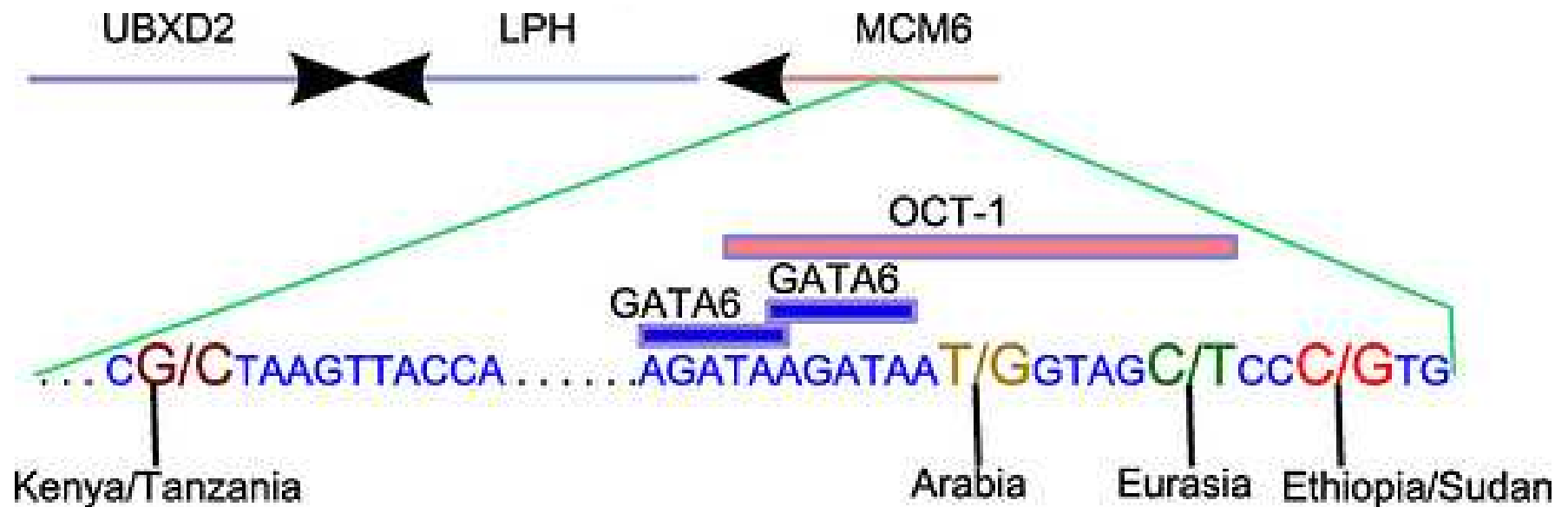
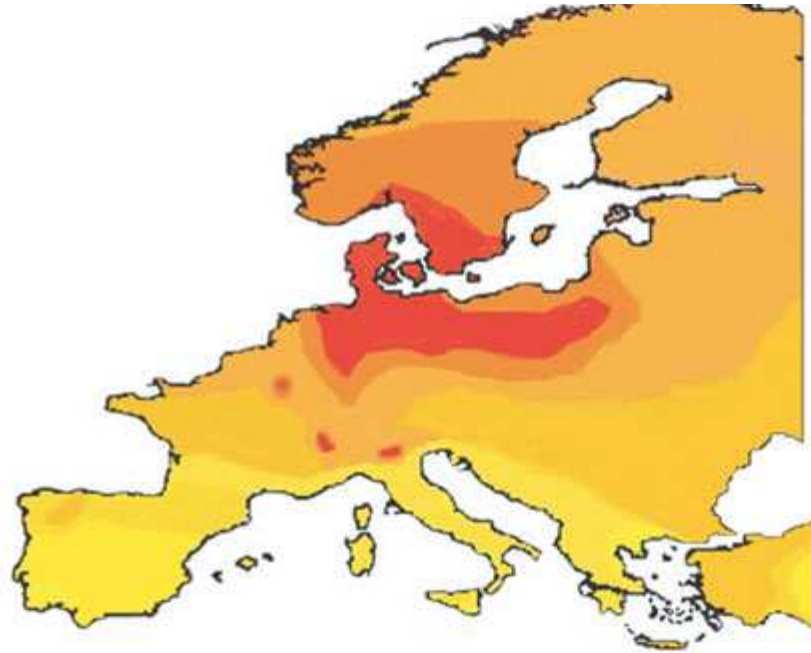


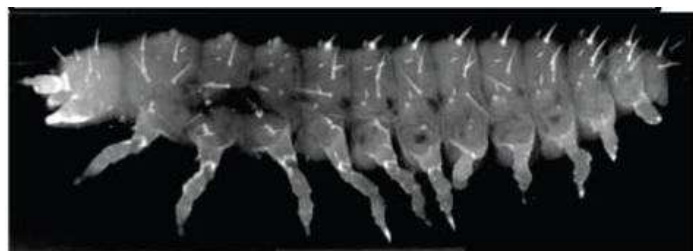
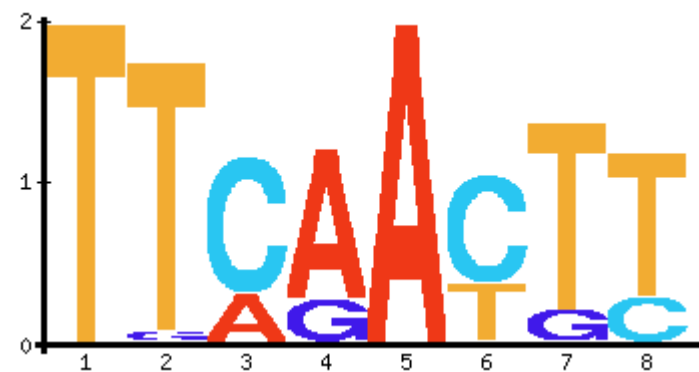
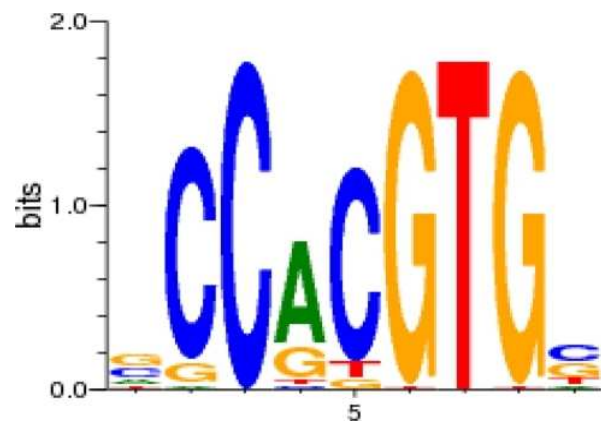
Leal & Cohen, 2014

Kvon et al., 2014

ZPA Regulatory Sequence

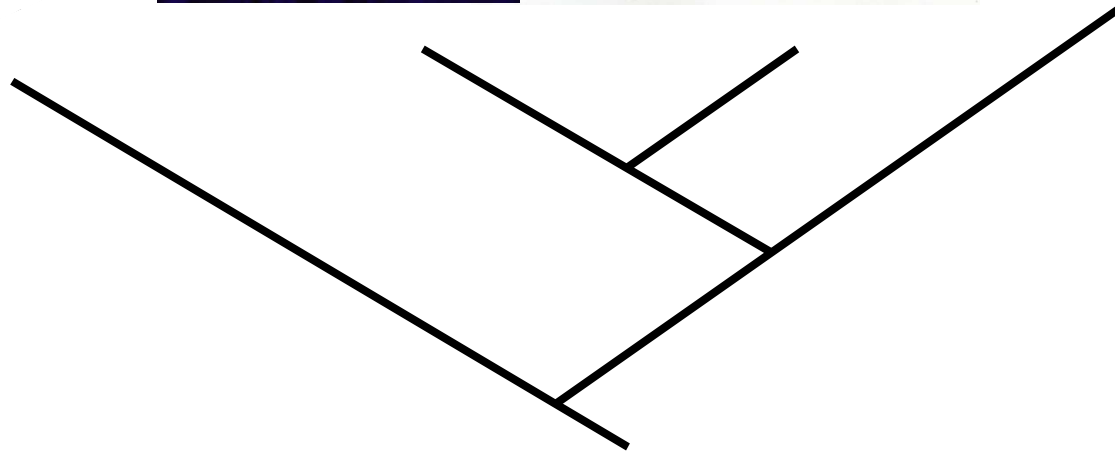
## Adulte lactose-tolerantie in mensen



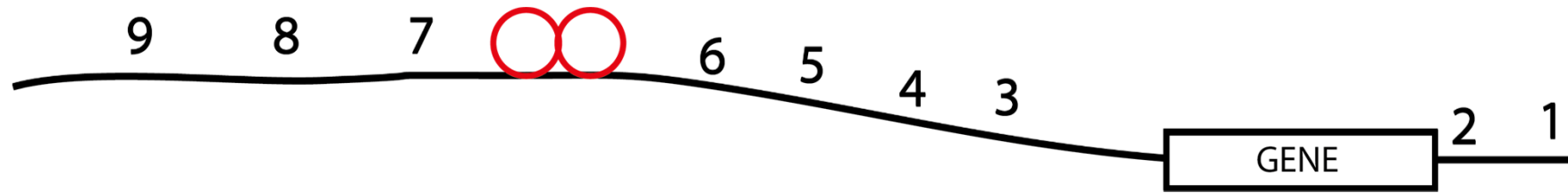


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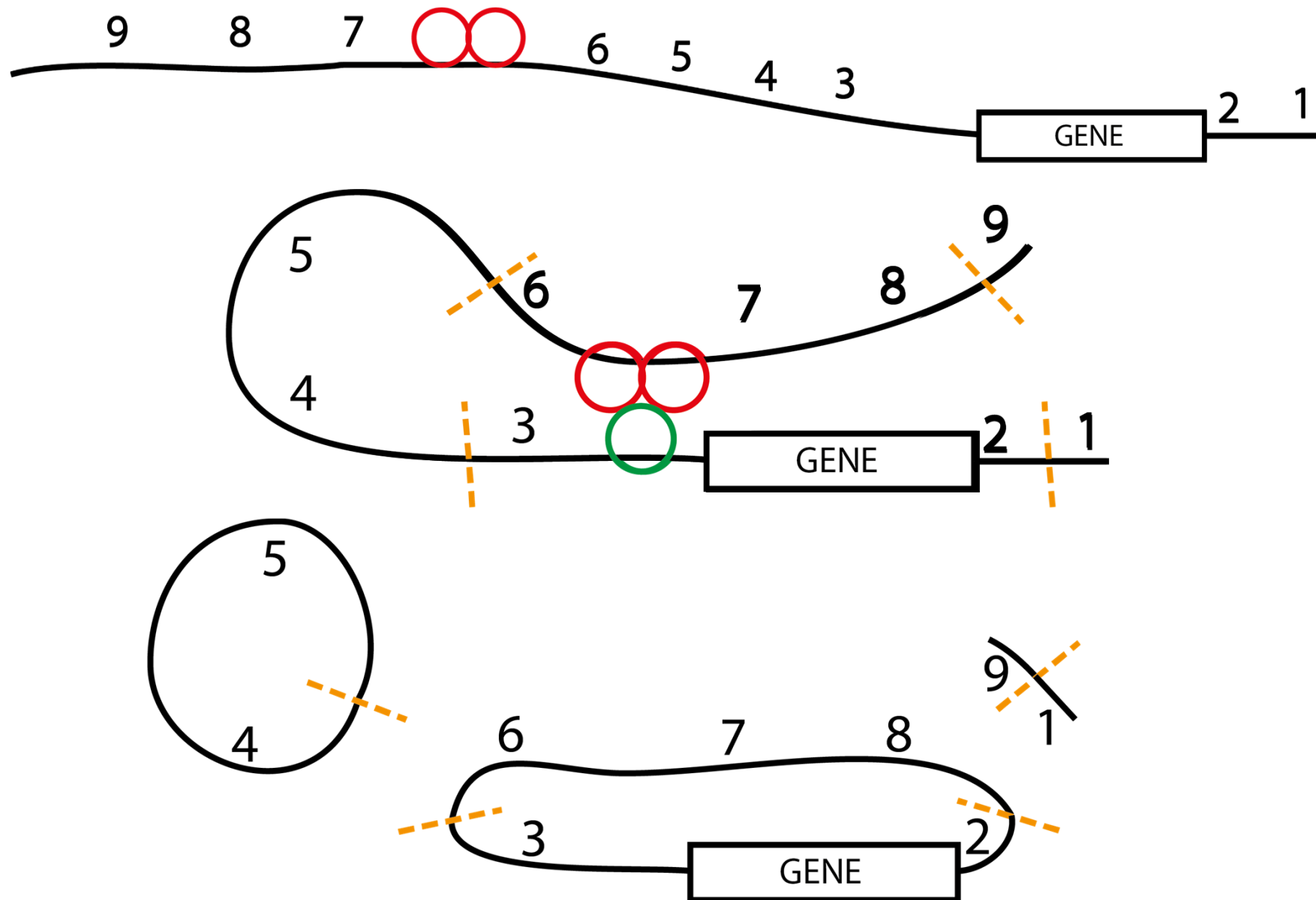




# Chromosome Conformation Capture



# Chromosome Conformation Capture






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Protein

dlx

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- Homo sapiens homeobox protein DLX-3
- Homo sapiens homeobox protein DLX-5
- Homo sapiens homeobox protein DLX-4
- Homo sapiens DLX1
- Mus musculus homeobox protein DLX-5
- Danio rerio homeobox protein Dlx3b
- Homo sapiens DLX3
- Homo sapiens homeobox protein DLX-6
- Homo sapiens DLX5
- Bos taurus homeobox protein DLX-5
- Danio rerio homeobox protein Dlx1a
- Danio rerio homeobox protein Dlx2b
- Danio rerio homeobox protein Dlx5a
- Homo sapiens homeobox protein DLX-2
- Rattus norvegicus homeobox protein DLX-5
- Homo sapiens DLX4
- Mus musculus homeobox protein DLX-3
- Mus musculus homeobox protein DLX-6
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## transcription factor DLX1 [Homo sapiens]

GenBank: AAO91939.1

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LOCUS AAO91939 255 aa linear PRI 24-DEC-2003

DEFINITION transcription factor DLX1 [Homo sapiens].

ACCESSION AAO91939

VERSION AAO91939.1

DBSOURCE accession [AY257976.1](#)

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM [Homo sapiens](#)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 255)

AUTHORS Chiba,S., Takeshita,K., Imai,Y., Kumano,K., Kurokawa,M., Masuda,S., Shimizu,K., Nakamura,S., Ruddle,F.H. and Hirai,H.

TITLE Homeoprotein DLX-1 interacts with Smad4 and blocks a signaling pathway from activin A in hematopoietic cells

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (26), 15577-15582 (2003)

PUBMED [14671321](#)

REFERENCE 2 (residues 1 to 255)

## unique identifier

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Maak er een handige naam van:

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	U	C	A	G	
U	UUU } Phe - F UUC } UUA } Leu - L UUG }	UCU } UCC } Ser - S UCA } UCG }	UAU } Tyr - Y UAC } UAA stop UAG stop	UGU } Cys - C UGC } UGA stop UGG } Trp - W	U C A G
C	CUU } CUC } Leu - L CUA } CUG }	CCU } CCC } Pro - P CCA } CCG }	CAU } His - H CAC } CAA } Gln - Q CAG }	CGU } CGC } Arg - R CGA } CGG }	U C A G
A	AUU } AUC } Ile - I AUA } AUG Met - M start	ACU } ACC } Thr - T ACA } ACG }	AAU } Asn - N AAC } AAA } Lys - K AAG }	AGU } Ser - S AGC } AGA } Arg - R AGG }	U C A G
G	GUU } GUC } Val - V GUA } GUG }	GCU } GCC } Ala - A GCA } GCG }	GAU } Asp - D GAC } GAA } Glu - E GAG }	GGU } GGC } Gly - G GGA } GGG }	U C A G

# Abbreviations for amino acids

<i>Amino acid</i>	<i>Three-letter abbreviation</i>	<i>One-letter symbol</i>
Alanine	Ala	A
Arginine	Arg	R
Asparagine	Asn	N
Aspartic acid	Asp	D
Asparagine or aspartic acid	Asx	B
Cysteine	Cys	C
Glutamine	Gln	Q
Glutamic acid	Glu	E
Glutamine or glutamic acid	Glx	Z
Glycine	Gly	G
Histidine	His	H
Isoleucine	Ile	I
Leucine	Leu	L
Lysine	Lys	K
Methionine	Met	M
Phenylalanine	Phe	F
Proline	Pro	P
Serine	Ser	S
Threonine	Thr	T
Tryptophan	Trp	W
Tyrosine	Tyr	Y
Valine	Val	V



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NCBI National Center for Biotechnology Information

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## Basic Local Alignment Search Tool

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NEWS

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New databases, better performance.  
Wed, 19 Dec 2018 17:00:00 EST

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nucleotide ► nucleotide

**blastx**  
translated nucleotide ► protein

**tblastn**  
protein ► translated nucleotide




**Protein BLAST**  
protein ► protein

### BLAST Genomes


Search

Human Mouse Rat Microbes


### Standalone and API BLAST



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Call BLAST from your application



**Use BLAST in the cloud**  
Start an instance at a cloud provider

## Standard Protein BLAST

blastn blastp **blastx** tblastn tblastx

BLASTP programs search protein databases using a protein

**Enter Query Sequence**

Enter accession number(s), gi(s), or FASTA sequence(s) [Clear](#)

YVNSVSSHASSPYISSVQSYPGSASLAQSRLEDPGADSEKSTVVEGGEVRFNGKGKKIRKPRTIYSS  
LQL  
QALNRRFQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKKLMKQGGALEGSALANGRALSA  
GSP  
PVPPGWNPNSSSGKGSGGNAGSYIPSYTSWYPSAHQEAMQQPQLM

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Job Title

Enter a descriptive title for your BLAST search

☐ Align two or more sequences

**Choose Search Set**

Database

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Exclude [Optional](#)

Entrez Query [Optional](#)

☐ exclude [+](#)

☐ will be shown.

☐ Uncultured/environmental sample sequences

[Create custom database](#)

chimpa  
chimpanzee (taxid:9598)  
chimpanzees (taxid:9596)  
Chimpanzee immunodeficiency virus (SIV(CPZ)) (taxi...  
Chimpanzee immunodeficiency virus (taxid:11723)  
pygmy chimpanzee (taxid:9597)

←

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Alignments

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	Description	Max score	Total score
<input type="checkbox"/>	<a href="#">homeobox protein DLX-1 [Pan troglodytes]</a>	517	517
<input type="checkbox"/>	<a href="#">DLX1 isoform 2 [Pan troglodytes]</a>	384	384
<input type="checkbox"/>	<a href="#">DLX1 isoform 1 [Pan troglodytes]</a>	348	348
<input type="checkbox"/>	<a href="#">DLX6 isoform 1 [Pan troglodytes]</a>	231	231
<input type="checkbox"/>	<a href="#">homeobox protein DLX-6 [Pan troglodytes]</a>	231	231

- ☐ [ventral anterior homeobox 1 isoform X1 \[Pan troglodytes\]](#)
- ☐ [diencephalon/mesencephalon homeobox protein 1 isoform X1 \[Pan troglodytes\]](#)

## Alignments

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homeobox protein DLX-1 [Pan troglodytes]

Sequence ID: [XP\\_009442039.1](#) Length: 255 Number of Matches: 1

[▶ See 1 more title\(s\)](#)

Range 1: 1 to 255 [GenPept](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
517 bits(1332)	0.0	Compositional matrix adjust.	255/255(100%)	255/255(100%)	0/255(0%)
Query 1	MTMTTMPESLNSPVSGKAVFMEFGPPNQMSPPMSHGHYSMHCLHSAGHSQPDGAYSSA	60			
Sbjct 1	MTMTTMPESLNSPVSGKAVFMEFGPPNQMSPPMSHGHYSMHCLHSAGHSQPDGAYSSA	60			
Query 61	SSFSRPLGYPYVNSVSSHASSPYISSVQSYPGSASLAQSRLEDPGADSEKSTVVEGGEVR	120			
Sbjct 61	SSFSRPLGYPYVNSVSSHASSPYISSVQSYPGSASLAQSRLEDPGADSEKSTVVEGGEVR	120			
Query 121	FNGKGKKIRKPRTIYSSLQLQALNRRFQQTQYLALPERAELAASLGLTQTQVKIWFQNK	180			
Sbjct 121	FNGKGKKIRKPRTIYSSLQLQALNRRFQQTQYLALPERAELAASLGLTQTQVKIWFQNK	180			
Query 181	SKFKKLMKQGGALEGSALANGRALSGSPVPVPGWNPNSSSGKSGGNAGSYIPSYTSW	240			
Sbjct 181	SKFKKLMKQGGALEGSALANGRALSGSPVPVPGWNPNSSSGKSGGNAGSYIPSYTSW	240			
Query 241	YPSAHQEAMQQPQLM	255			
Sbjct 241	YPSAHQEAMQQPQLM	255			

>NP\_835221.2 homeobox protein DLX-1 isoform 1 [Homo sapiens]  
MTMTTMPESLNSPVSGKAVFMEFGPPNQMSPPMSHGHYSMHCLHSAGHSQPDGAYSSASSFSRPLGYP  
YVNSVSSHASSPYISSVQSYPGSASLAQSRLEDPGADSEKSTVVEGGEVRFNGKGKKIRKPRTIYSSLQL  
QALNRRFQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKKLMKQGGAALEGSALANGRALSAGSP  
PVPPGWNPNSSSGKSGGNAGSYIPSYTSWYPSAHQEAMQQPQLM

>XP\_009442039.1 homeobox protein DLX-1 [Pan troglodytes]  
MTMTTMPESLNSPVSGKAVFMEFGPPNQMSPPMSHGHYSMHCLHSAGHSQPDGAYSSASSFSRPLGYP  
YVNSVSSHASSPYISSVQSYPGSASLAQSRLEDPGADSEKSTVVEGGEVRFNGKGKKIRKPRTIYSSLQL  
QALNRRFQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKKLMKQGGAALEGSALANGRALSAGSP  
PVPPGWNPNSSSGKSGGNAGSYIPSYTSWYPSAHQEAMQQPQLM

Of, met handige namen:

>MensDistalless  
MTMTTMPESLNSPVSGKAVFMEFGPPNQMSPPMSHGHYSMHCLHSAGHSQPDGAYSSASSFSRPLGYP  
YVNSVSSHASSPYISSVQSYPGSASLAQSRLEDPGADSEKSTVVEGGEVRFNGKGKKIRKPRTIYSSLQL  
QALNRRFQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKKLMKQGGAALEGSALANGRALSAGSP  
PVPPGWNPNSSSGKSGGNAGSYIPSYTSWYPSAHQEAMQQPQLM

>ChimpanseeDistalless  
MTMTTMPESLNSPVSGKAVFMEFGPPNQMSPPMSHGHYSMHCLHSAGHSQPDGAYSSASSFSRPLGYP  
YVNSVSSHASSPYISSVQSYPGSASLAQSRLEDPGADSEKSTVVEGGEVRFNGKGKKIRKPRTIYSSLQL  
QALNRRFQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKKLMKQGGAALEGSALANGRALSAGSP  
PVPPGWNPNSSSGKSGGNAGSYIPSYTSWYPSAHQEAMQQPQLM



Gewervelden (bijvoorbeeld):

Koe: *Bos taurus*

Kip: *Gallus gallus*

Kikker: *Xenopus laevis*

Zebravis: *Danio rerio*

>Mens

MTMTTMPESLNSPVSGKAVFMEFGPPNQQMSPSPMSHGHYSMHCLHSAGHSQPDGAYSSASSFSRPLGYPYVNSVSSHASSPYISSVQSYPGSASLAQSRLEDP  
GADSEKSTVVEGGEVRFNGKGKKIRKPRTIYSSLQLQALNRRFQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKKLMKQGGAALEGSALANGRALSAG  
SPPVPPGWNPNSSSGKGSGGNAGSYIPSYTSWYPSAHQEAMQQPQLM

>Chimpansee

MTMTTMPESLNSPVSGKAVFMEFGPPNQQMSPSPMSHGHYSMHCLHSAGHSQPDGAYSSASSFSRPLGYPYVNSVSSHASSPYISSVQSYPGSASLAQSRLEDP  
GADSEKSTVVEGGEVRFNGKGKKIRKPRTIYSSLQLQALNRRFQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKKLMKQGGAALEGSALANGRALSAG  
SPPVPPGWNPNSSSGKGSGGNAGSYIPSYTSWYPSAHQEAMQQPQLM

>Koe

MTMTTMPESLNSPVSGKAVFMEFGPPNQQMSPSPMSHGHYSMHCLHSAGHSQPDGAYSSASSFSRPLGYPYVNSVSSHASSPYISSVQSYPGSASLTQSRLEDP  
GADSEKSTVVEGGEVRFNGKGKKIRKPRTIYSSLQLQALNRRFQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKKLMKQGGAALEGSALANGRALSAG  
SPPVPPGWNPNSSSGKGSGGSAGSYIPSYTSWYPSAHQEALQQPQLM

>Kip

MTMTTMPESLNSPVSGKAVFMEFGPPGQQMSPSPMSHGHYSMHCLHSAGHSQPD SAYSTASSFSRPLGYPYVNSVSSHSGNPYISSVQPYPNSSGLAQPRLEET  
GAESEKSTVVEGGEVRFNGKGKKIRKPRTIYSSLQLQALNRRFQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKKLMKQGGAALESGALSNGRALSAG  
SPPVPAVWNTSSASGKASSGSAGTYIPSYTSWYPSAHQEAMQQPQLM

>Kikker

MMTMTTMADGLEAQDSSKSAFMEFGQQQSHSQSSPVMAAGHYPSLHCLHSGSHHHPQH QHDTNYSGSNSYSRSLAAYPYMSHSQHSPYLQSCNSNTTTQSRAE  
EPDQQKTTVIENGEIRFNGKGKKIRKPRTIYSSLQLQALNRRFQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKYKKLIKQGNPLEIDQLAGTVALSPR  
SPAIPPVWDVSASKGVSMAPNSYMPGYSHWYSSPHQDTMQRSQMM

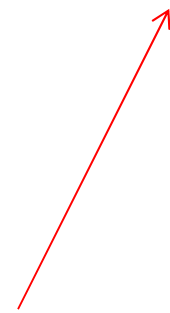
>Zebravis

MTMSTIPESLNSPVSGKSVFMEFGPPSQQMSPSSMTHGHYSMHCLHSSGHPQHDSAYSPAPSFPRSLPYPYVNSVSGSHSSPYLSTVQTYPNNSALAQTRLEDP  
APESEKNTVVEGGEVRFNGKGKKIRKPRTIYSSLQLQALNRRFQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKKLMKQGGGTIDTNALANGRGLSTG  
SPSVAPVWNTTATVKTSTPTSYIPSYTSWYPTAHQDTMQQPQLM

*Zeester Pisaster ochraceus*

Annelide *Platynereis dumerillii*

Oester *Pinctada fucata*



echinoderms

hemichordates

tunicates

vertebrates

flatworms

annelids

mollusks

arthropods

nematodes



Lophotrochozoa

Ecdysozoa

Deuterostomia

Protostomia

- ☐ [Pitx \[Clytia hemisphaerica\]](#)
- ☐ [dachous protocadherin \[Clytia hemisphaerica\]](#)

## Alignments

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Dll1 distalless homeodomain protein [Clytia hemisphaerica]

Sequence ID: [ACM62726.1](#) Length: 352 Number of Matches: 1

Range 1: 191 to 264 [GenPept](#) [Graphics](#)

Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
110 bits(276)	1e-31	Compositional matrix adjust.	51/74(69%)	63/74(85%)	1/74(1%)
Query 122	NGKGKKI-RKPRTIYSSLQLQALNRRFQQTQYLALPERAELAASLGLTQTQVKIWFQNKR 180				
	NGKG K+ RKPRTI++S QL+ LNR F++T YL+LPERAELA +LGLTQTQ+KIWFQNKR				
Sbjct 191	NGKGGKLPRKPRTIFTSSQQLRELNRAFERTHYLSLPERAELAHALGLTQTQIKIWFQNKR 250				
Query 181	SKFKKLMKQGGAAL 194				
	SKFKK++K G +				
Sbjct 251	SKFKKIIKANGGQM 264				

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Dll2 distalless homeodomain protein, partial [Clytia hemisphaerica]

Sequence ID: [ACM62727.1](#) Length: 195 Number of Matches: 1

Range 1: 2 to 51 [GenPept](#) [Graphics](#)

Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
91.7 bits(226)	1e-25	Compositional matrix adjust.	40/50(80%)	44/50(88%)	0/50(0%)
Query 143	LNRRFQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKKLMKQGGA 192				
	LNRRF +TQYLALPERAELAA L LTQTQ+KIWFQNKRSK KK++K GG				
Sbjct 2	LNRRFSRTQYLALPERAELAAELNLTQTQIKIWFQNKRSKLKKIVKSGGV 51				

# De uiteindelijke fasta-file:

>Mens

MTMTTMPESLNSPVSGKAVFMEFGPPNQQMSPSPMSHGHYSMHCLHSAGHSQPDGAYSSASSFSRPLGYPYVNSVSSHASSPYISSVQSYPGSASLAQSRLEDPGADSEKSTVVEGGEVRFNGKGKKIRKPRTIYSSLQL  
QALNRRFQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKKLMKQGGAALEGSALANGRALSGSPVPVPGWNPNSSSGKSGGNAGSYIPSYTSWYPSAHQEAMQQPQLM

>Chimpansee

MTMTTMPESLNSPVSGKAVFMEFGPPNQQMSPSPMSHGHYSMHCLHSAGHSQPDGAYSSASSFSRPLGYPYVNSVSSHASSPYISSVQSYPGSASLAQSRLEDPGADSEKSTVVEGGEVRFNGKGKKIRKPRTIYSSLQL  
QALNRRFQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKKLMKQGGAALEGSALANGRALSGSPVPVPGWNPNSSSGKSGGNAGSYIPSYTSWYPSAHQEAMQQPQLM

>Koe

MTMTTMPESLNSPVSGKAVFMEFGPPNQQMSPSPMSHGHYSMHCLHSAGHSQPDGAYSSASSFSRPLGYPYVNSVSSHASSPYISSVQSYPGSASLTQSRLEDPGADSEKSTVVEGGEVRFNGKGKKIRKPRTIYSSLQL  
QALNRRFQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKKLMKQGGAALEGSALANGRALSGSPVPVPGWNPNSSSGKSGGSAGSYIPSYTSWYPSAHQEALQQPQLM

>Kip

MTMTTMPESLNSPVSGKAVFMEFGPPNQQMSPSPMSHGHYSMHCLHSAGHSQPD SAYSTASSFSRPLGYPYVNSVSSHSGNPYISSVQPYPNSSGLAQPRL EETGAESEKSTVVEGGEVRFNGKGKKIRKPRTIYSSLQL  
QALNRRFQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKKLMKQGGAALESGALSNGRALSGGSPVPVAVWNTSSASGKASSGSAGTYIPSYTSWYPSAHQEAMQQPQLM

>Kikker

MMTMTTMADGLEAQDSSKSAFMEFGQQQSHSQSSPVMAAGHYPSLHCLHSGSHHHPQHQHDTNYSGSNSYSRSLAAYPYMSHSQHSPYLQSCNSNTTTSRAEEPDQQKTTVIENGEIRFNGKGKKIRKPRTIYSSLQL  
QALNHRFQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKYKKLIKQGNPLEIDQLAGTVALSPRSPAIPPVWDVSAASKGVSMAPNSYMPGYSHWYSSPHQDTMQRSQMM

>Zebravis

MTMTTIPESLNSPVSGKSVFMEFGPPSQQMSPSSMTHGHYSMHCLHSSGHPQHDSAYSPAPSFPRSLPYPYVNSVSGSHSSPYLSTVQTYPNNSALAQTRLEDPAPESEKNTVVEGGEVRFNGKGKKIRKPRTIYSSLQL  
QALNRRFQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKKLMKQGGGTIDTNALANGRGLSTGSPSVAPVWNTTATVKTSTPTSYIPSYTSWYPTAHQDTMQQPQLM

>Zeester

GKKLRKPRTIYSSLQLQKLNHRFTKTQYLALPERADLAASLGLTQTQVKIWFQNRRSKYKKILKHGSTPTSSSTGSQDPEQDPPQSHTPASQQGSLSPAPPPTSAPHPQGTPTMSGPSSTGLGSACYSSQQHVPSHHHHH  
HHPHHQMPTDGSSTHSSPVPPWDYVGDIPTPAVRSSSGTVDNNPYPFHQQHYQH HHYPWFVGGQDGTSGMSAQQHMLASAPSVDKTILQLAKECDFLELKNAFHTNA

>Annelide

MTLEKGYSMNLNMGSGEGLGPDQDVSKSAFMEIQQQQMNASMPNPIARGGYPGNAGQMEGFPGQQTRGHIGYPFSMTPMGSHGTYNPTS YHHFSAPGYQTSAPSVTPPTSRESMYDLPNYSSYDKLENKYIYRKGLFED  
SPPNSDEKPSMDELRVNGKGKKMRKPRTIYSSLQLQQLNKRFORQTQYLALPERAELAASLGLTQTQVKIWFQNRRSKYKKLMKQNP GIGGPGGAQNGPPMDQGGMSPPPTHPTSTGQAPTSPQGAQGPPXPNGQPNGP  
HHGHAGAHGAGHGANPATPSMMGGPPPNMSMPPVSWGAAADFQLKSEINCSSNSTNSTPTPTHNTYMSQYPWYSQNPLAAQQHSLLT

>Oester

MLNVGSVEGMEQEMAGKSAFMELQQSGGMPMGHPAYPMRSSYQPPHHGGQHGESVFSNPQGRGPLAGYPFHMNASPTAYNPSSGHHFSMPYPYQSPSPTRDDKSQMDELRINGKGKKMRKPRTIYSSLQLQQLNRRFQRT  
QYLALPERAELAASLGLTQTQVKIWFQNRRSKAKKIMKQGGTPPGPNQPPPTVTSPPANQMQPPSSPVQHSPTSNTHAHTPHQQLP PNGLKMEAPEQQHNLMVSPSSSASPEPENHWN DHMSGMTSSHHAHASQPYM  
SMPSMPSSSMMPSGMPMSYYHSAWYSQPMVNQQSCLT

>Fruitvlieg

MDAPDAPHTPKYMDGGNTAASVTPGINIPGKSAFVELQQHAAAGYGGIRSTYQHFGPQGGQDSGFSPRSALGYFPFPMHQNSYSGYHLGSYAPPCASPPKDDFSISDKCEDSGLRVNGKGKKMRKPRTIYSSLQLQQLN  
RRFQRTQYLALPERAELAASLGLTQTQVKIWFQNRRSKYKKMMKAAQGP GTNSGMPLGGGGPNPGQHSPNQMHSGGNNGGGSNSGSPSHYLP PGHSPTPSSTPVSELSPEFPPTGLSPPTQAPWDQKPHWIDHKPPQM T  
PQPPHPAATLHPQTHHHNPPPMQGGYVPQYWYQPETNPSLTVWPAV

>Kwal

MIEMKMSPHQQAVLSQQVPMSSFLPPSKAPEAYRPLNYTPTSFVTNFKEMSQQIDSNNNNNNNNNPHSESEGKFSPRPATQFSPMGDLRSH PSTQDTHPFKTFDDSKSFLNNNTPNGSMPEQDSISSSLQSFHSSGLPTS  
YTSSYNNNSMQTTLSPPSSITSNMSRSFSSSSYVKQESDEEDEGDLTQSKNGKGKGLPRKPRTIFTSQQLERLNRAFER THYLSLPERAELAHALGLTQTQIKIWFQNKRSKFKKIIKANGQMPPPSLVS GGNPGLWP  
SGYGKSFSGGPPMHLSPFSPPPSSHSVPGDSWYYRMQSAGGYGSHETMFYPYGGTSGTDVTRTTRPNFSYHM

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# Clustal Omega

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Tools > Multiple Sequence Alignment > Clustal Omega

## Multiple Sequence Alignment

Clustal Omega is a new multiple sequence alignment program that uses seeded guide trees and HMM profile-profile techniques to generate **or more** sequences. For the alignment of two sequences please instead use our [pairwise sequence alignment tools](#).

**Important note:** This tool can align up to 4000 sequences or a maximum file size of 4 MB.

### STEP 1 - Enter your input sequences

Enter or paste a set of

PROTEIN

sequences in any supported format:

```
>Mens
MTMTTMPESLNSPVSGKAVFMEFGPPNQMQSPSPMSHGHYSMHCLHSAGHSQPDGAYSSASSFSRPLGYP
YVNSVSSHASSPYISSVQSYPGSASLAQSRLEDPGADSEKSTVVEGGEVRFNGKGKKIRKPRTIYSSLQL
QALNRRFQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKKLMKQGGALEGSALANGRALSAGSP
PVPPGWNPNSSSGKSGGNAGSYIPSYTSWYPSAHQEAMQQPQLM
```

>Chimpansee

MTMTTMPESLNSPVSGKAVFMEFGPPNQMQSPSPMSHGHYSMHCLHSAGHSQPDGAYSSASSFSRPLGYP

Or, upload a file:

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Use a example sequence | Clear





Oester	--MGHPAYPMRSSYQ-----PPHH---GGQHG-----ESVFSNPQ-GRG---PLAGY	68
Kwal	PEQDSISSSLQSFHSSGLPTSSTSYNNNSMQTTLSPPSSITSN-----MS-----	165
Zeester	-----	0
Fruitvlieg	PFPPMHQNSYSGYHLG-----SYAP-----PC	96
Kikker	PYMSH-----SQH-SPYLQ-----SC	93
Zebravis	PYVNSVGS-----HSS-SPYLS-----TV	87
Kip	PYVNSVSS-----HSG-NPYIS-----SV	87
Mens	PYVNSVSS-----HAS-SPYIS-----SV	87
Chimpansee	PYVNSVSS-----HAS-SPYIS-----SV	87
Koe	PYVNSVSS-----HAS-SPYIS-----SV	87
Annelide	PFSMTPMGSHGTYNPT-----SYHHFSAPGYQTSAPSVTPPTSRESMYDLPNYYSSY	124
Oester	PFHMNAMS-PTAYNPS-----SGHHFSMPPYQSP-----	96
Kwal	RSFSSSS-Y---V---KQESDEEDEGDLTQ-SKNGKGGKLPKRPRTIFTSQQQLRELNRA	216
Zeester	-----GKKLRKPRTIYSSLQLQQLNHR	22
Fruitvlieg	AS-----PPKDDFSISDKCEDSGLRVNGK-GKKMRKPRTIYSSLQLQQLNRR	142
Kikker	NS---NTTQSRAE--EPDQKTTVIENG EIRFNGK-GKKIRKPRTIYSSLQLQALNHR	146
Zebravis	QTYPNNSALAQTRLEDPAPESEKNTVVEGGEVRFNGK-GKKIRKPRTIYSSLQLQALNRR	146
Kip	QPYPNSSGLAQPRLEETGAESEKSTVVEGGEVRFNGK-GKKIRKPRTIYSSLQLQALNRR	146
Mens	QSYPGSASLAQSRLEDPGADSEKSTVVEGGEVRFNGK-GKKIRKPRTIYSSLQLQALNRR	146
Chimpansee	QSYPGSASLAQSRLEDPGADSEKSTVVEGGEVRFNGK-GKKIRKPRTIYSSLQLQALNRR	146
Koe	QSYPGSASLTQSRLEDPGADSEKSTVVEGGEVRFNGK-GKKIRKPRTIYSSLQLQALNRR	146
Annelide	DKLENKYIYRKGLFEDSPPNSD--EKPSMDEL RVNGK-GKKMRKPRTIYSSLQLQQLNKR	181
Oester	-----SPTRD--DKSQMDEL RINGK-GKKMRKPRTIYSSLQLQQLNRR	136
	** *****:;* **: **:	
Kwal	FERTHYLSLPERAELAHALGLTQTQIKIWFQNKRSKFKKIIKANGGQMPPPS---LVS	272
Zeester	FTKTQYLALPERADLAASLGLTQTQVKIWFQNNRSKYKKILKQHGSTPTSSTGSQDPE--	80
Fruitvlieg	FQRTQYLALPERAELAASLGLTQTQVKIWFQNNRSKYKKMMKAAQPGTNSGM---PLG	198
Kikker	FQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKYKKLIKQGNPLEIDQLAGTVALS	206
Zebravis	FQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKKLMKQGGGTIDTNALANGRGLS	206
Kip	FQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKKLMKQGGAALESGALSNGRALS	206
Mens	FQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKKLMKQGGAALEGSALANGRALS	206
Chimpansee	FQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKKLMKQGGAALEGSALANGRALS	206
Koe	FQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKKLMKQGGAALEGSALANGRALS	206
Annelide	FQRTQYLALPERAELAASLGLTQTQVKIWFQNNRSKYKKLMKQNP GIGPGGAQNGPPMD	241
Oester	FQRTQYLALPERAELAASLGLTQTQVKIWFQNNRSKAKKIMKQGGTTPPGPNQQ---PPT-	192
	* :*:**:*****:* :*:*****:*****:*** **:*	

Browser window showing the Clustal Omega web interface. The URL is <https://www.ebi.ac.uk/Tools/services/web/tool>. The page title is "Clustal Omega". Navigation links include "Input form", "Web services", "Help & Documentation", and "Bioinformatics Tools FAQ".

Tools > Multiple Sequence Alignment > Clustal Omega

## Results for job clustalo-l20190109-142418-0795-79569343-p1m

Navigation tabs: Alignments, Result Summary, Phylogenetic Tree, Submission Details. Action buttons: Download Alignment File, Show Colors, View result with Jalview, Send to Simple Phylogeny, Sen.

CLUSTAL O(1.2.4) multiple sequence alignment

Kwal	MIEMKMSPHQQAVLSQQVPMSSFLPPSKAPEAYRPLNYTPTSFVTNFKEMSQQIDSNNN	60
Zeester	-----	0
Fruitvlieg	-MDAPDAPHTPKYMDGGN----TA---ASVTPG-----INIPGKSAFVELQQHAAAG--	44
Kikker	-----MMTMTTMADGLEA-----QDSSKSAFMEFGQQQSHS--	31
Zebravis	-----MTMSTIPESLNS-----PVSGKSVFMEFGPPSOO---	29

# Clustal Omega

Input form | Web services | Help & Documentation | Bioinformatics Tools FAQ

Tools > Multiple Sequence Alignment > Clustal Omega

## Results for job clustalo-l20190109-142418-0795-79569343-p1m

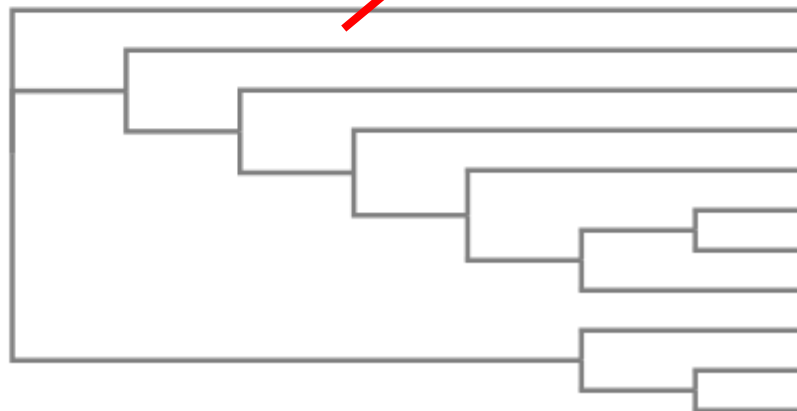
Alignments | Result Summary | **Phylogenetic Tree** | Submission Details

### Phylogenetic Tree

*This is a Neighbour-joining tree without distance corrections.*

Download Phylogenetic Tree Data

Branch length: ☒ Cladogram ☐ Real



Kwal 0.37164  
Zeester 0.22611  
Kikker 0.21523  
Zebravis 0.10773  
Kip 0.05561  
Mens 0  
Chimpansee 0  
Koe 0.00631  
Fruitvlieg 0.29532  
Annelide 0.26272  
Oester 0.25887

# Clustal Omega

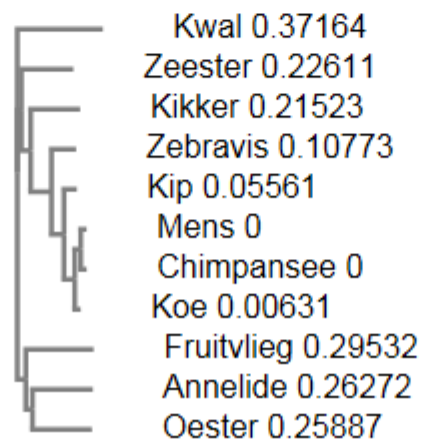
[Input form](#)[Web services](#)[Help & Documentation](#)[Bioinformatics Tools FAQ](#)[Tools](#) > [Multiple Sequence Alignment](#) > [Clustal Omega](#)

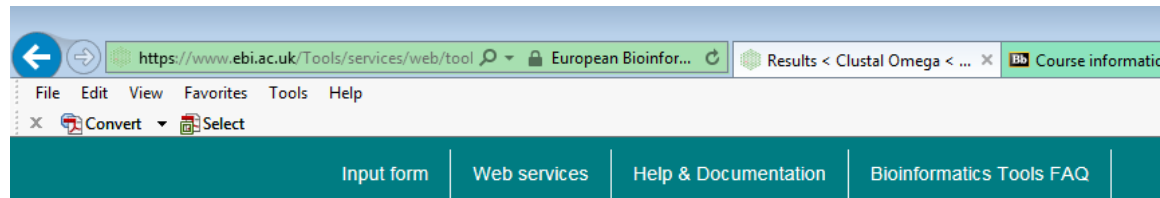
## Results for job clustalo-l20190109-142418-0795-79569343-p1m

[Alignments](#)[Result Summary](#)[Phylogenetic Tree](#)[Submission Details](#)

## Phylogenetic Tree

*This is a Neighbour-joining tree without distance corrections.*

[Download Phylogenetic Tree Data](#)Branch length: ☐ Cladogram ☒ Real



Zebravis 0.10773  
 Kip 0.05561  
 Mens 0  
 Chimpansee 0  
 Koe 0.00631  
 Fruitvlieg 0.29532  
 Annelide 0.26272  
 Oester 0.25887

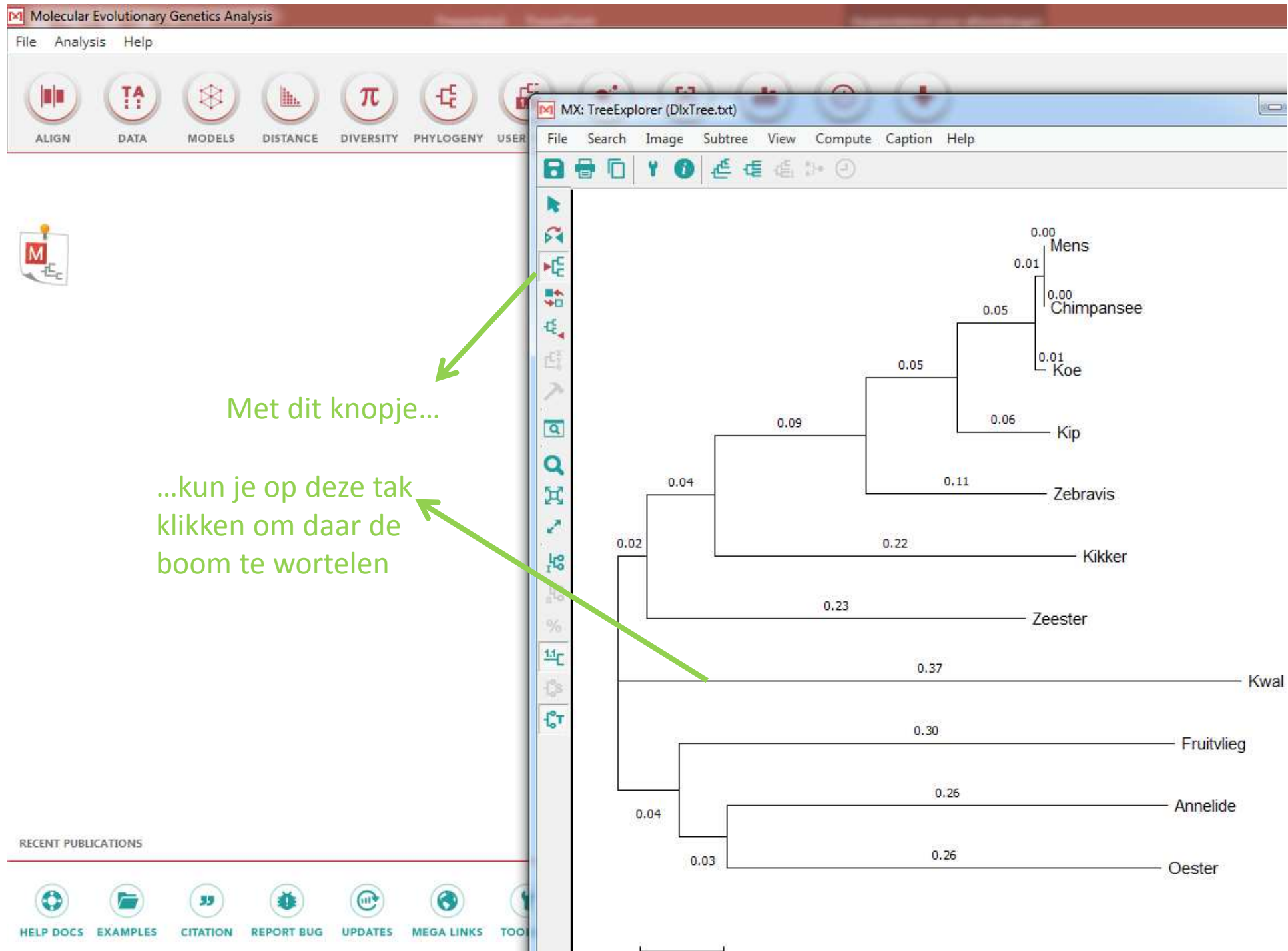
## Tree Data

```

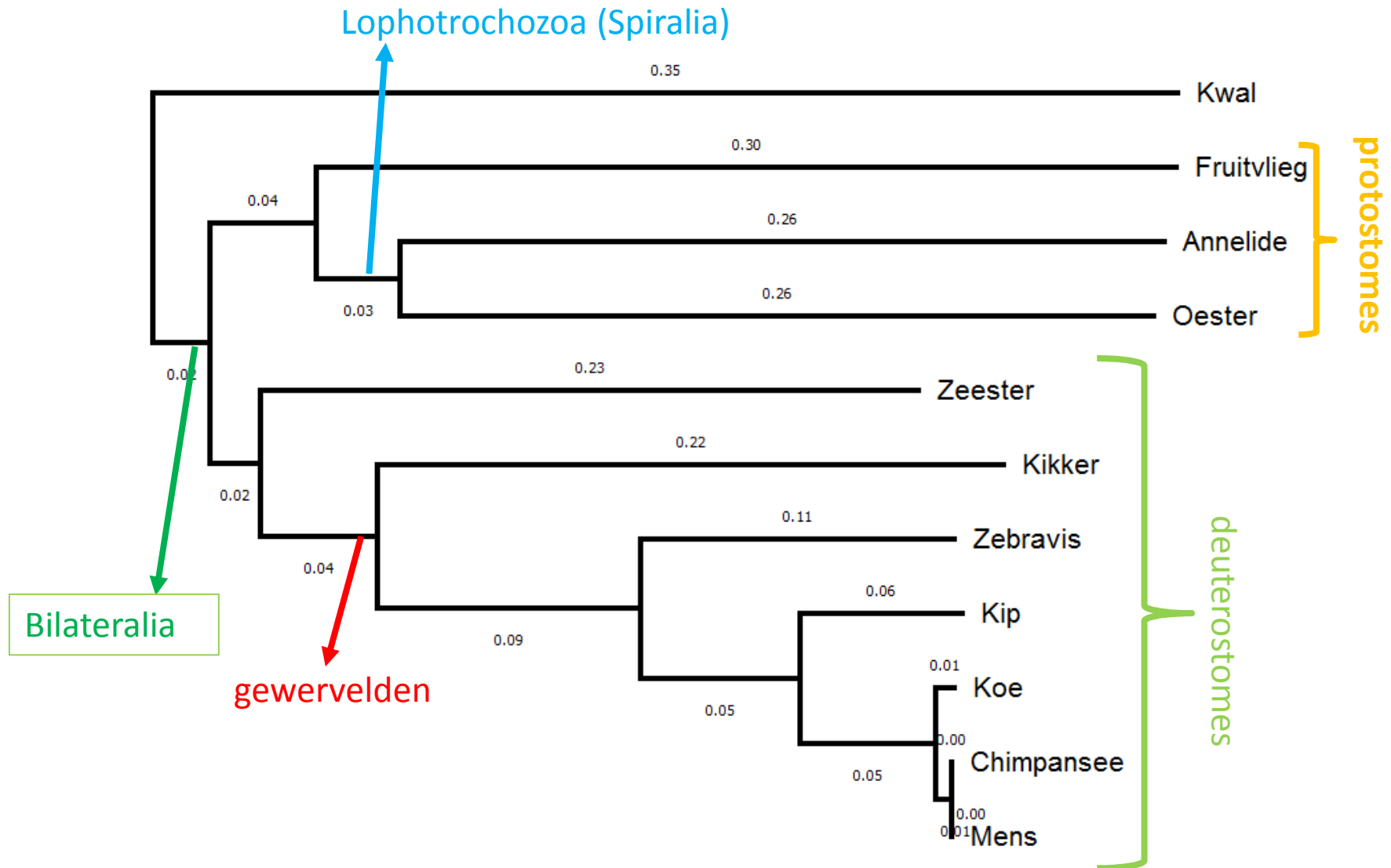
(
  Kwal:0.37164,
  (
    (
      Zeester:0.22611,
      (
        Kikker:0.21523,
        (
          Zebravis:0.10773,
          (
            Kip:0.05561,
            (
              (
                Mens:0.00000,
                Chimpansee:0.00000)
              :0.00545,
              Koe:0.00631)
            :0.04635)
          :0.05462)
        :0.09040)
      :0.04030)
    :0.01735,
    (
      Fruitvlieg:0.29532,
      (
        Annelide:0.26272,
        Oester:0.25887)
      :0.02869)
    :0.03671);
  
```



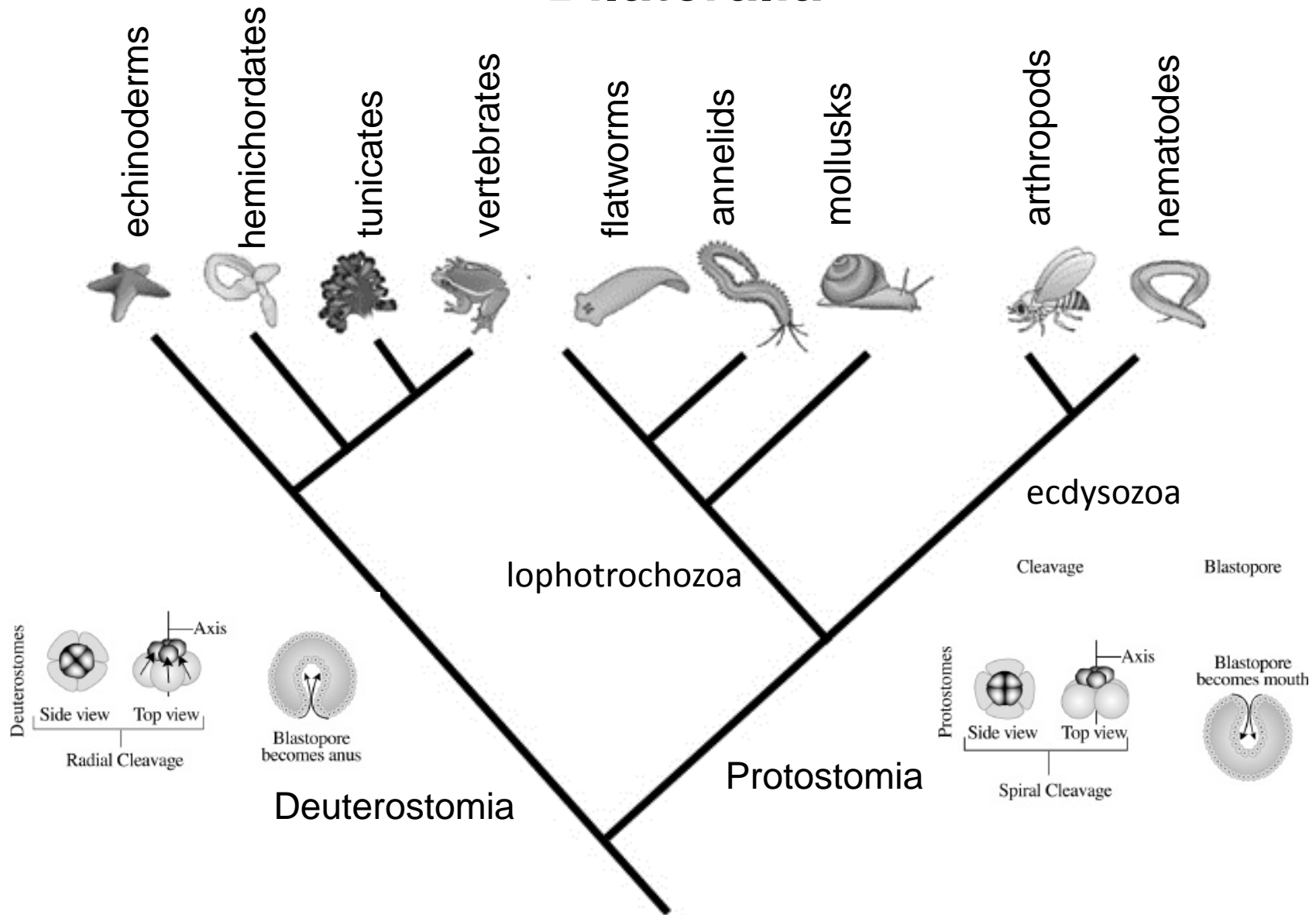




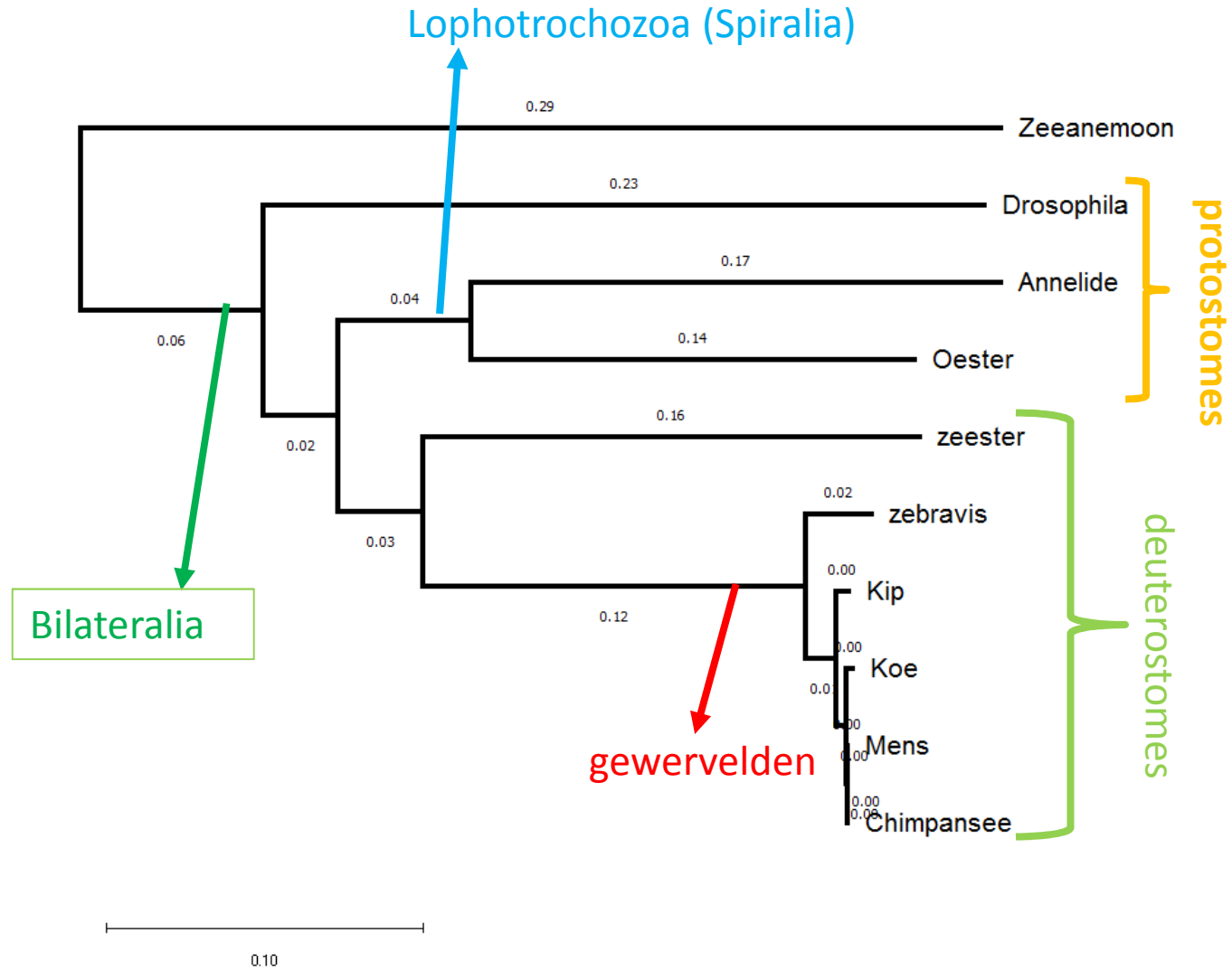
# Boom gebaseerd op Distalless:



# Bilateria



## Boom gebaseerd op Pax6:



# Waarom?

- Brengt leerlingen in contact met bioinformatica (databases, fasta-files, etc.)
- Laat zien hoe eiwitten in elkaar zitten (functionele domeinen)
- Doordringt leerlingen van de diepe verbondenheid van alle levende dieren die alleen maar door evolutie verklaard kan worden
- Laat een belangrijke fylogenetische methode zien (genetische afstand)
- Laat de taxonomische indeling van de dieren zien





# Evolution and development

1. Embryo's vertellen je iets over evolutie.
2. Evo-devo onthult diepe homologieën.
3. Evo-devo zoekt de genetische en ontwikkelingsbiologische basis van evolutionaire veranderingen.
4. Evo-devo bestudeert de oorsprong van *novelties*
5. Embryonale ontwikkeling kan de evolutie in bepaalde richtingen sturen.

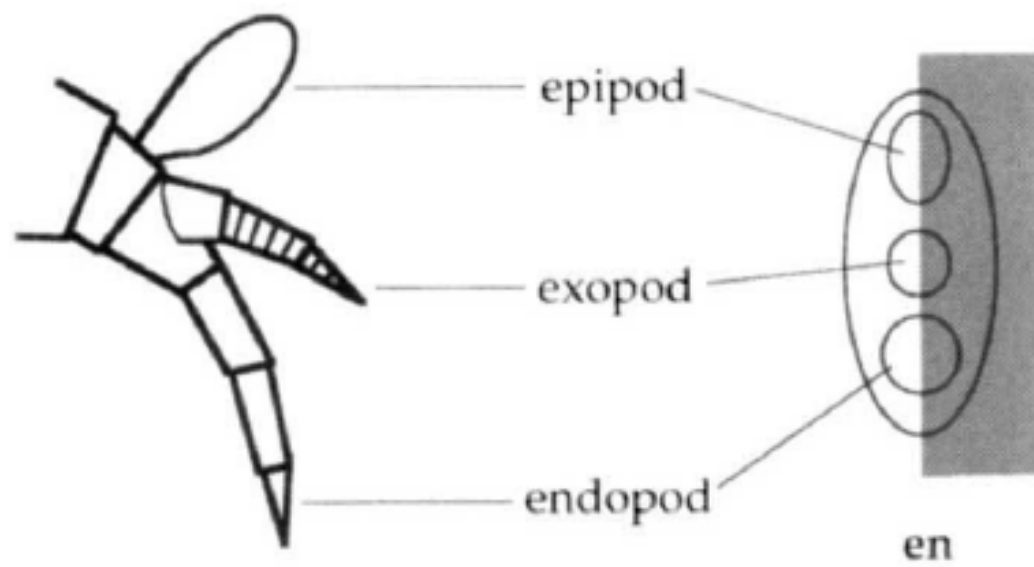
# Evolution and development

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5. Embryonale ontwikkeling kan de evolutie in bepaalde richtingen sturen.

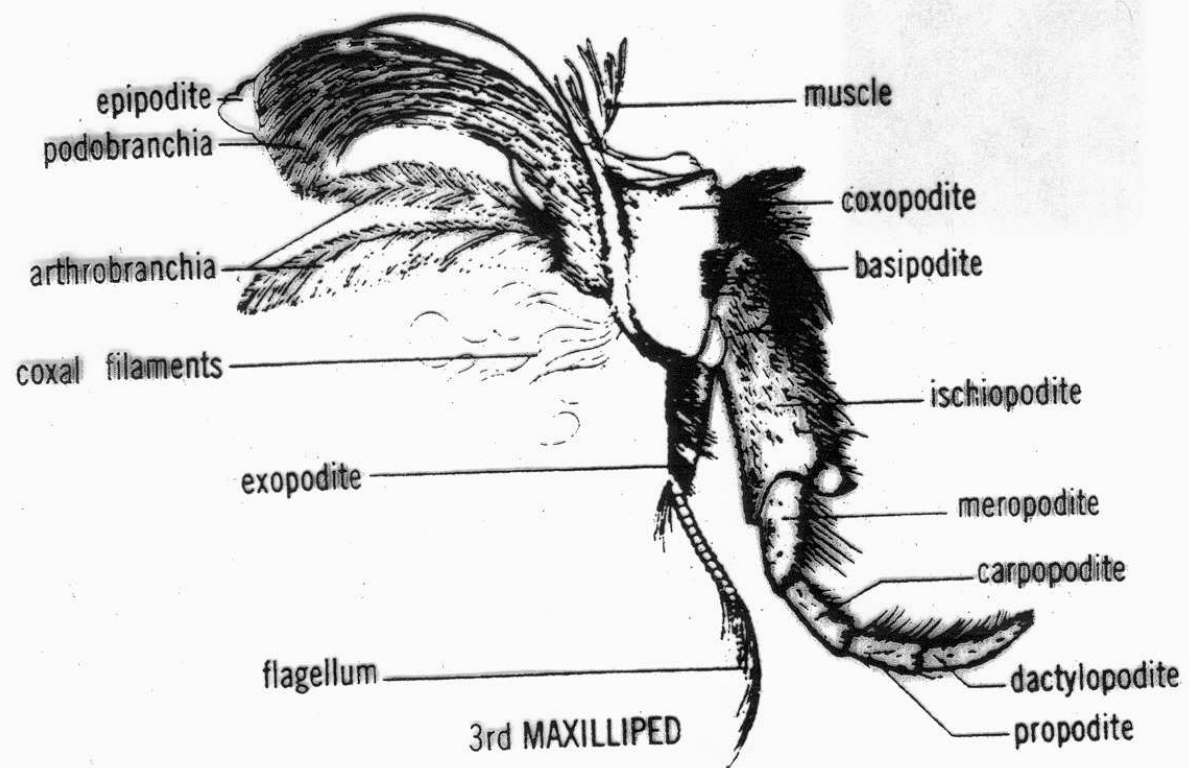
# The origin of insect wings



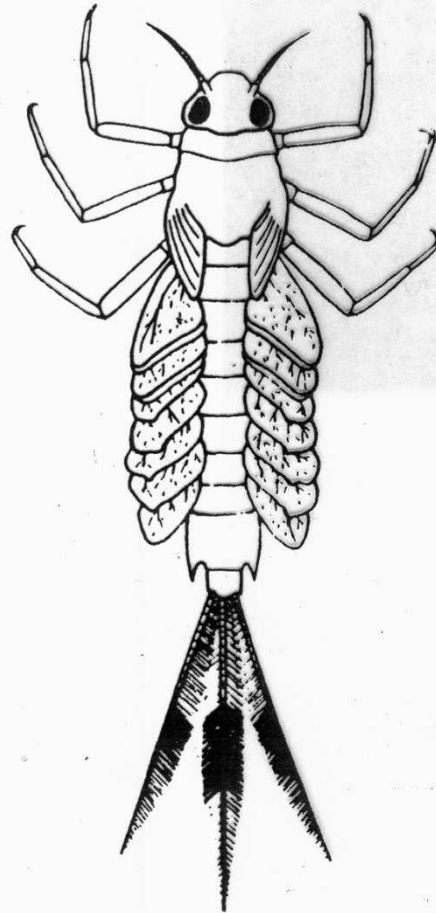
**b**





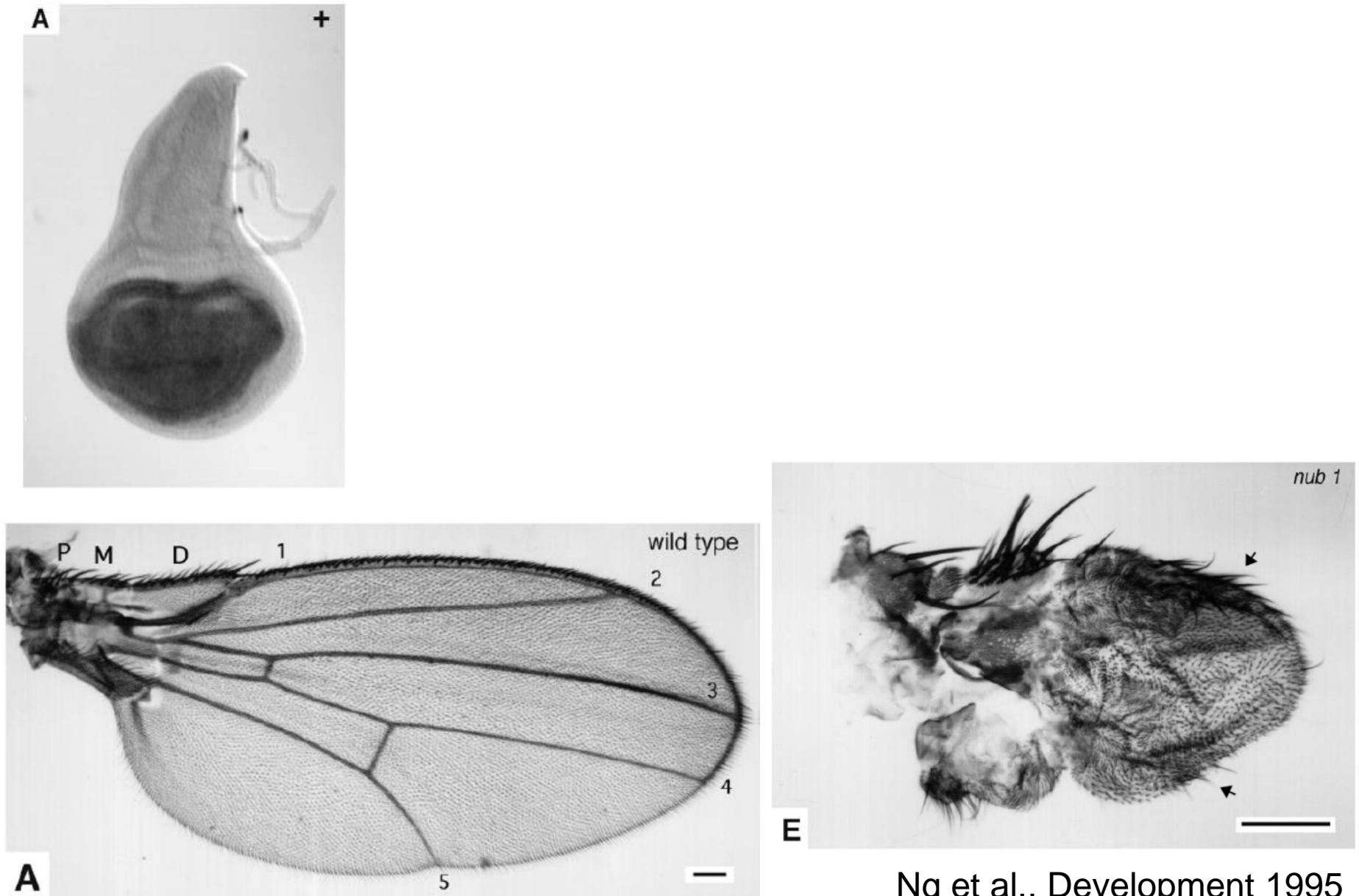


**Fig. 6** A crayfish leg



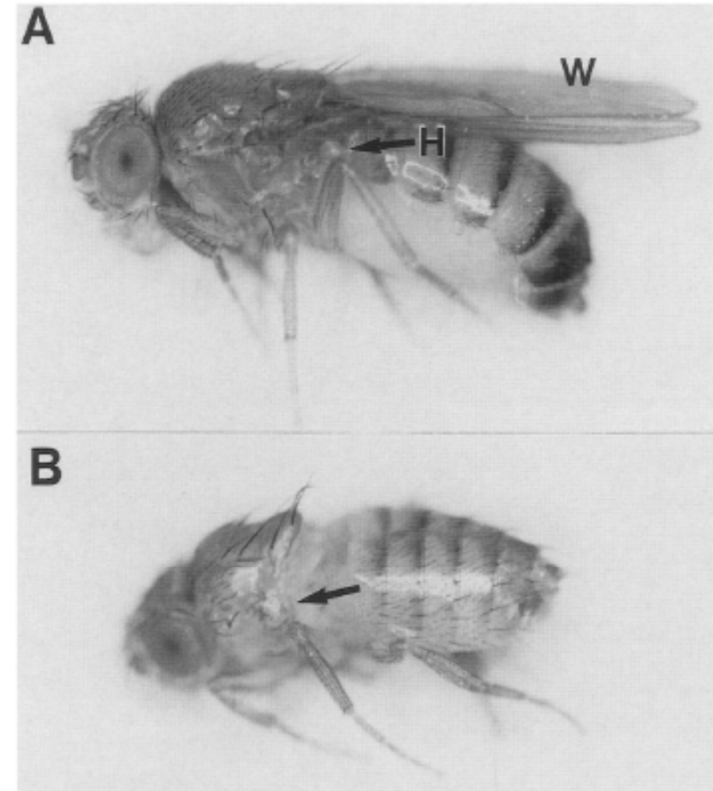
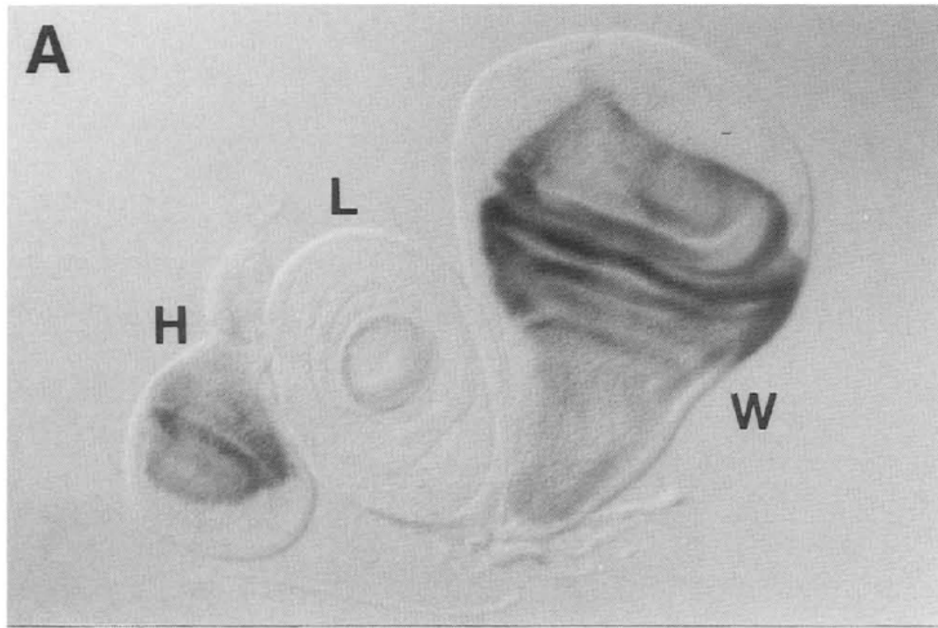
**Fig. 1** *Siphonurus* sp.

# Nubbin (pdm) is required for wing development

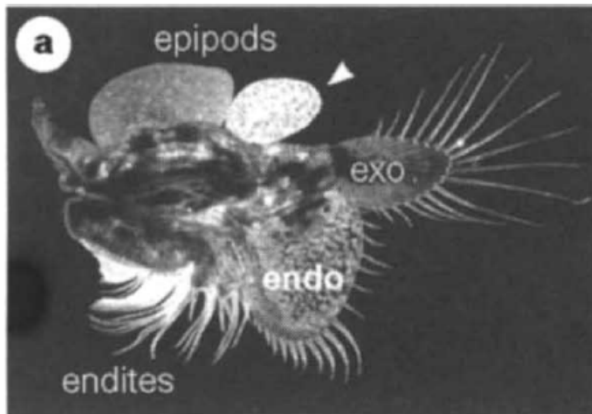


Ng et al., Development 1995

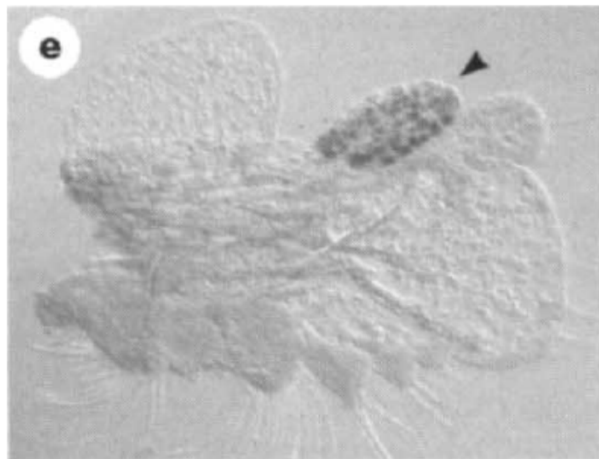
# Apterous is required for wing development



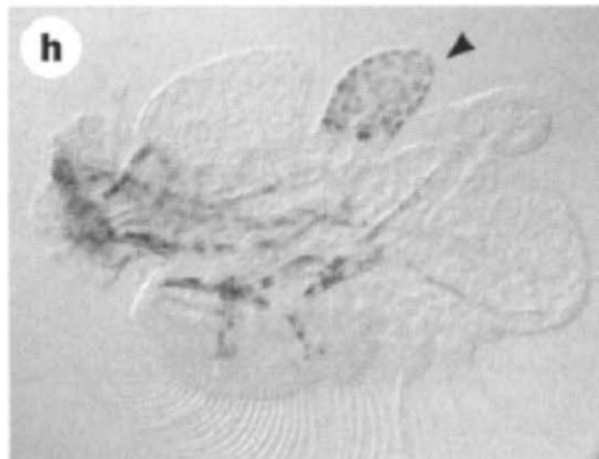
**Figure 2.** Morphological defects in *ap* mutants. (A) Side view of a wild-type fly, showing the normal appearance of the wing (W), haltere (H), and the pattern of bristles on the dorsal thorax. (B) Comparable view of an *ap* null mutant fly of genotype *ap*<sup>UG035</sup>/*ap*<sup>UG035</sup>. The wing is reduced to a small stump [arrow]. The haltere is similarly reduced (not visible in the picture). A number of large bristles (macrochaetae) are missing from the thorax near the wing, and this region appears reduced in size relative to the rest of the thorax. These flies are short lived and females are nonvitellogenic.



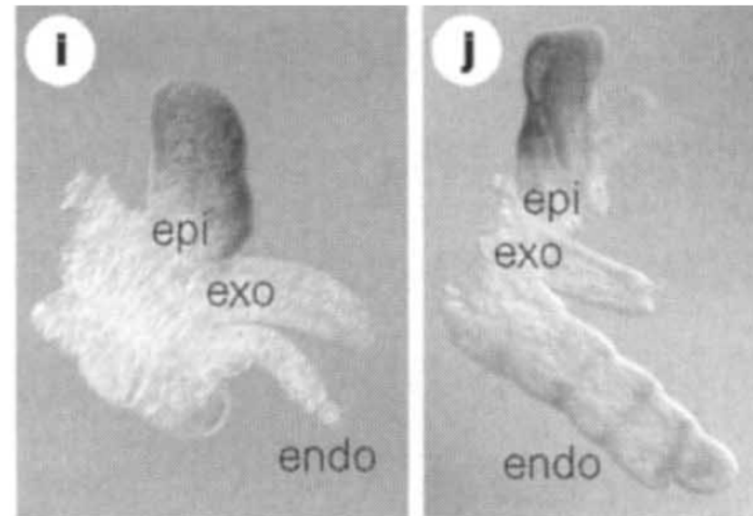
Nubbin and Apterous is expressed in the epipods in the shrimp *Artemia fransiscana*



Artemia  
pdm



Artemia  
ap

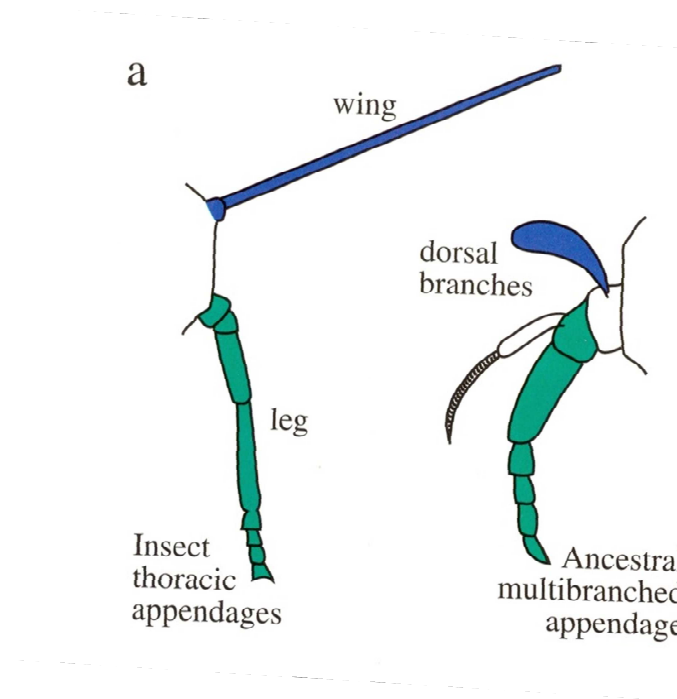


As well as in the crayfish  
*Pacifastacus leniusculus*

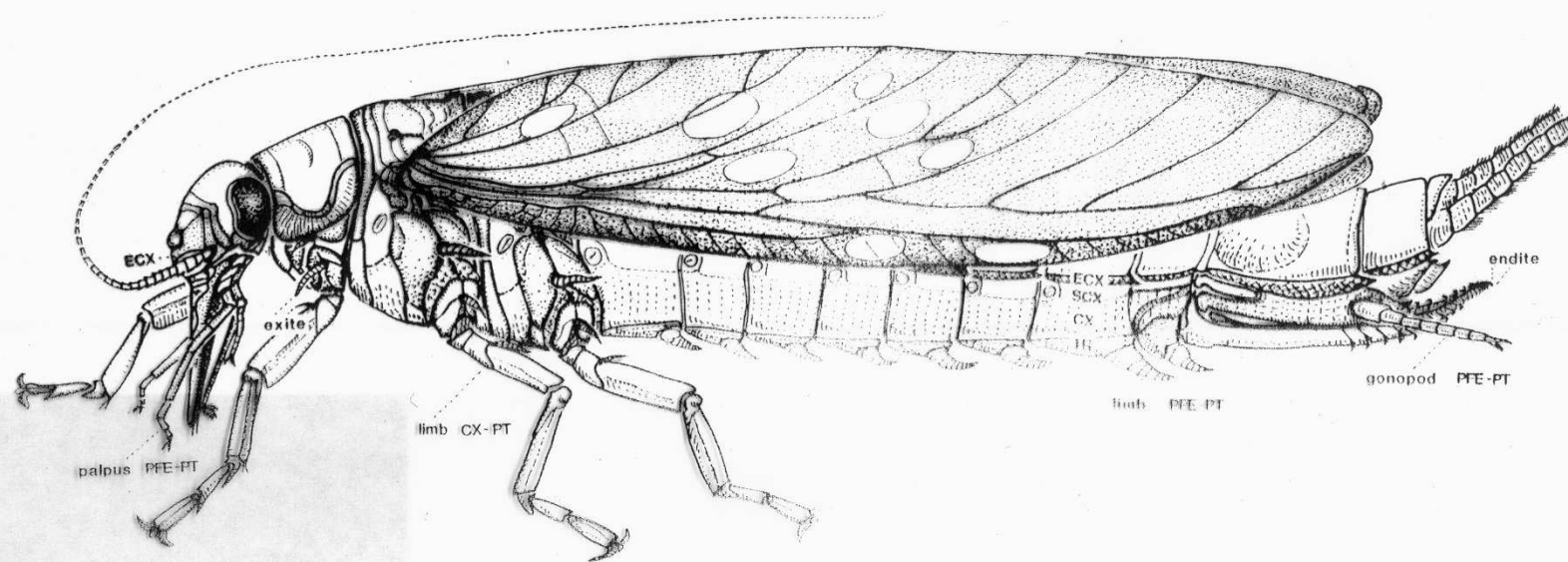
Averof & Cohen, Nature 1997



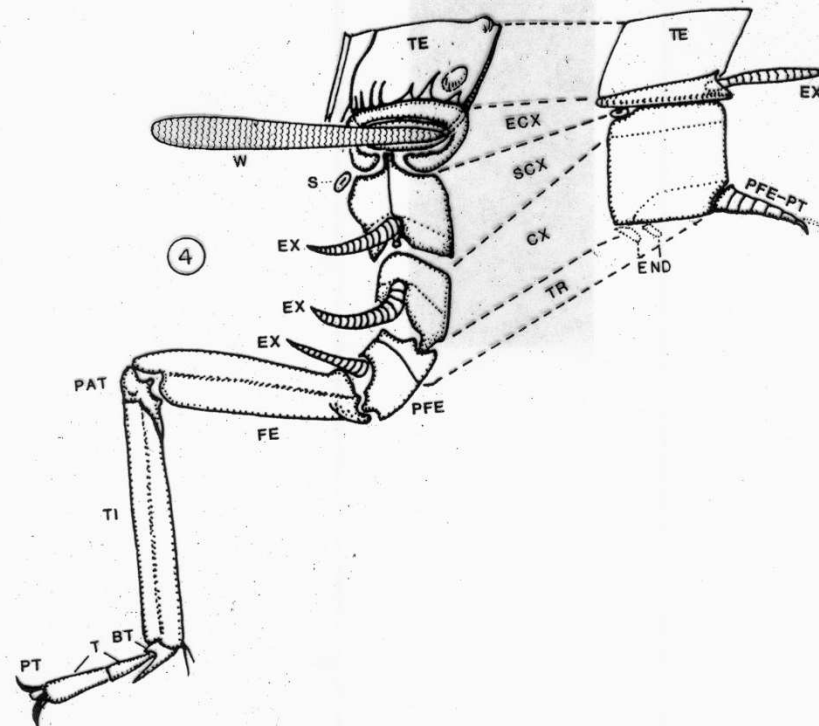
Wings evolved from epipodites...



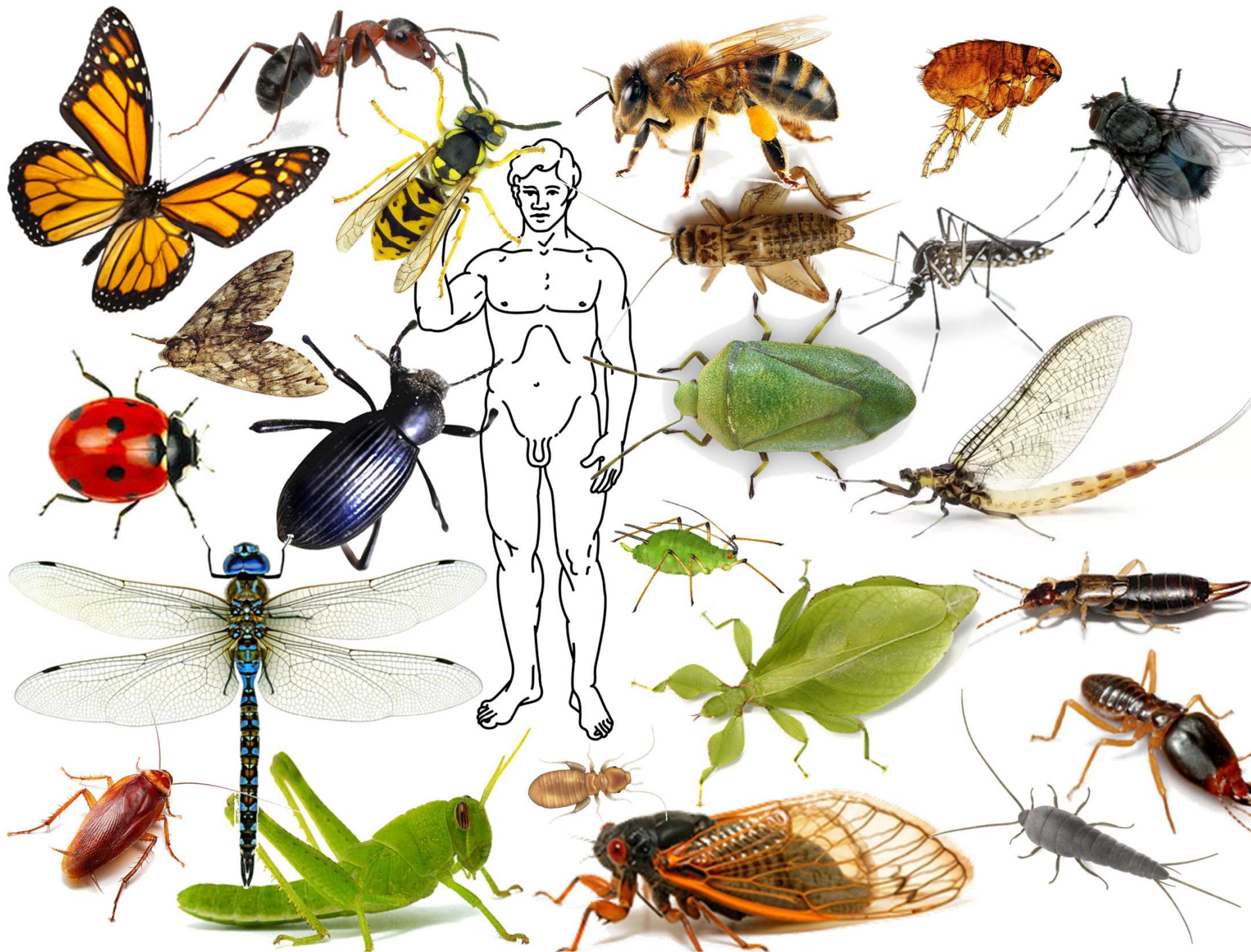
..that might have had a gill function



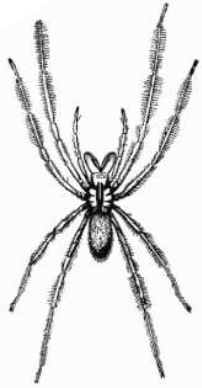
**Fig.4** Reconstruction of a Pterygote insect from fossils (Kuckalova-Peck, 1982)



**Fig. 5** Schematic drawing of the leg of the same insect (Kuckalova-Peck, 1982)



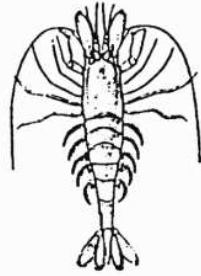
# Insecten hebben massaal de stap naar het land gemaakt



Chelicerata



Myriapoda



Crustacea



Entognatha  
Collembola + Diplura)



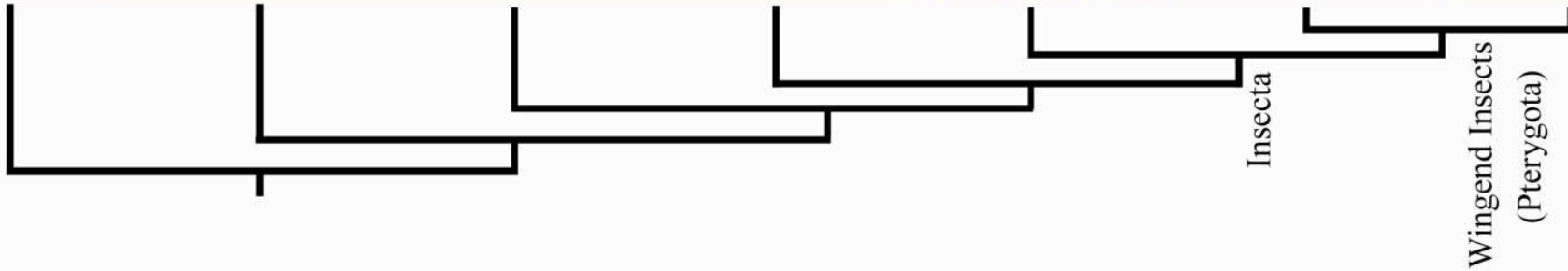
Apterygote insects  
(Archaeognatha +  
Zygentoma)



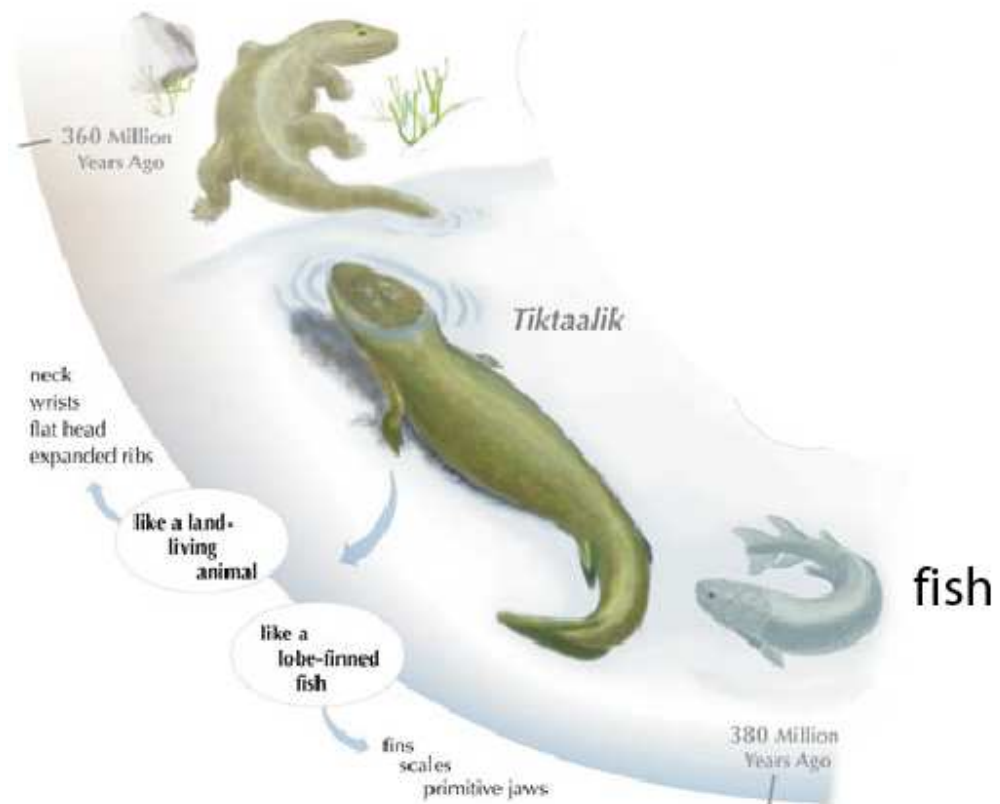
Most insects  
(Other Pterygota)



Higher Flies  
(Schizophora)







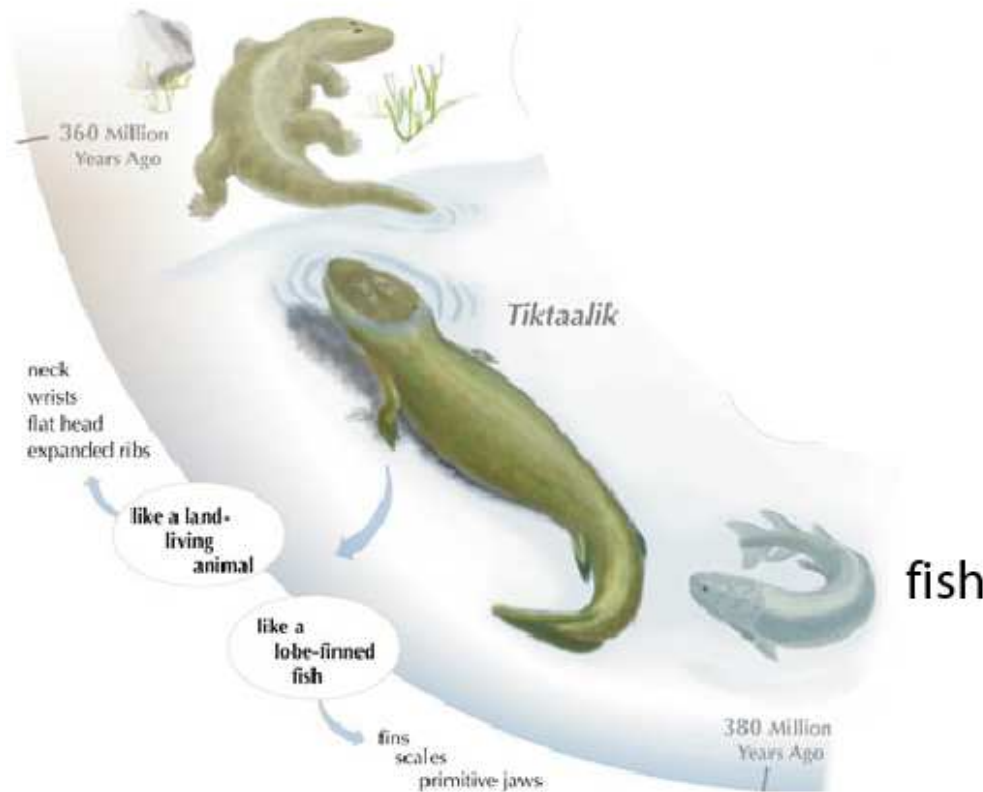


amphibians

birds

reptiles

mammals



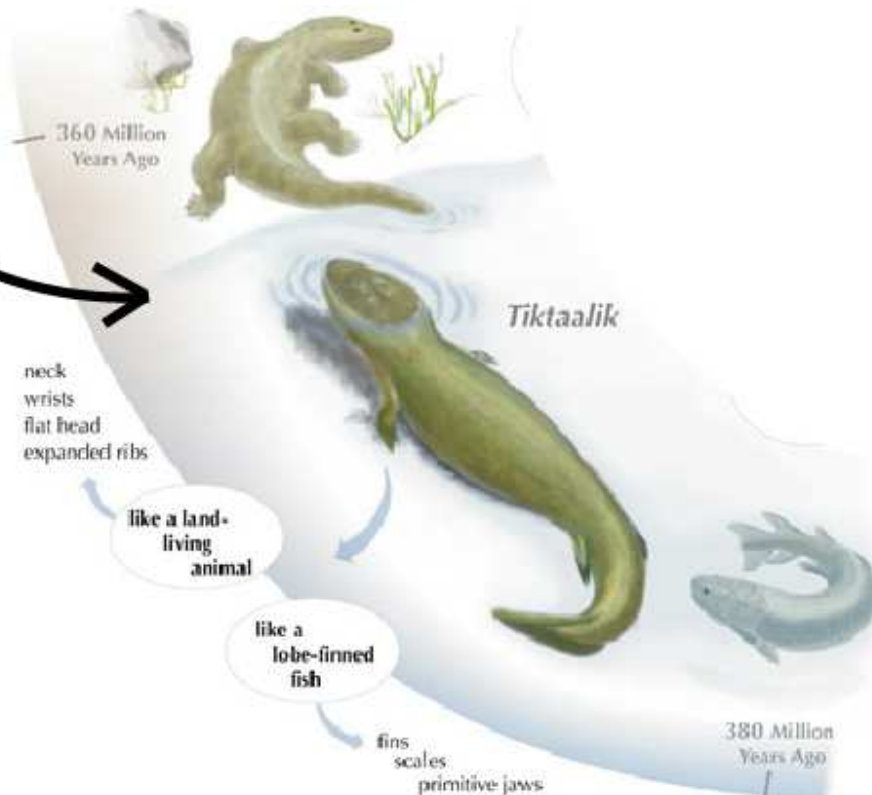
amphibians

birds

reptiles

mammals

reproductive



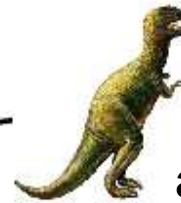
amphibians

birds

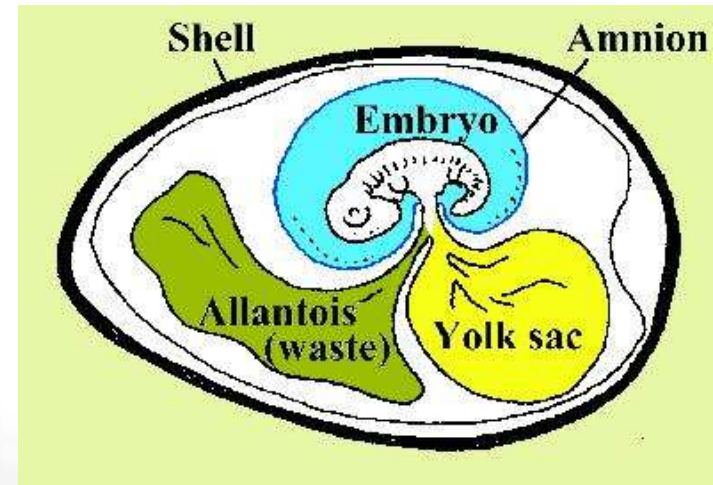
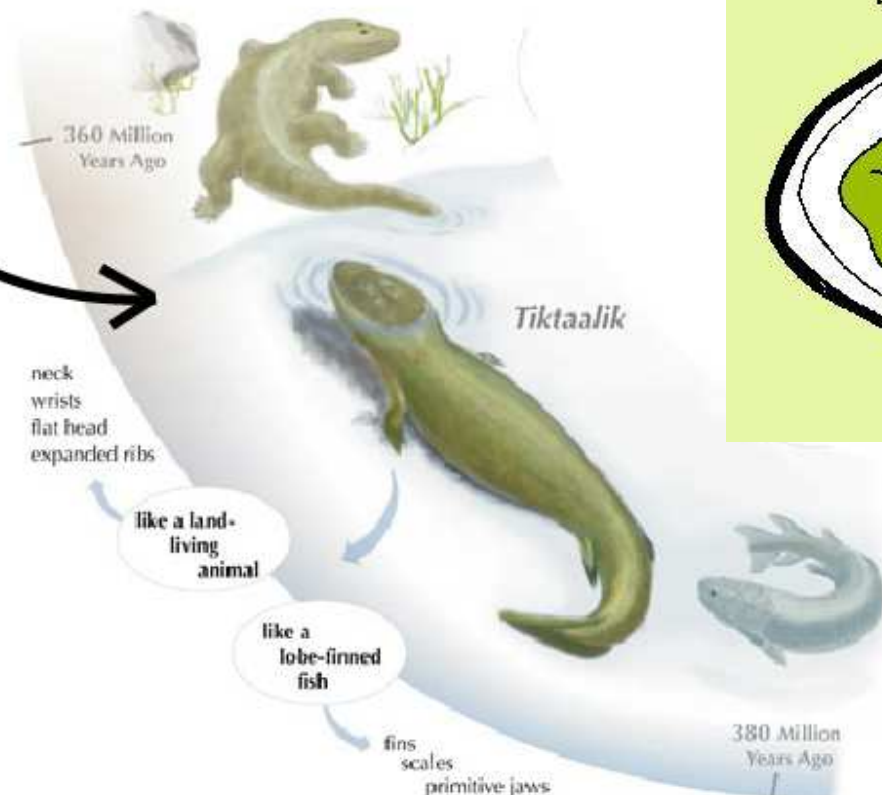
reptiles

mammals

reproduction



amniote ei

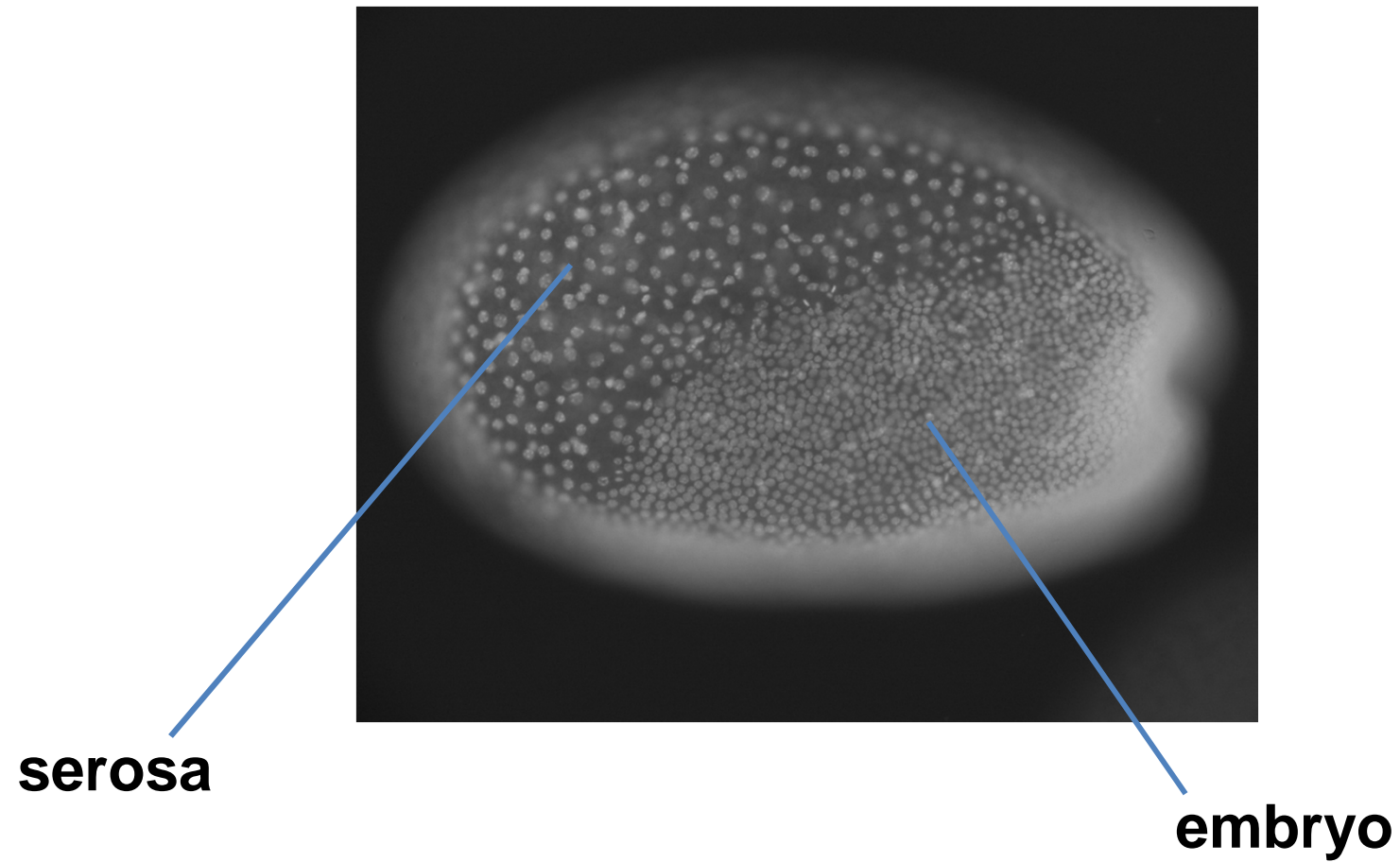




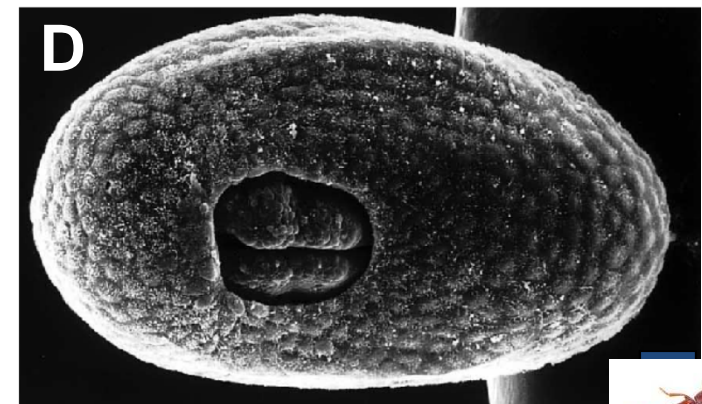
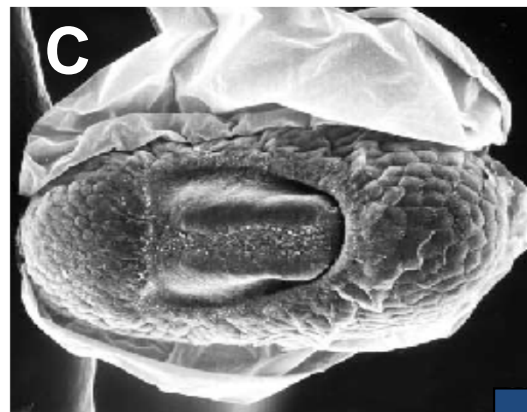
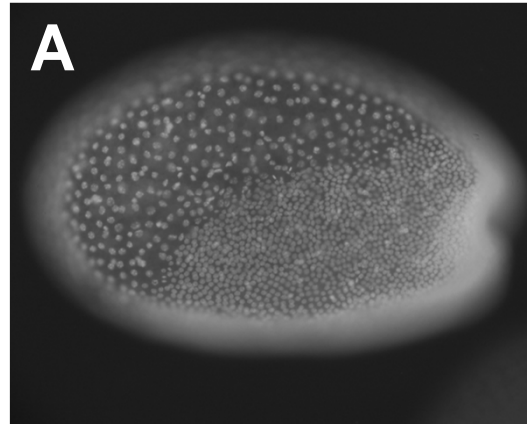
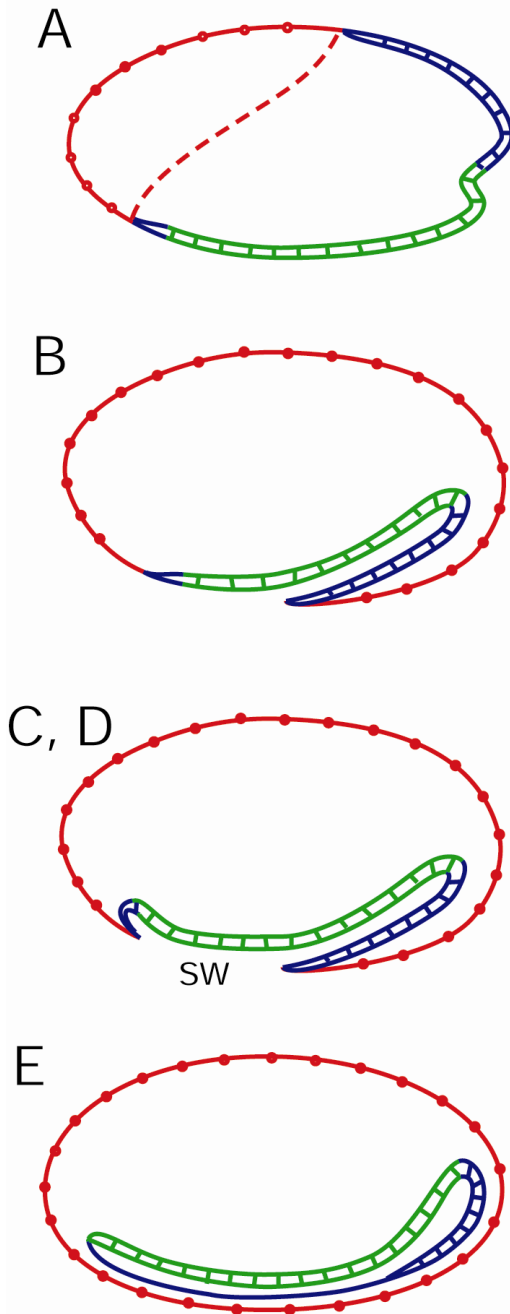
***Tribolium castaneum***



# The serosa



# Development of the serosa

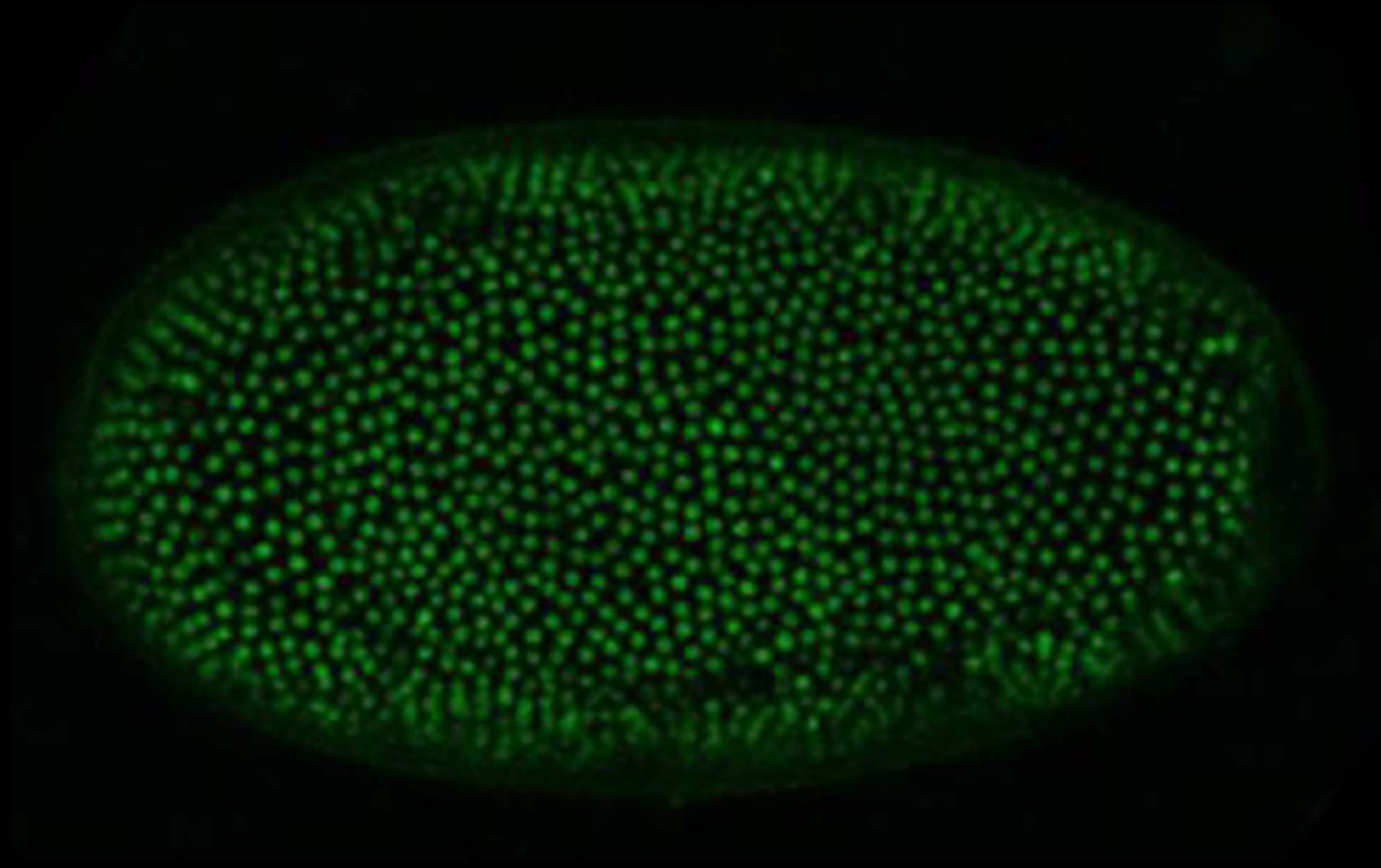


SEM: Handel et al., 2000



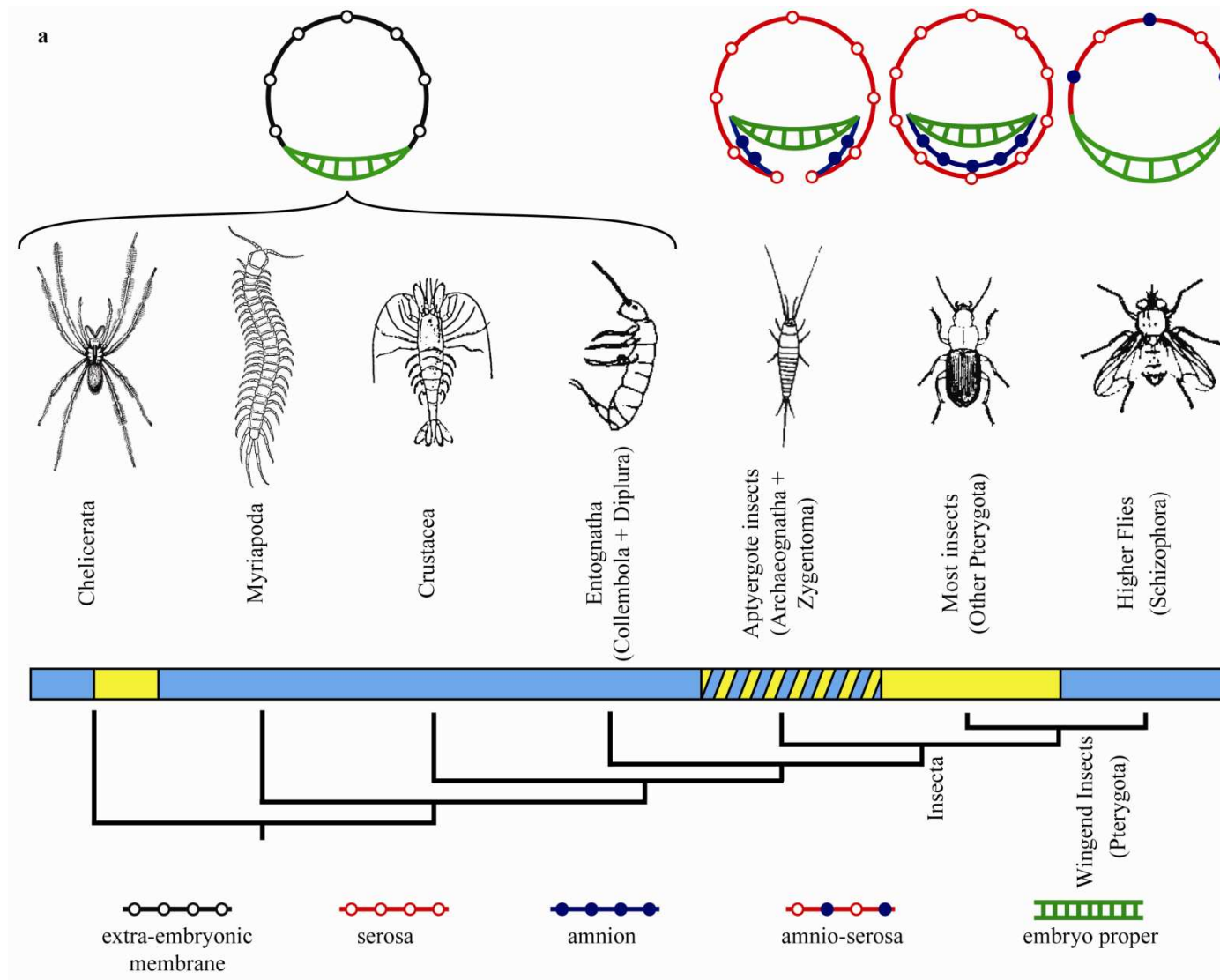


# Development of the serosa



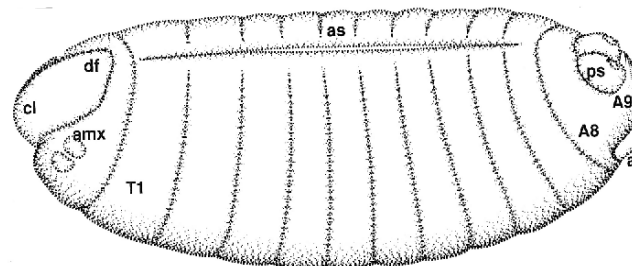
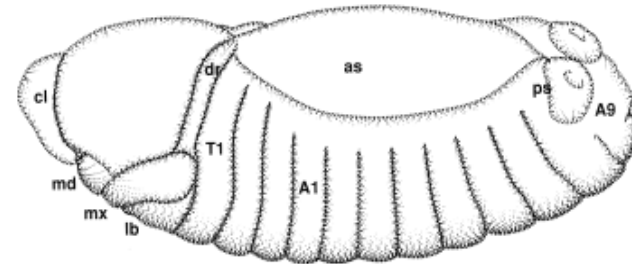
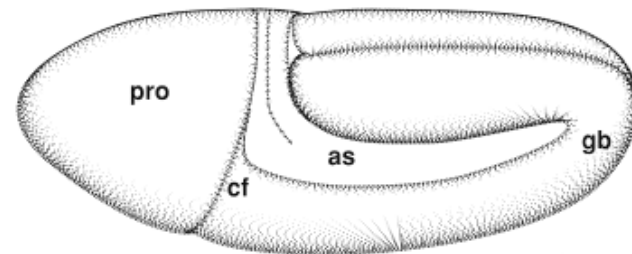
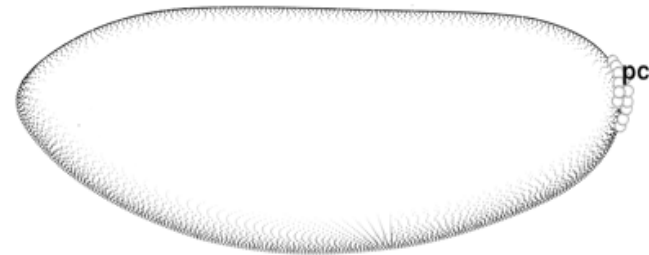
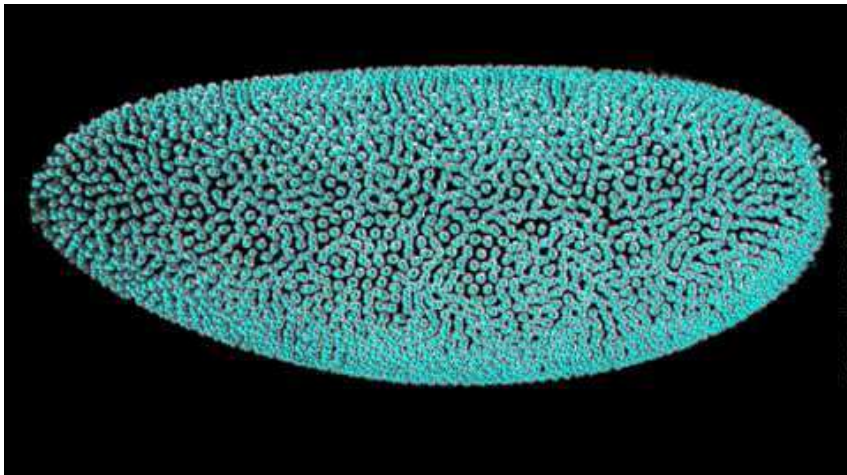
Tania Vazquez Faci

# The serosa is an evolutionary innovation of the insects



# *Drosophila* does not have a serosa

*Drosophila melanogaster*



Hartenstein, 1993

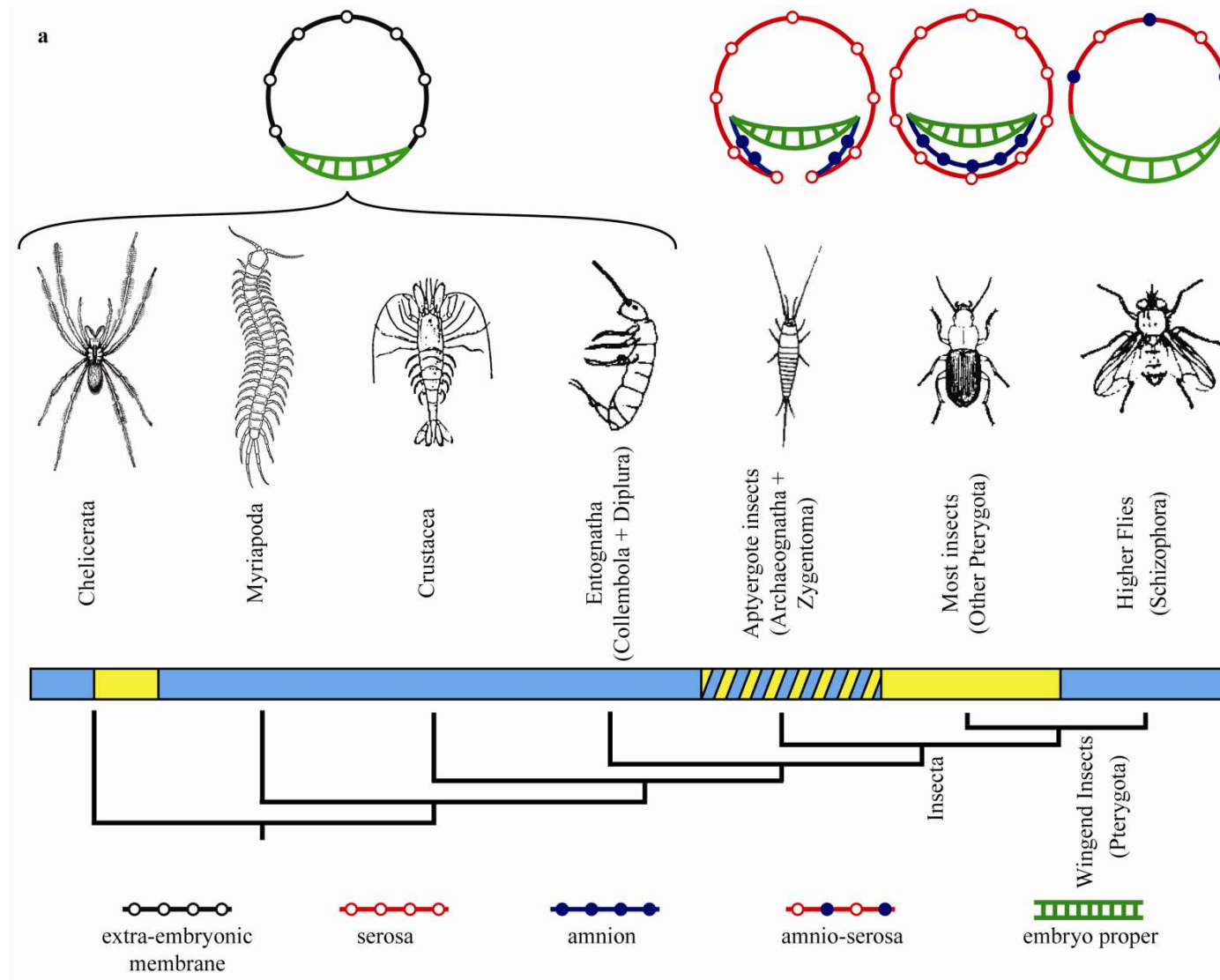
# *Drosophila* eggs are very sensitive to desiccation

Table 1. The incubation periods of eggs of *D. melanogaster* (MDE) at different temperatures and humidities

Temperature (°C)	Relative humidity (%)	Vapour pressure deficit (hP)	Mean duration (h)	SE	Mortality (%)	N
25	100	0.0	24.59	0.29	15.8	189
	95	1.6	26.30	0.22	14.0	200
	90	3.2	27.88	0.25	15.7	140
	85	4.8	31.58	0.20	23.2	168
	80	6.4	31.65	0.20	41.6	233
	75	8.0	—	—	100	150

N = Number of eggs hatching. SE = Standard Error. hP = Hecto Pascal.

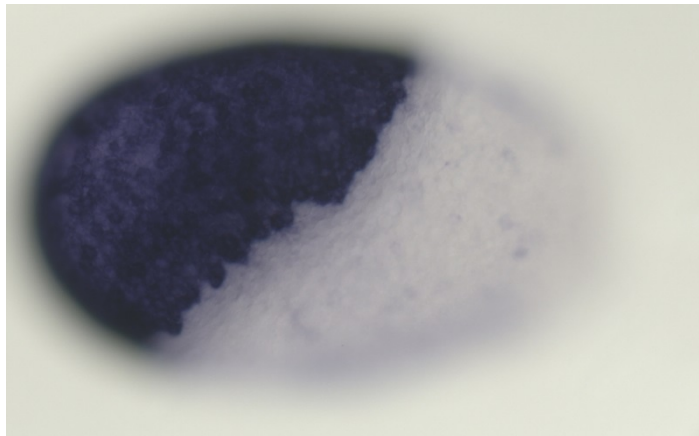
# The serosa is an evolutionary innovation of the insects





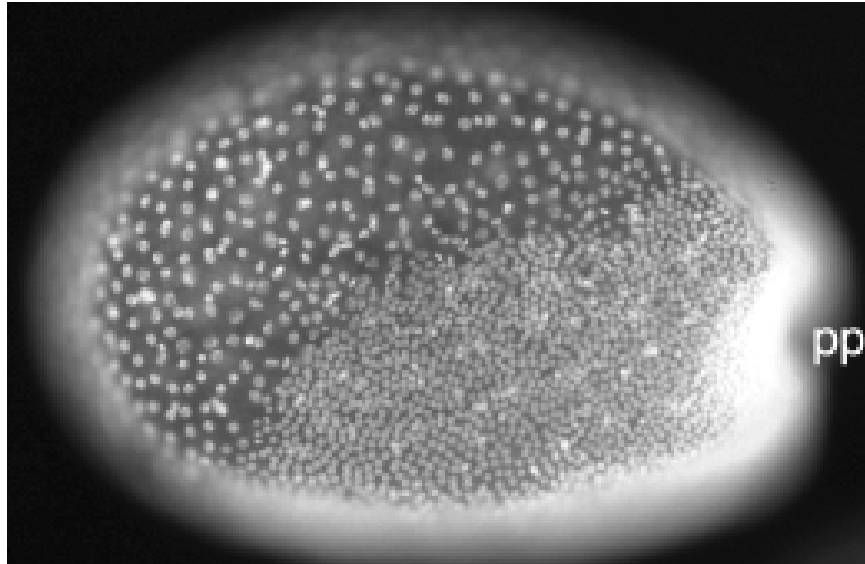
***zerknüllt (zen)* specificeert de serosa**

*Tribolium*

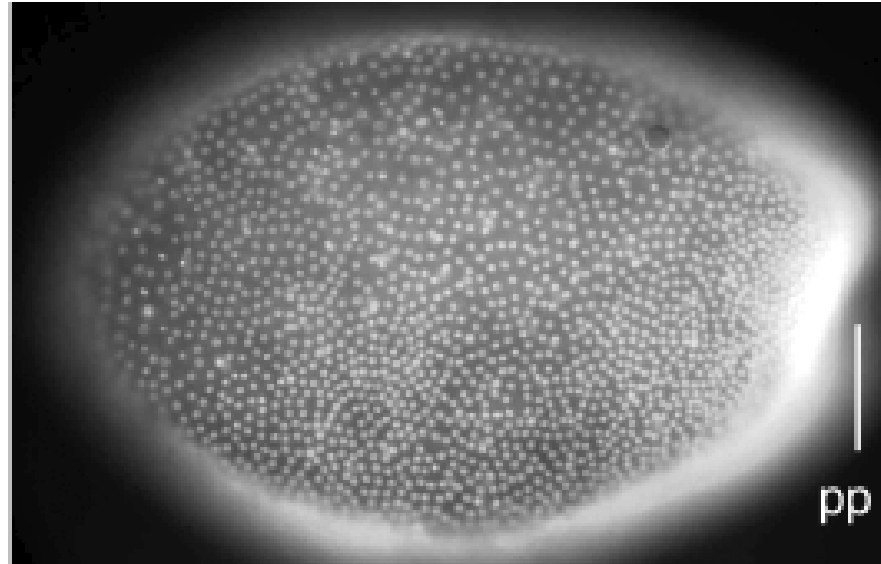


# ***Tc-zen* RNAi schakelt de serosa uit**

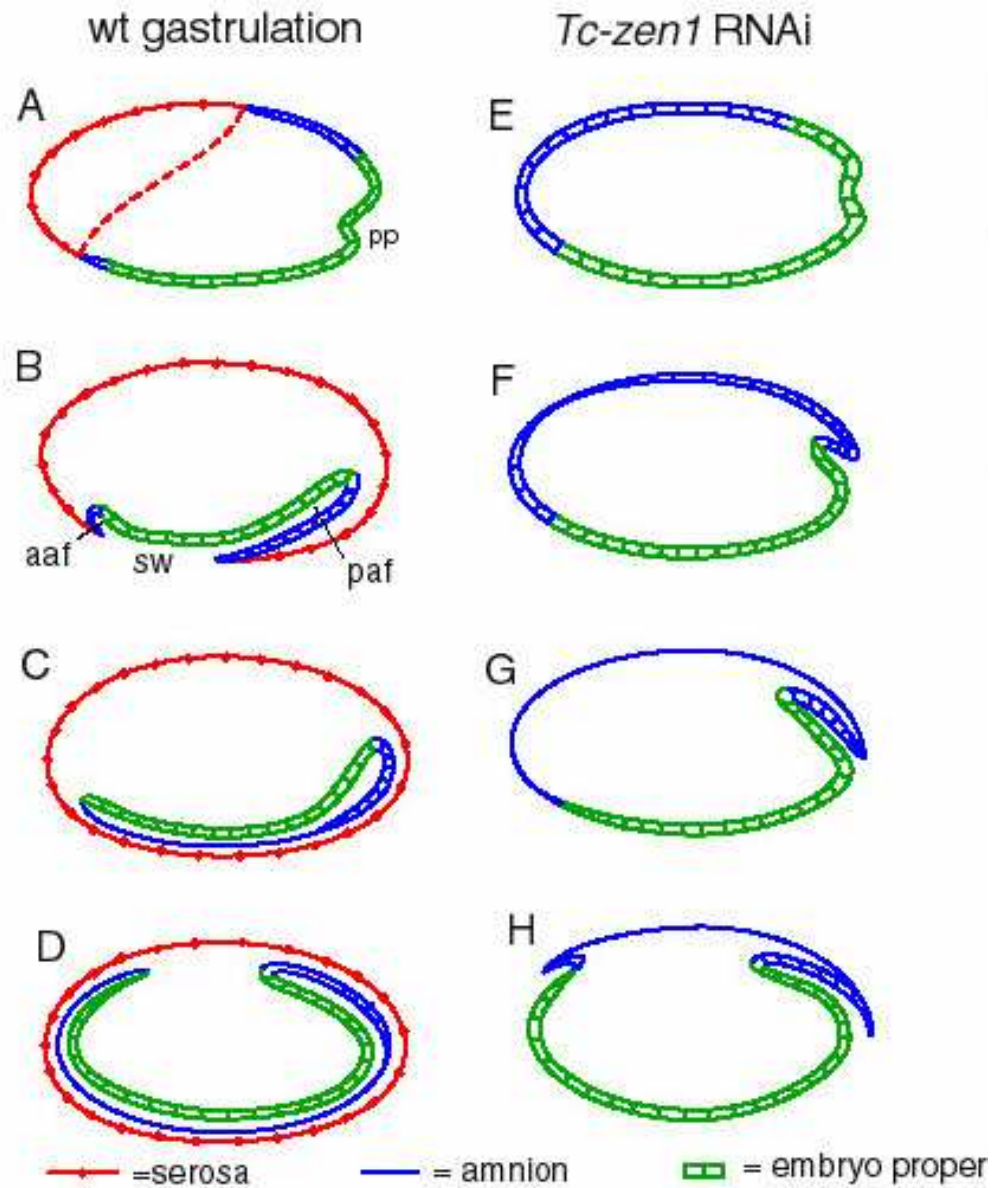
wild-type



*Tc-zen* RNAi



# Ontwikkeling na *Tc-zen* RNAi

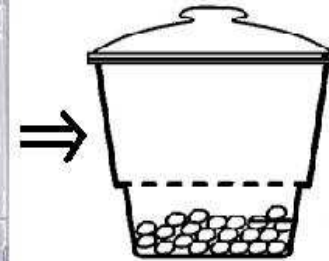
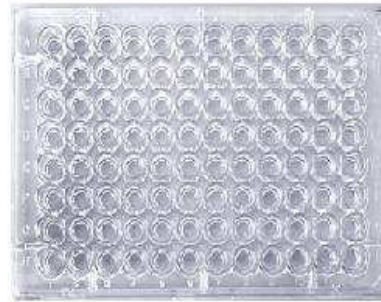


# Setup

## Treatments

- Wild type
- Control (non-targeting ds RNA)
- Tc-zen1* RNAi

⇒ Collect eggs ⇒



⇒ Count

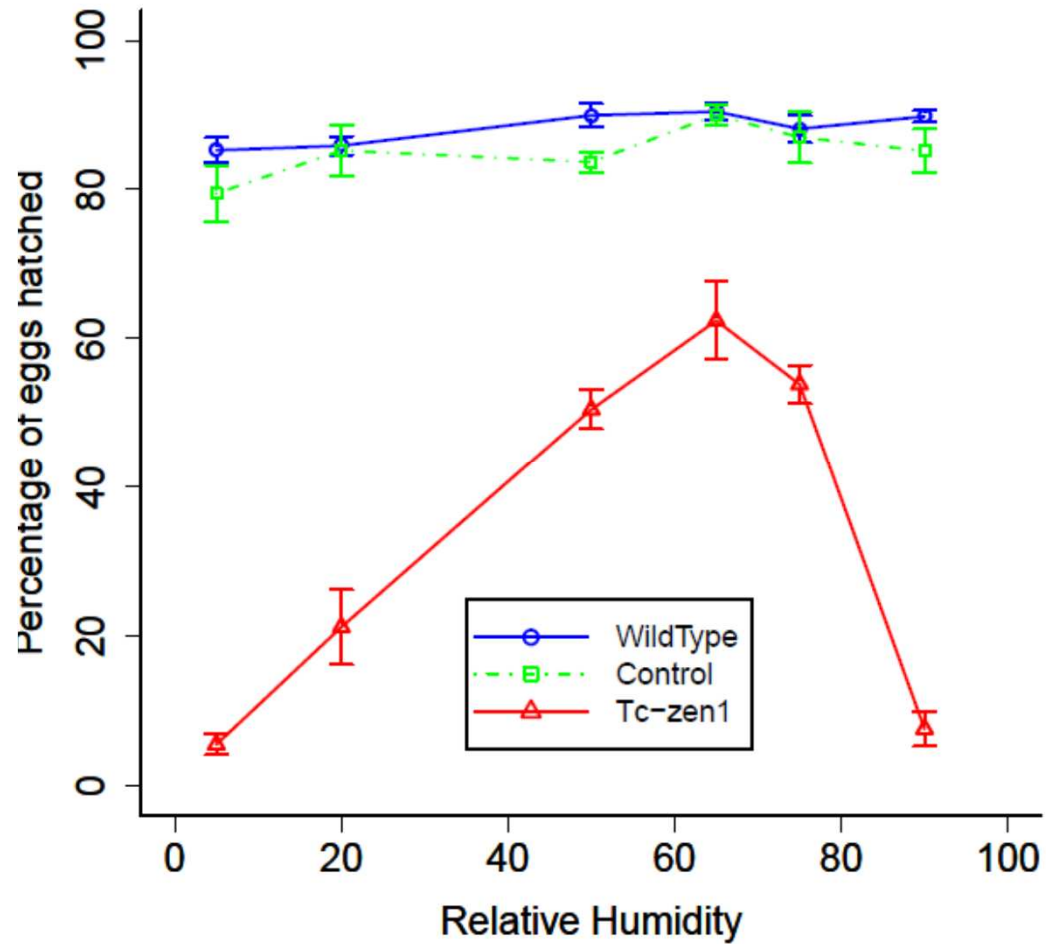
5%, 20%, 50%, 65%, 75% and 90% Relative Humidity

All experiments were repeated 2 to 9 times.



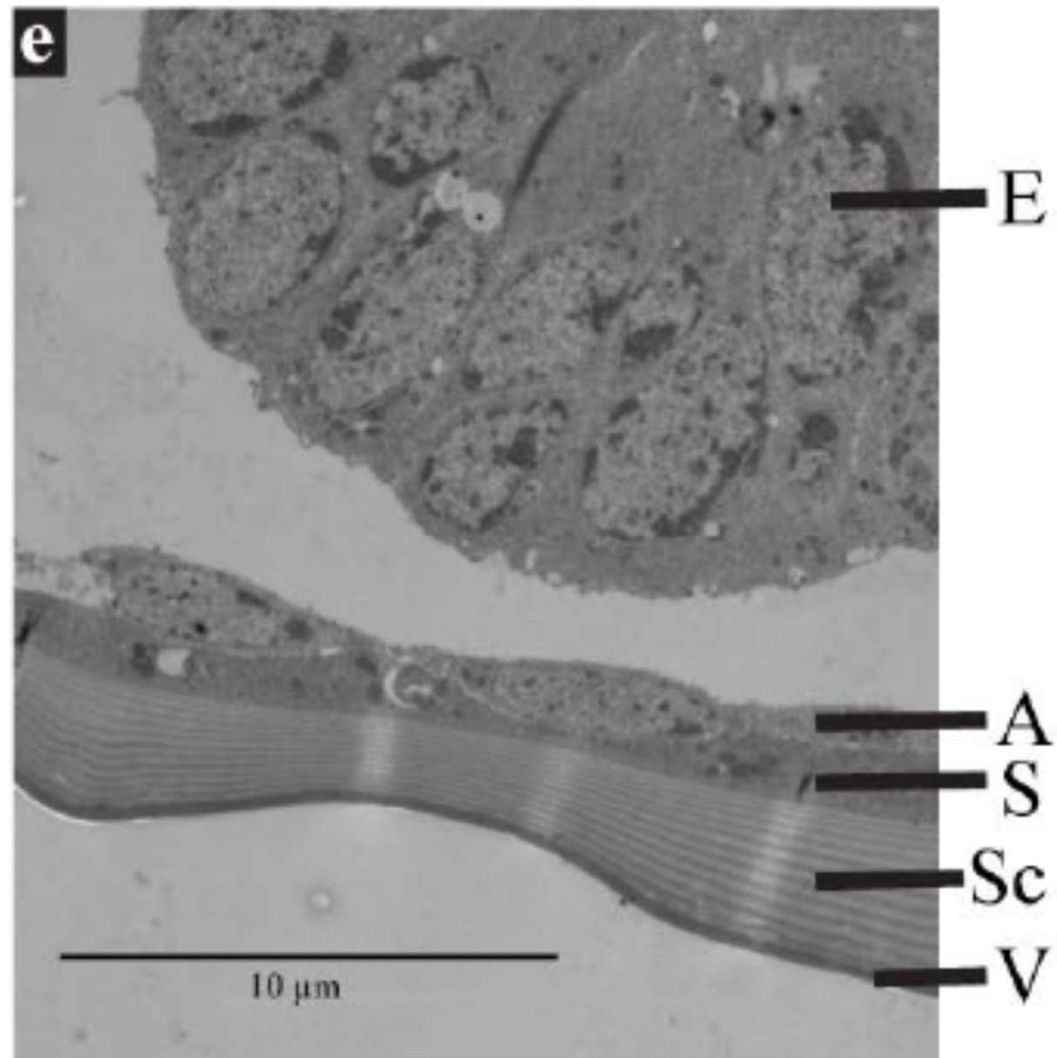
Chris Jacobs

# Serosa-loze kevereieren drogen snel uit



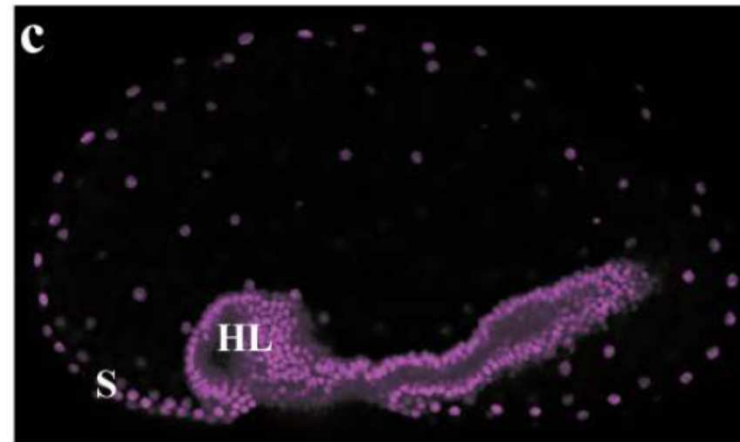
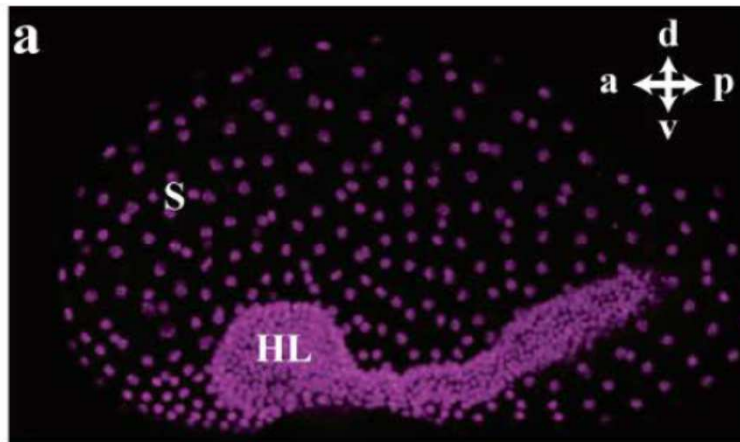


De serosa scheidt een cuticula af

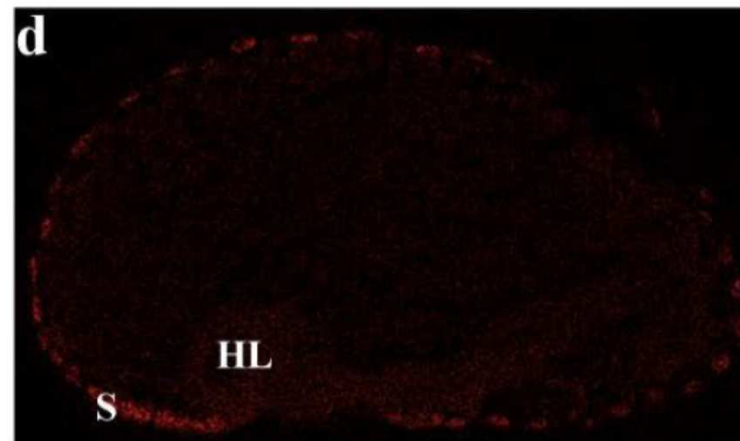
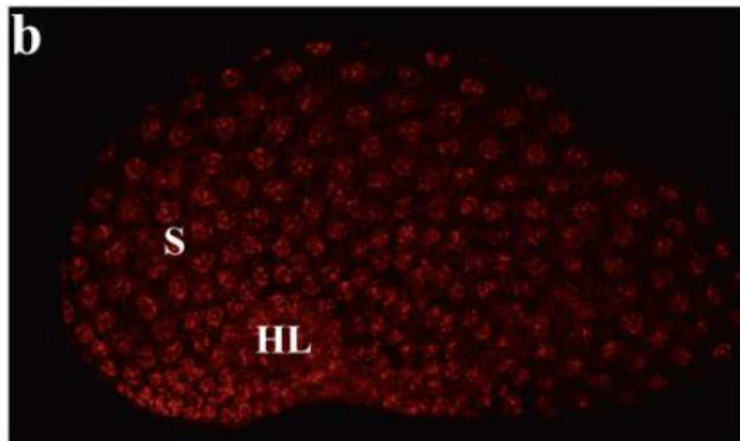


# *chitin synthase1* komt tot expressie in de serosa

*Tc-chs1* in situ



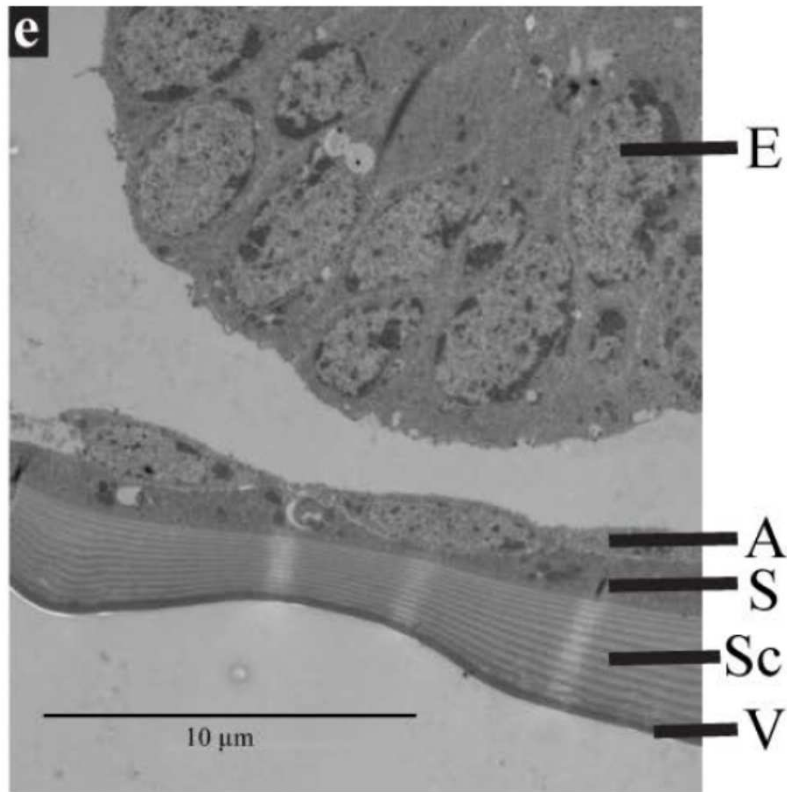
Draq5  
(nuclei)



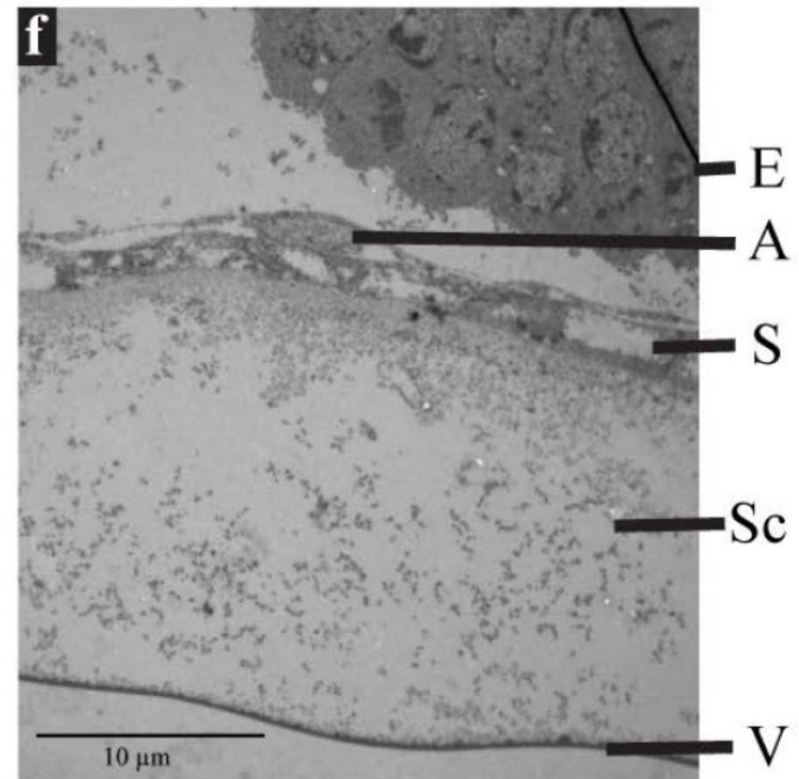
*chs1*  
in situ

## *Tc-chs1* RNAi schakelt de cuticula uit

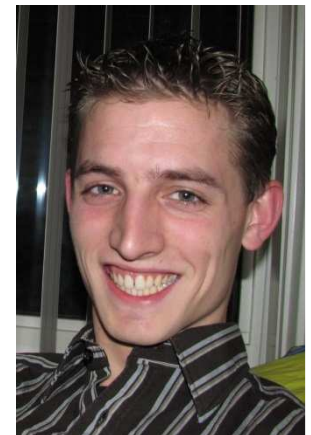
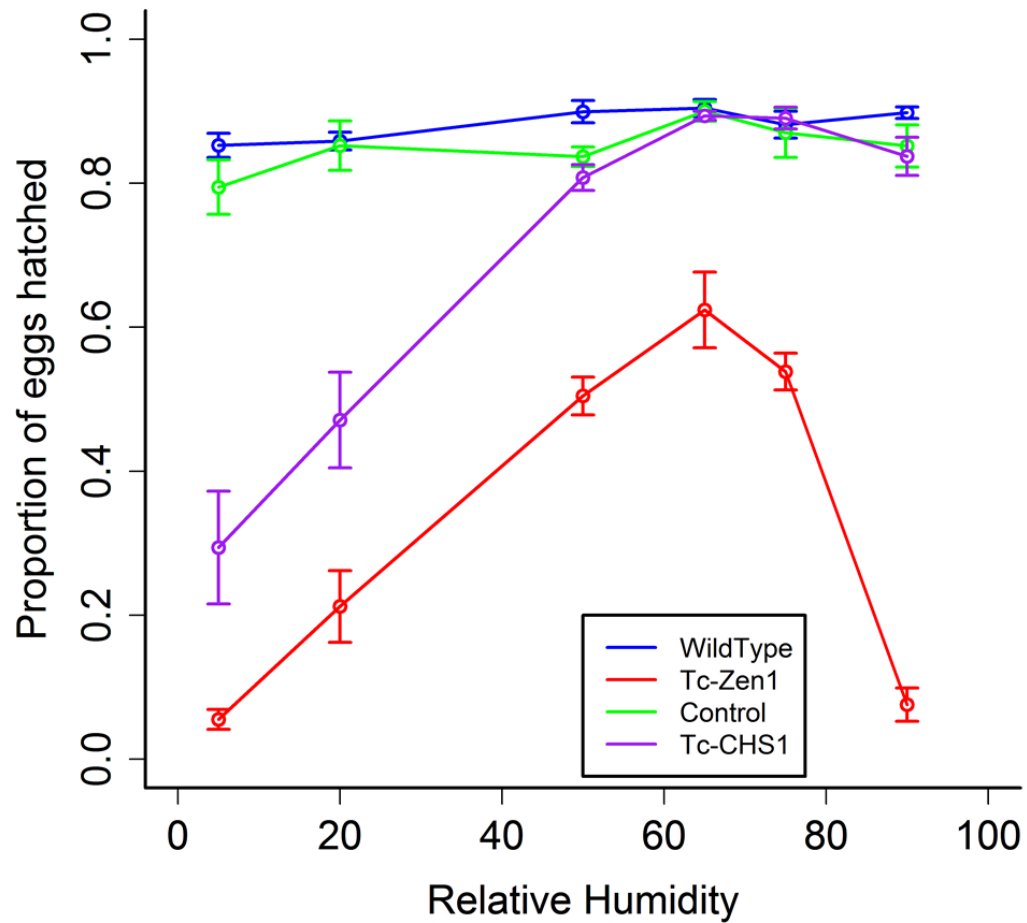
Wildtype



*Tc-chs1* RNAi

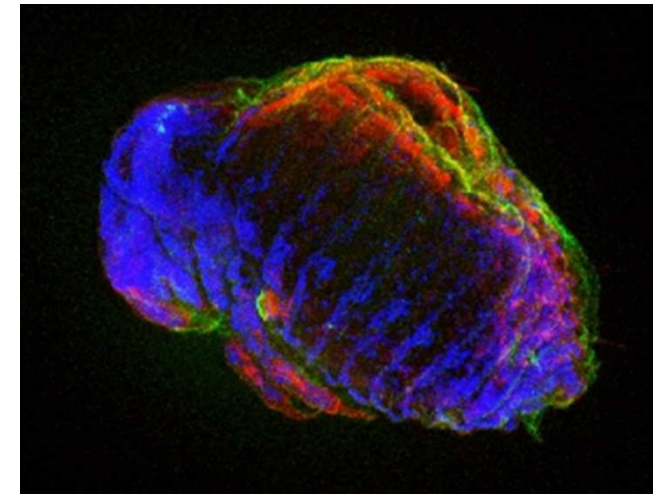
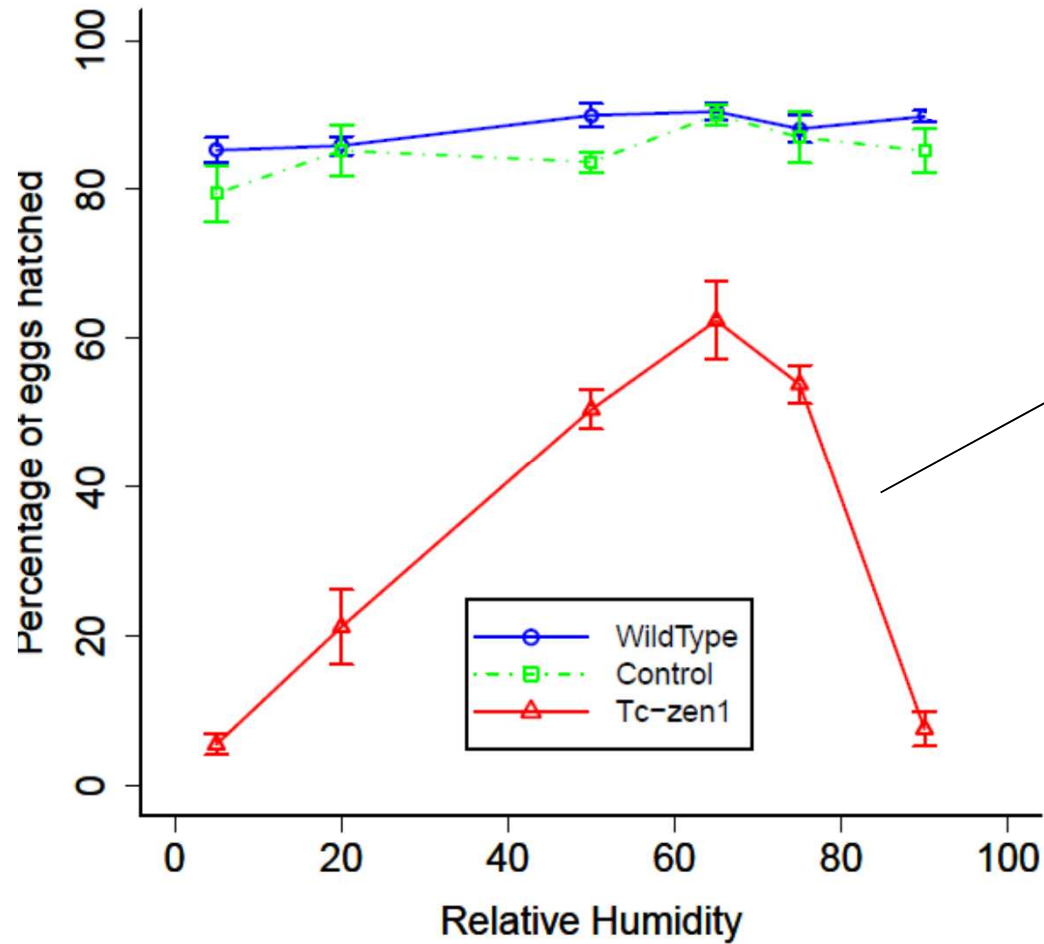


# De cuticula beschermt tegen uitdroging



Chris Jacobs

Op hoge luchtvochtigheid, zijn de cellen van de serosa nodig voor dorsale sluiting.



- De serosa beschermt tegen uitdroging



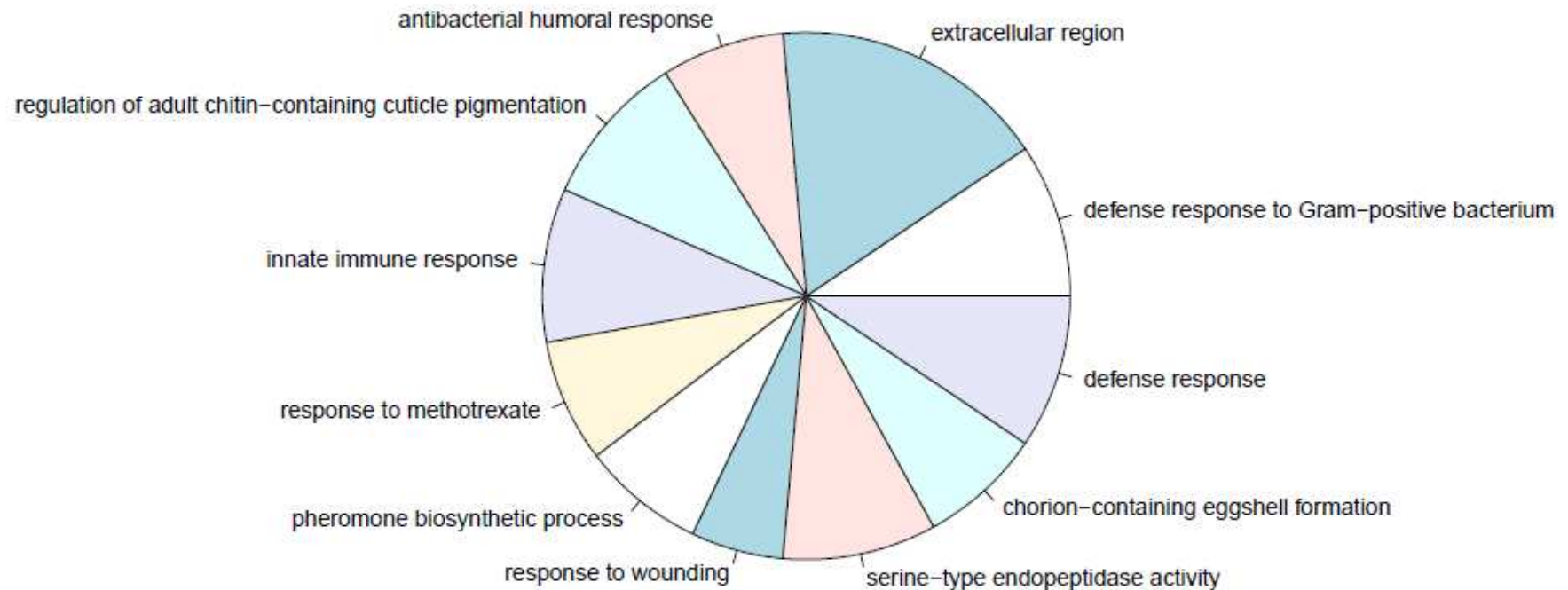
# RNA sequencing

→ kind of eggs tested

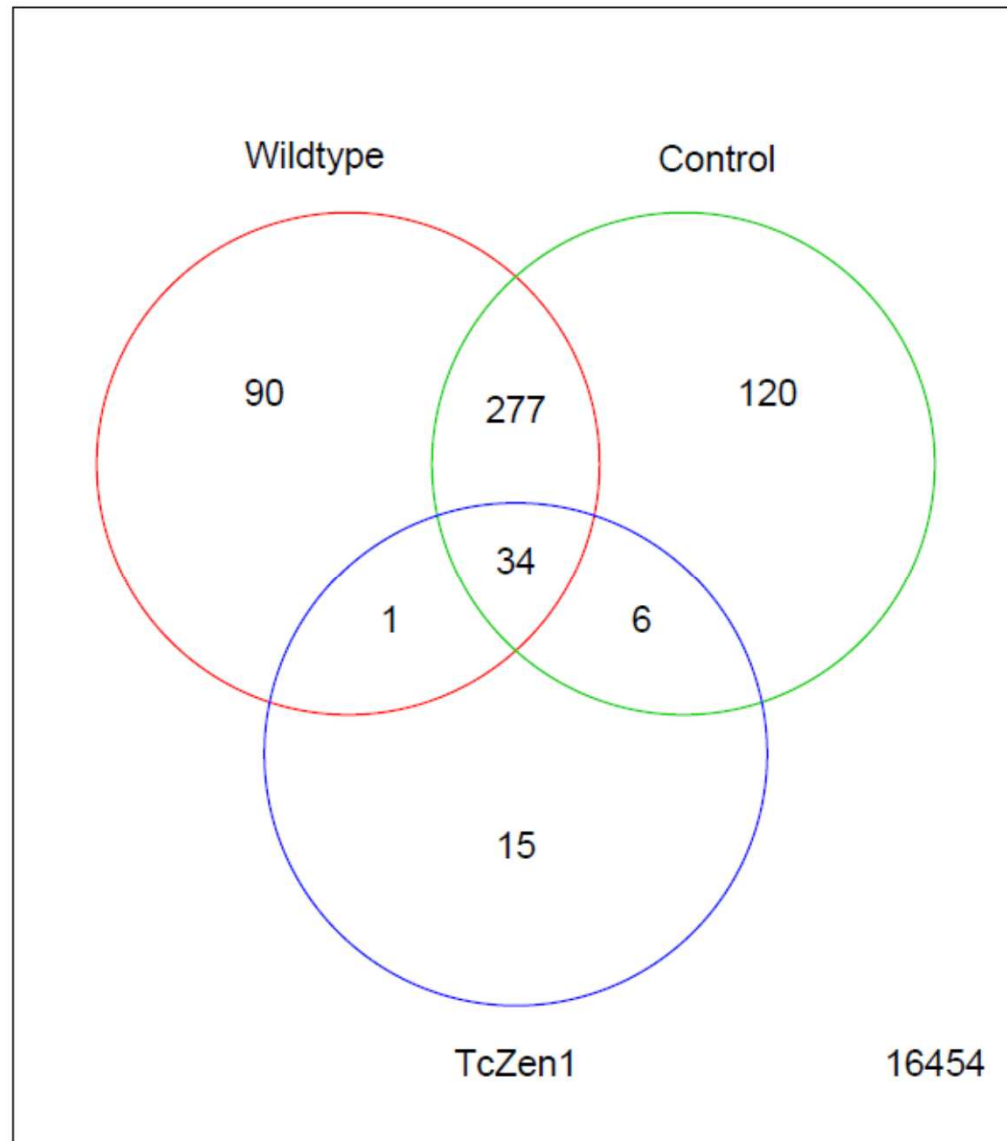
↓ treatments

Wildtype non-treated	Control RNAi non-treated	<i>Tc-zen1</i> RNAi non-treated
Wildtype sterile injury	Control RNAi sterile injury	<i>Tc-zen1</i> RNAi sterile injury
Wildtype septic injury	Control RNAi septic injury	<i>Tc-zen1</i> RNAi septic injury

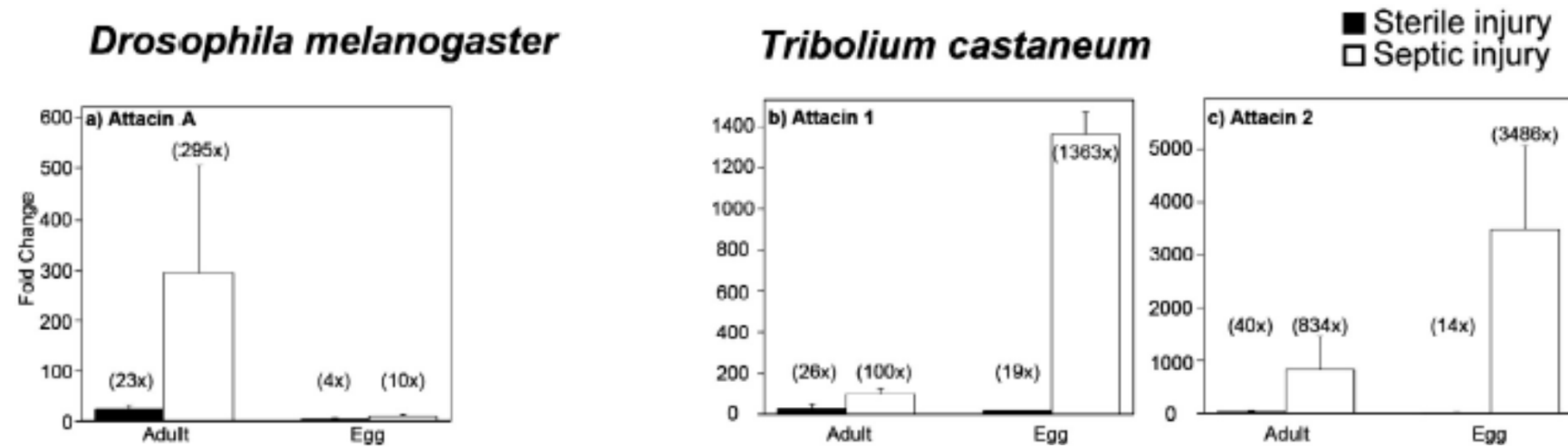
# Significantly overrepresented categories after septic injury in wild-type eggs



# Genes significantly ( $p < 0.01$ ) upregulated after septic injury



# Upregulation of antimicrobial peptides upon septic injury

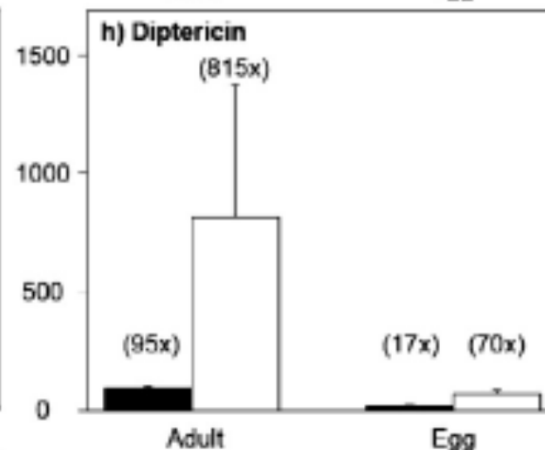
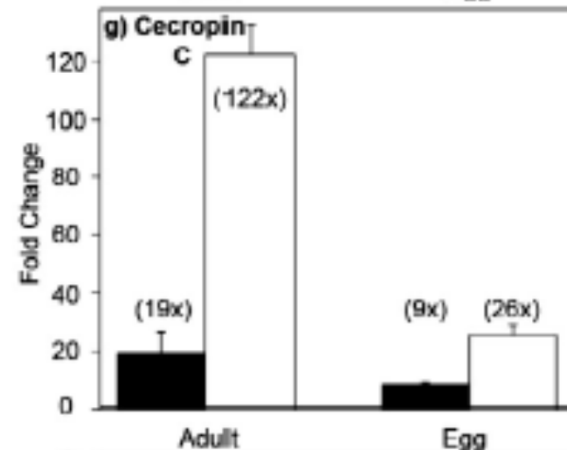
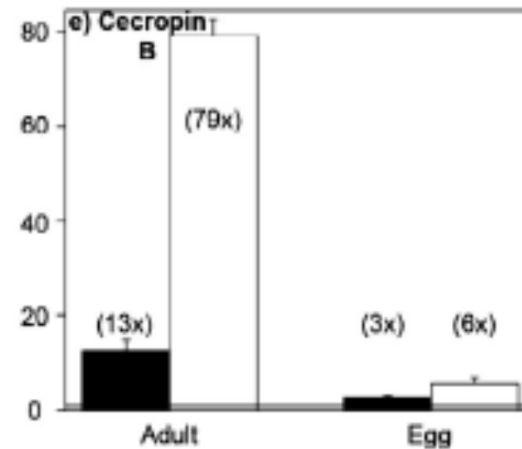
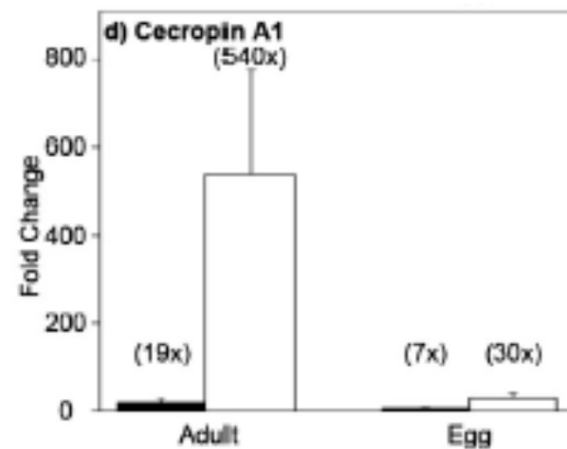


Chris Jacobs

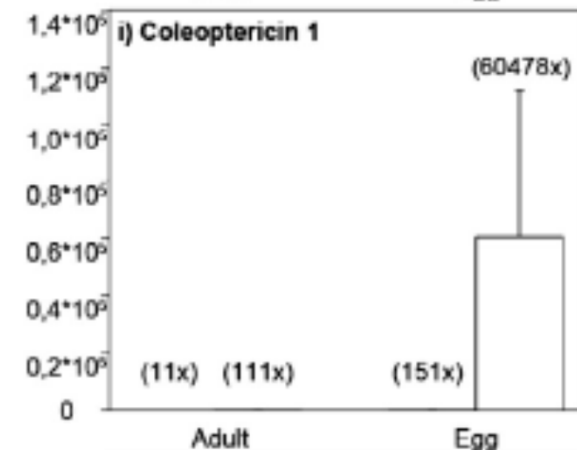
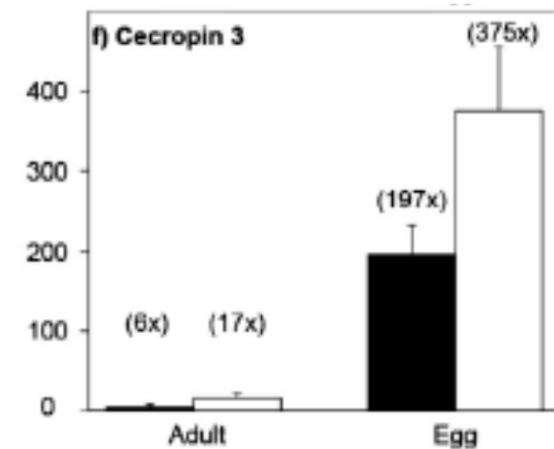


# Upregulation of antimicrobial peptides upon septic injury

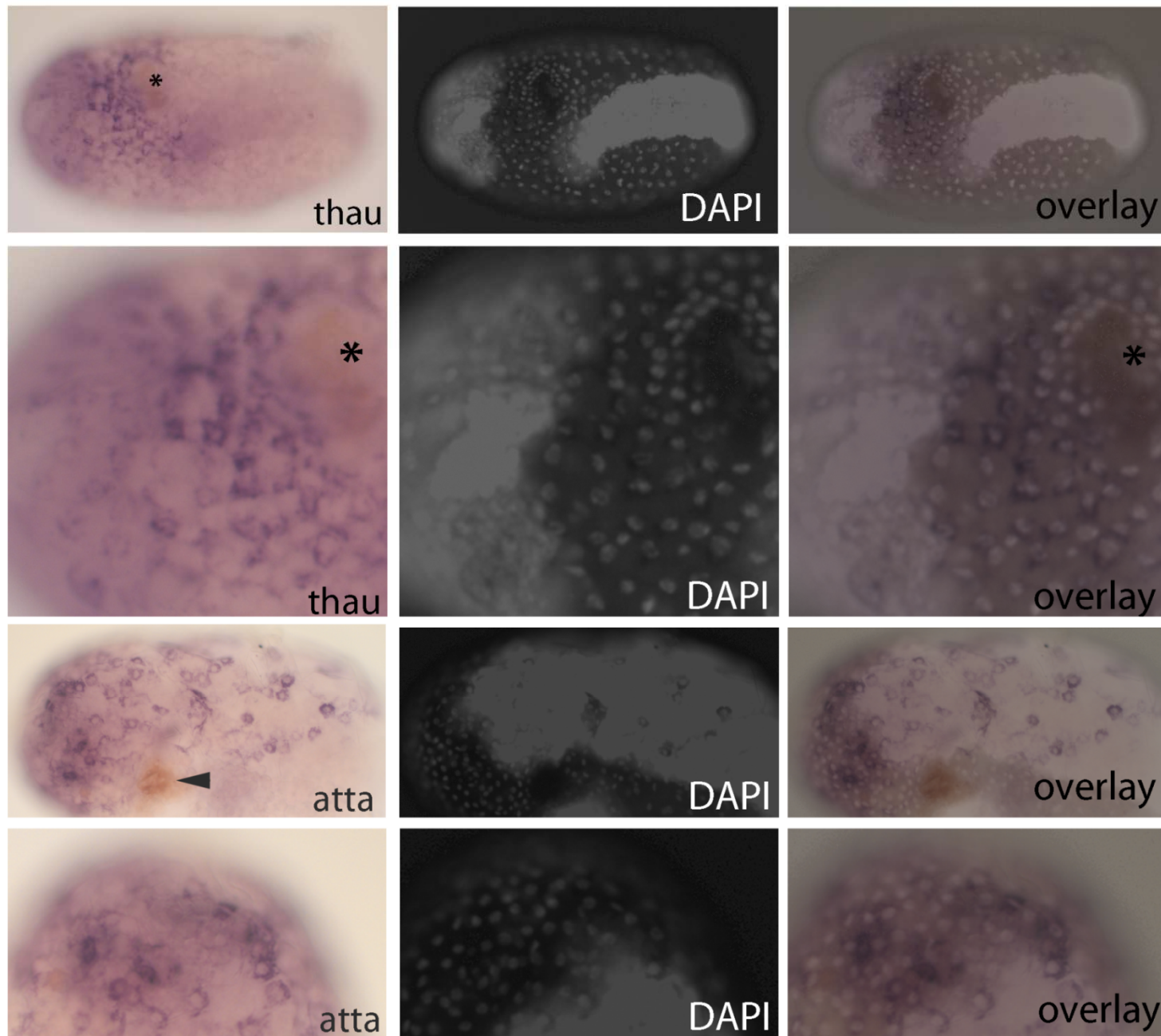
## *Drosophila*



## *Tribolium*

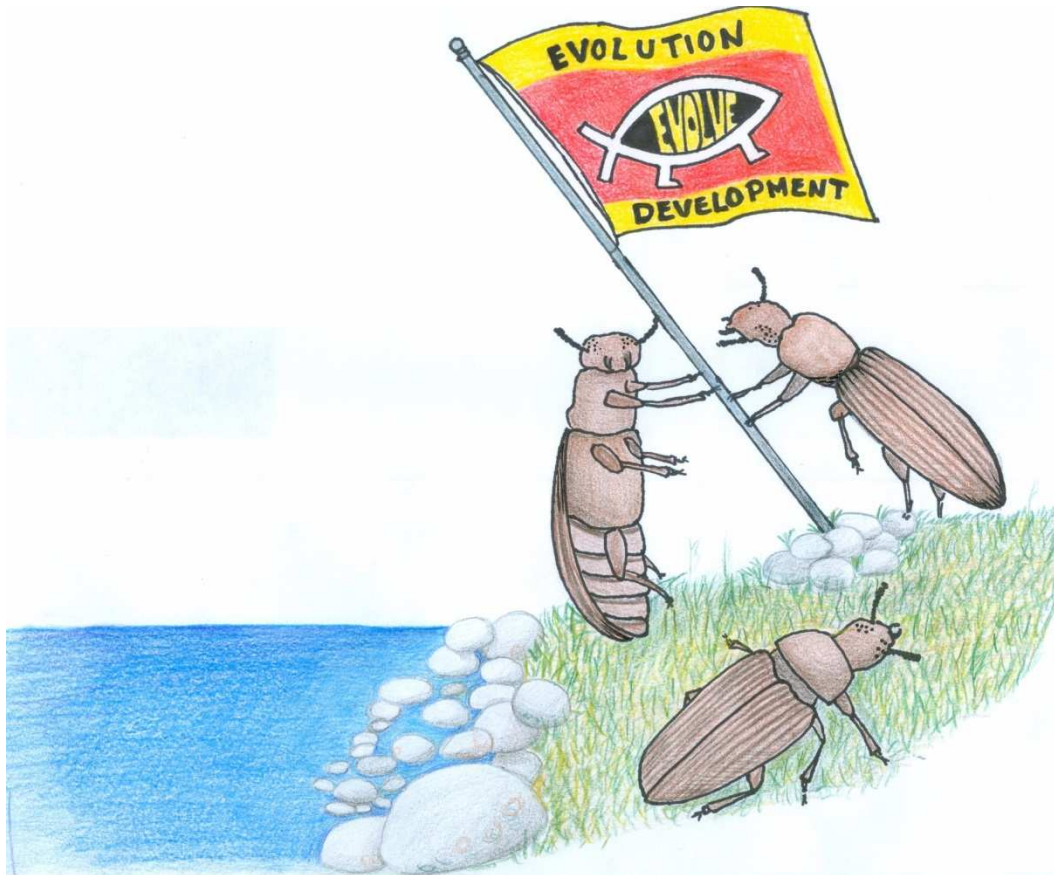


# Antimicrobial peptides are expressed in the serosa upon septic injury





- De serosa beschermt tegen uitdroging en bacteriën en zou wel eens een belangrijke rol kunnen hebben gespeeld bij de verovering van het land.



Leidse bioloog brengt spectaculaire stap evolutie in beeld door onderzoek met eitjes meelkevers

# Hoe insecten te land kwamen

**nature**

International weekly journal of science

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News &amp; Comment

» Nature's news

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22 juni 2013 | jaargang 23

## Insecten op land dankzij nieuw ei

NATURE | NEWS

### Waterproof eggs let insects conquer dry land

Membrane that protects eggs from drying out freed critters from need to stay close to water.

Ed Yong

19 June 2013

Insects were among the first animals to invade the land around 400 million years ago, and they have diversified so greatly that they now account for three-quarters of all animal species.

This success, according to a new study, depended to a great extent on the serosa — a membrane that makes insect embryos waterproof as they develop inside the eggs. By genetically removing the serosa from embryos of the red flour beetle (*Tribolium castaneum*), Maurijn van der Zee at



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For authors

E-alert

20 juni 2013 • Mare 7

Wetenschap

### Insecteneitjes

Rondom de eitjes van veel insecten zit aan de binnenkant van de eischal een speciaal laagje, de zogeheten serosa. De eieren van andere geleedpotige dieren hebben niet zo'n serosa. Als je met wat biotechnologisch knutselwerk zorgt dat een kever eitjes legt zonder serosa, komen die in het laboratorium nog steeds

3. 'Corkscr  
Nature | 2

## Membraan om ei was grote troef insecten

Door onze redactie wetenschap

AMSTERDAM. Een genetische verandering heeft het enorme evolutionaire succes van insecten mogelijk gemaakt. Insecten waren de eerste dieren die het land veroverden, 400 miljoen jaar geleden en nog steeds behoort driekwart van alle diersoorten tot de orde van insecten. De Leidse bioloog Maurijn van der Zee heeft nu, samen met zijn promovendus Chris Jacobs en twee Braziliaanse biologen, vastgesteld dat dit mede te danken is aan een unieke eigenschap van het insectenei. Het embryo in het ei droogt niet uit, dankzij de serosa. Dat is een membraan dat het embryo zelf produceert en dat andere geleedpotigen (zoals krabben en duizendpoten) missen.

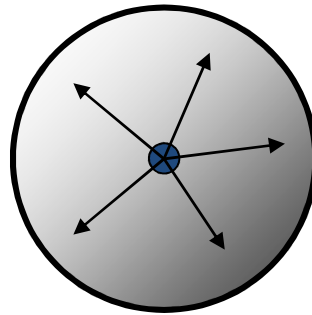
In de *Proceedings of the Royal Society B* van deze week beschrijft Van der Zee hoe hij erin slaagde om in eitjes van de kastanjebruine rijstmeelkever het gen *Tc-zen1* uit te schakelen, dat verantwoordelijk is voor de serosa. Bij lage luchtvochtigheid droogden de eitjes snel uit en kwamen ze niet uit. Onverwacht, trouwens, bleken de serosa-loze eitjes ook slecht uit te komen in hoge luchtvochtigheid, omdat het ei dan juist te veel vocht opnam. Ook ontdekte Van der Zee dat het keratinelaagje van de membraan cruciaal was voor de overleving in la-

# Evolution and development

1. Embryo's vertellen je iets over evolutie.
2. Evo-devo onthult diepe homologieën.
3. Evo-devo zoekt de genetische en ontwikkelingsbiologische basis van evolutionaire veranderingen.
4. Evo-devo bestudeert de oorsprong van *novelties*
5. Embryonale ontwikkeling kan de evolutie in bepaalde richtingen sturen.

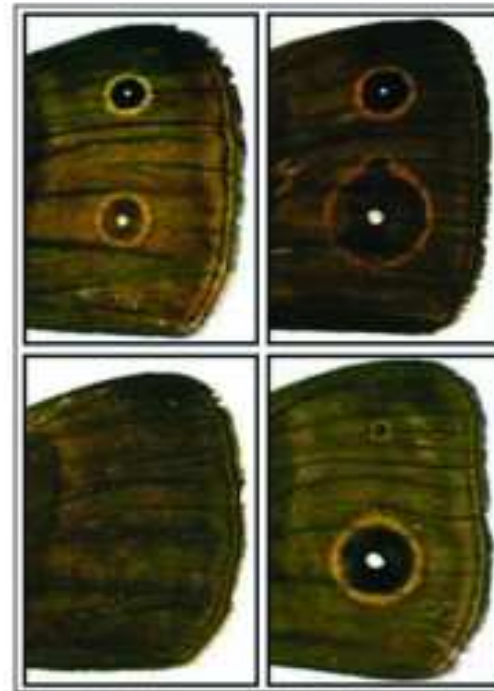
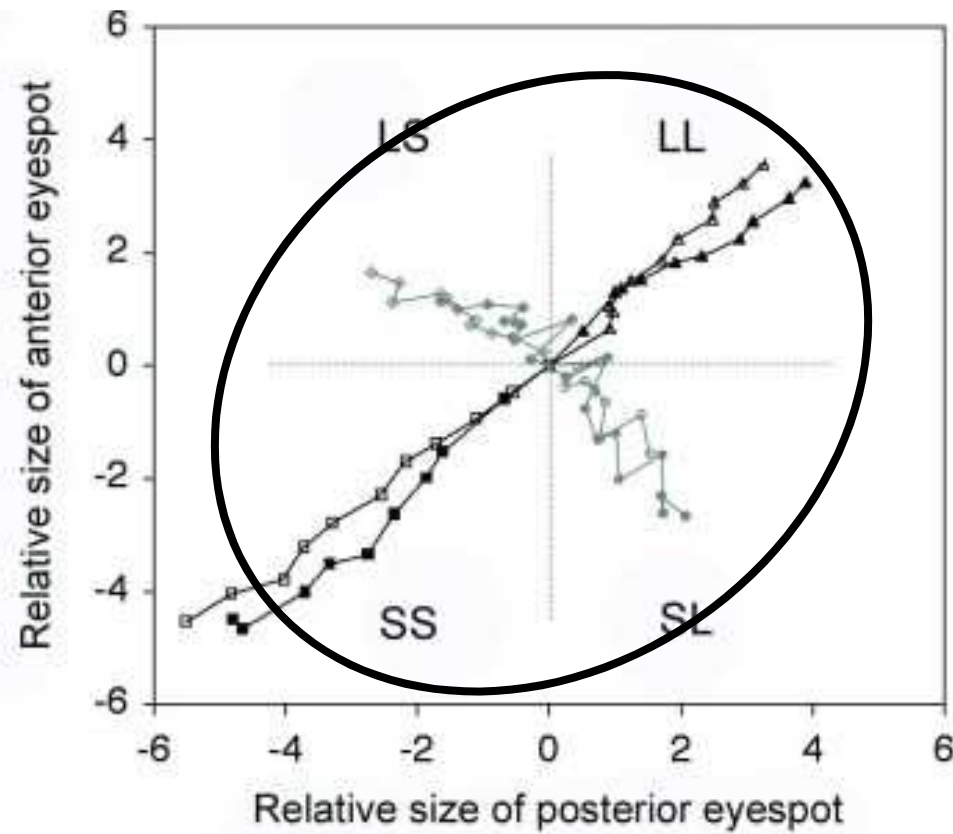
# Darwin:

- Variation is isotropic (random and in every direction)

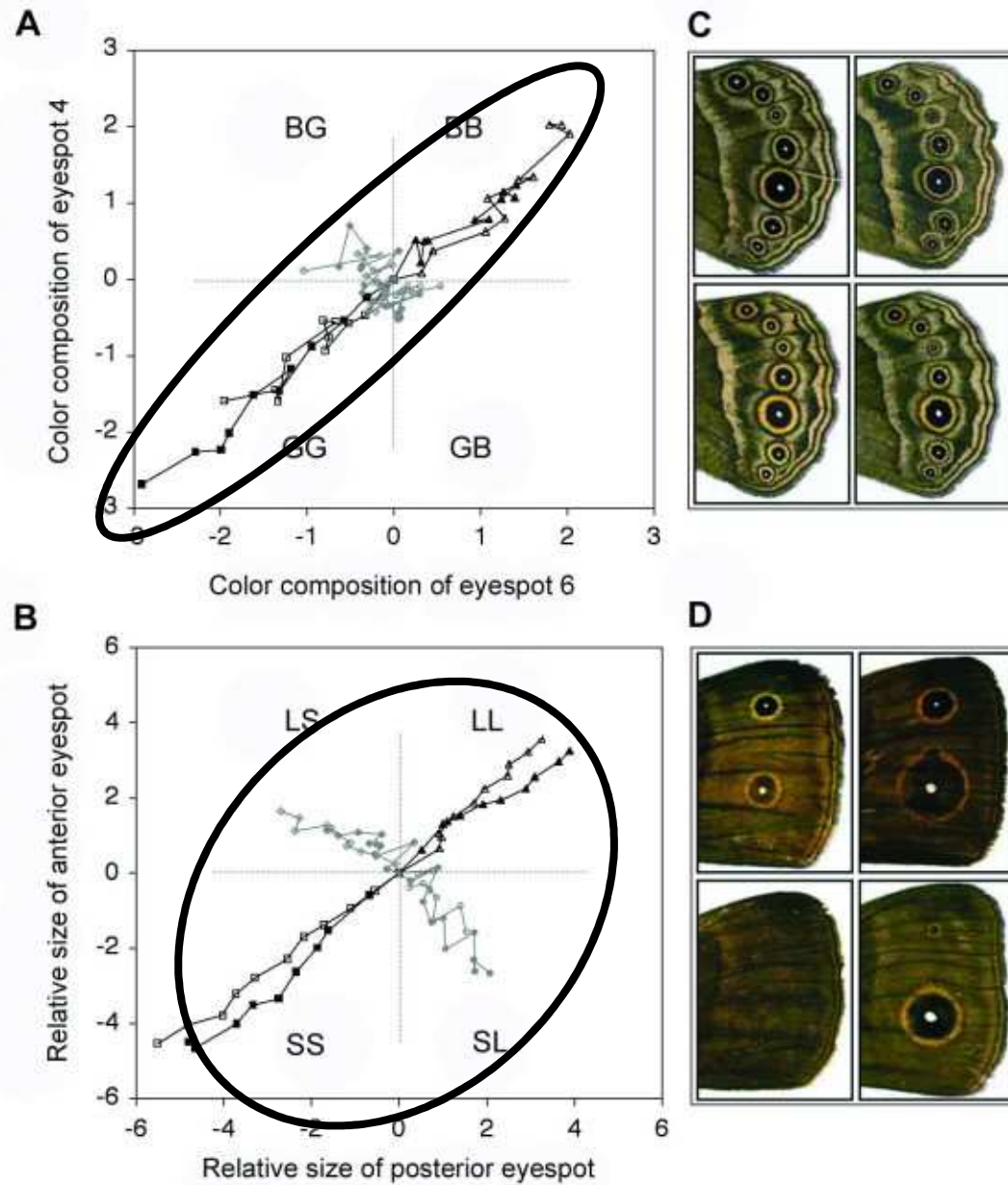




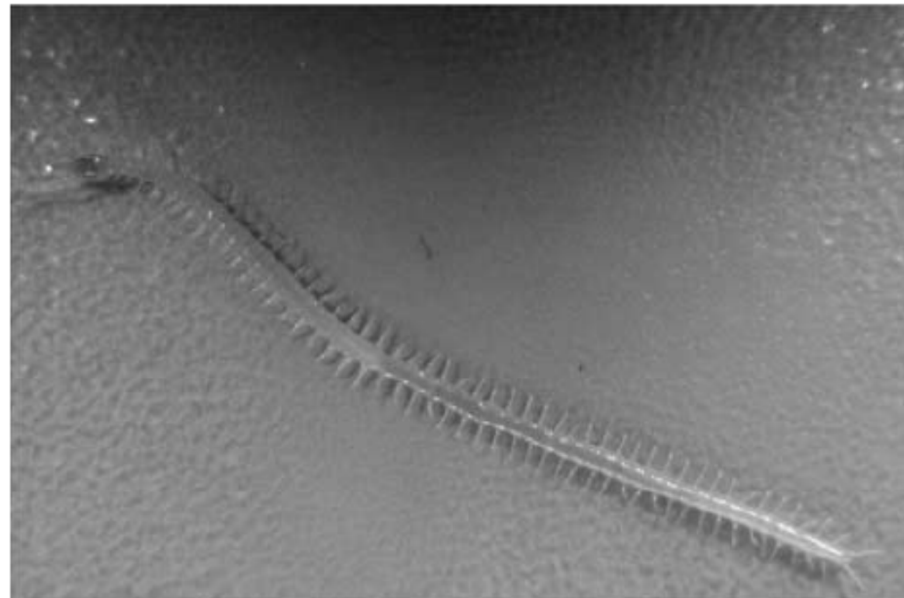
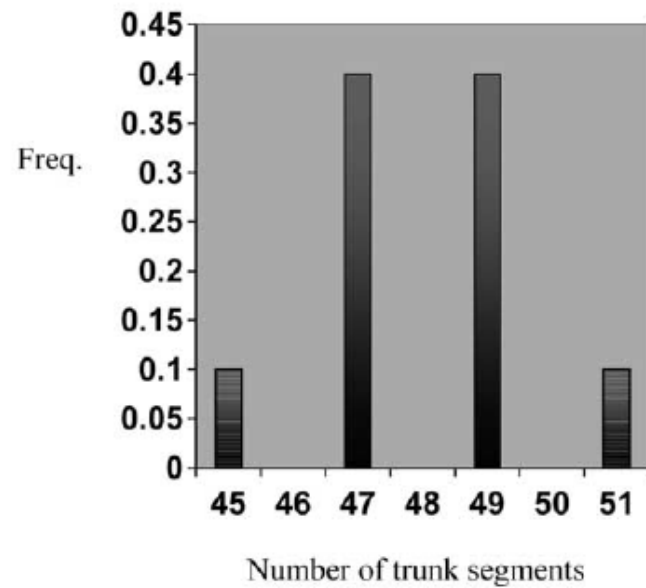
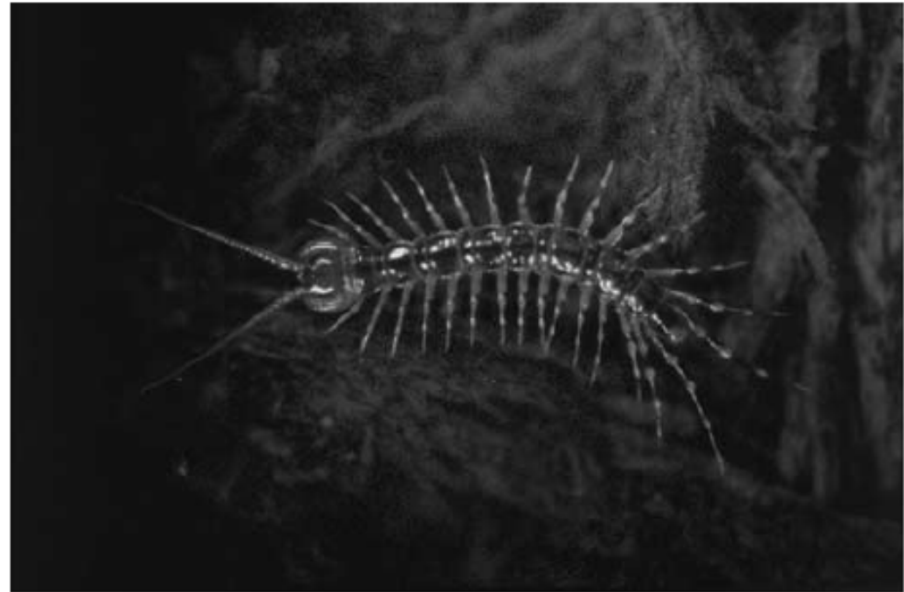
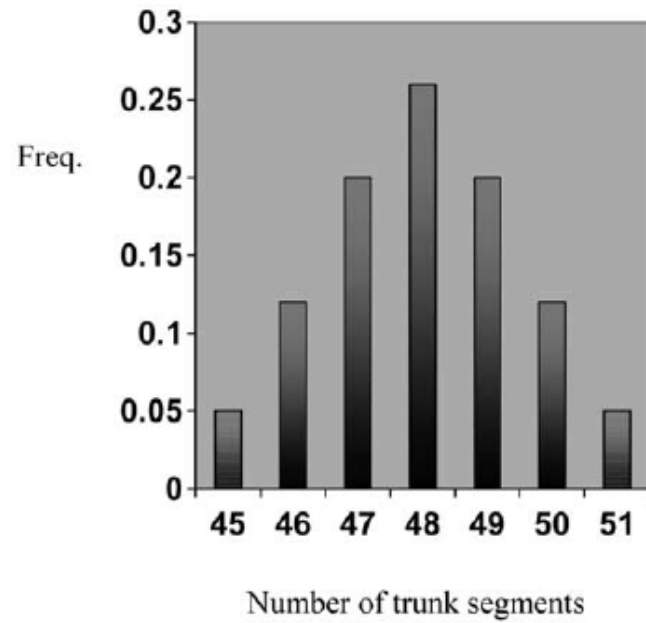
Variation and selection seems to be possible in every direction



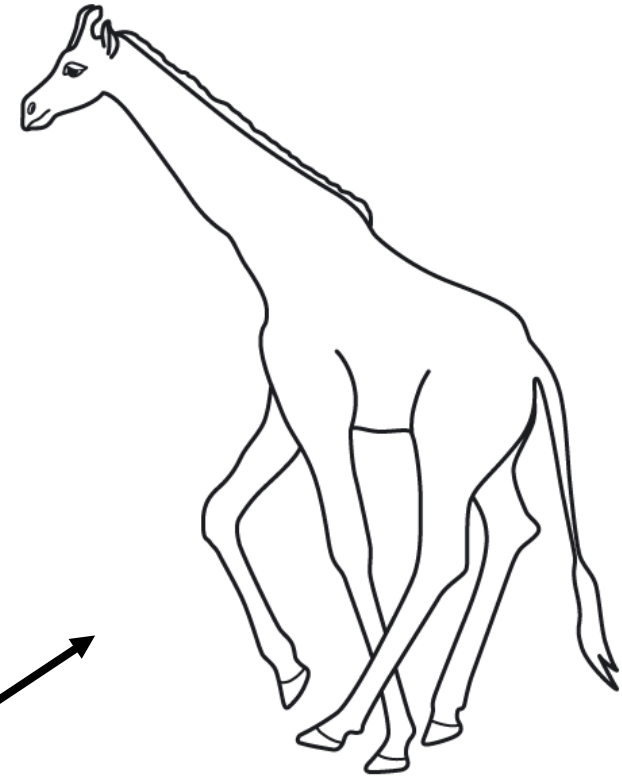
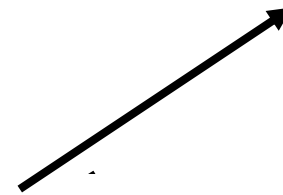
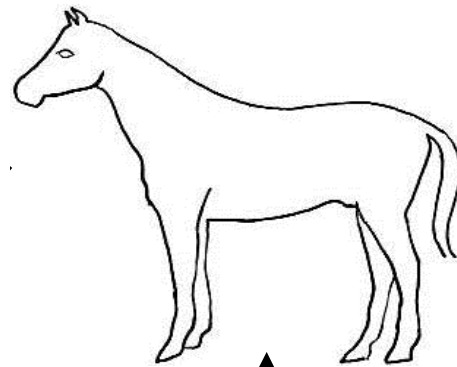
...but not for eyespot color!

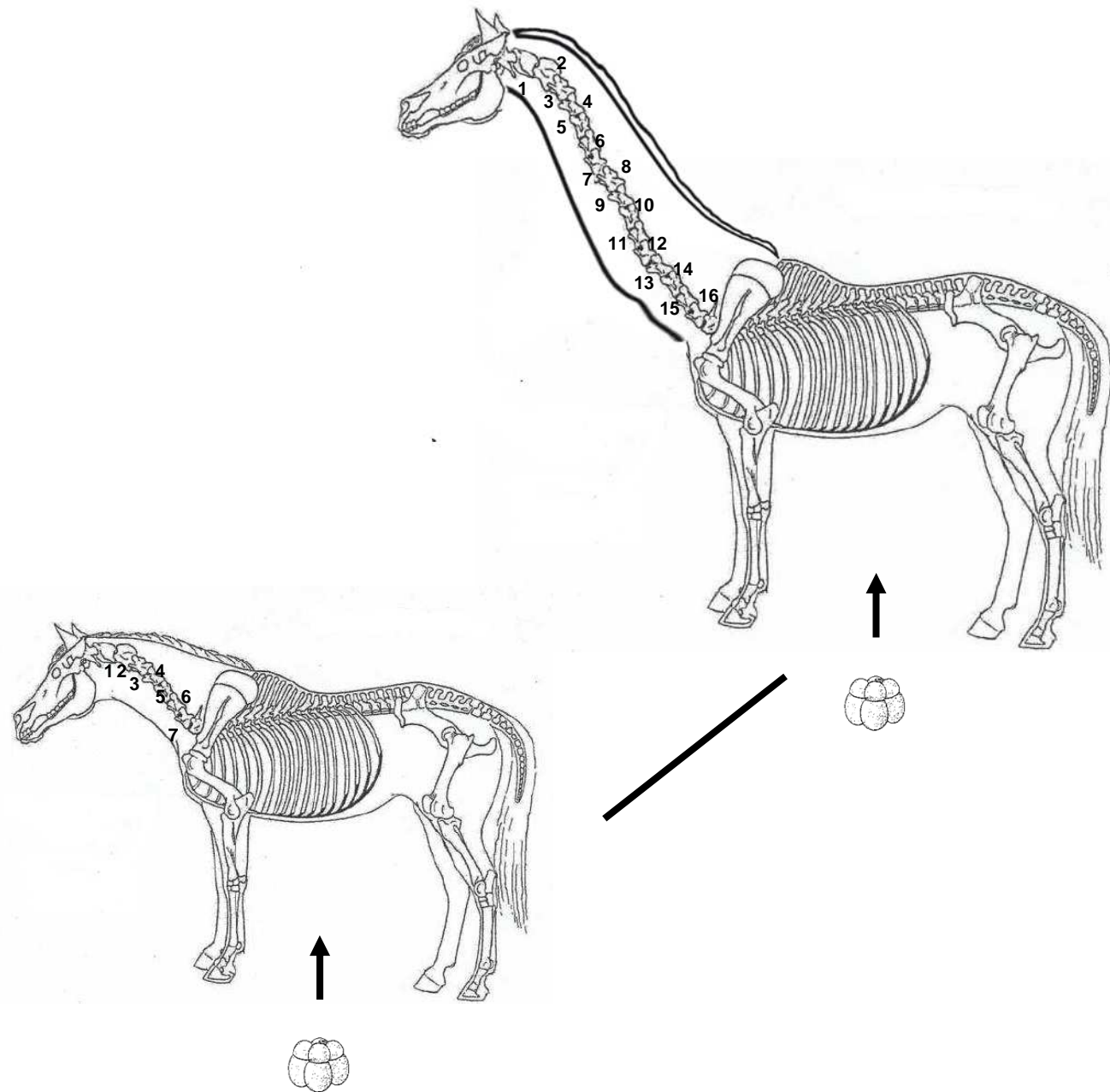


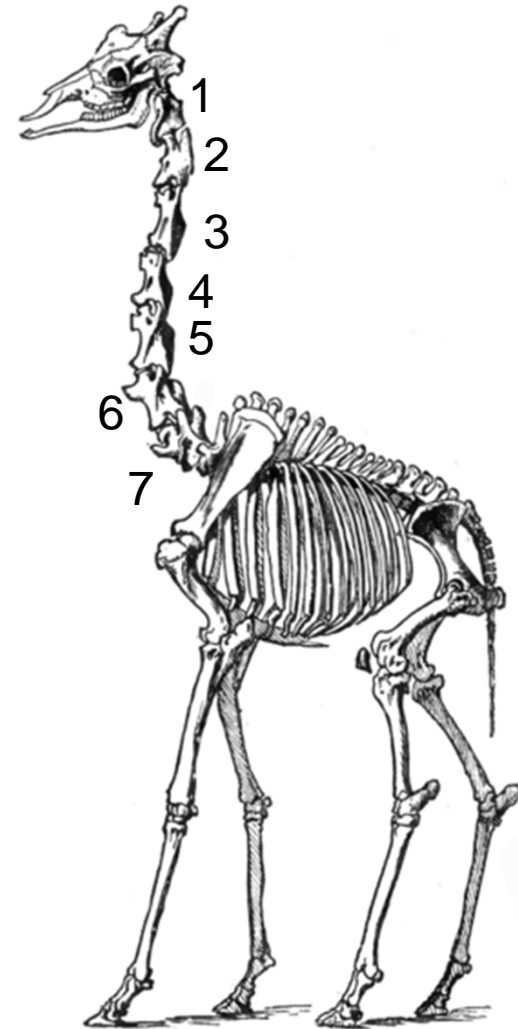
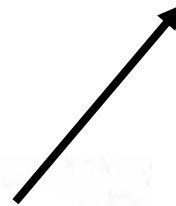
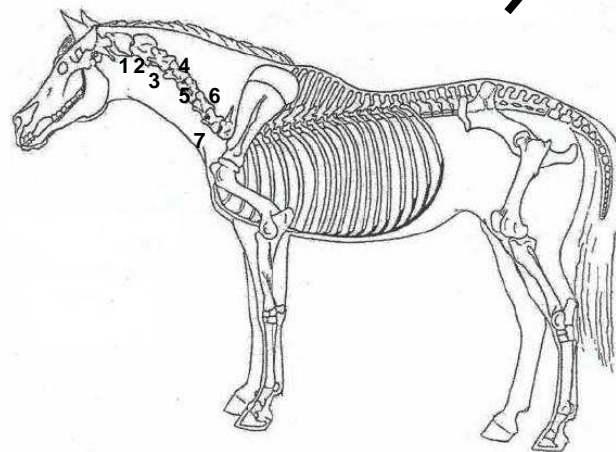




Arthur, *Heredity*, 2002

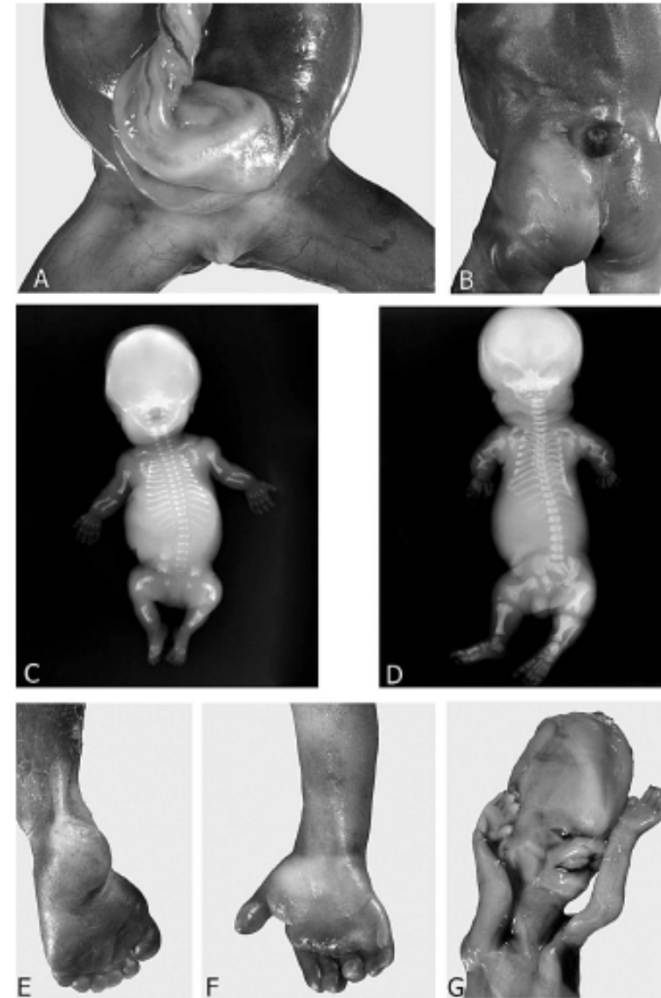
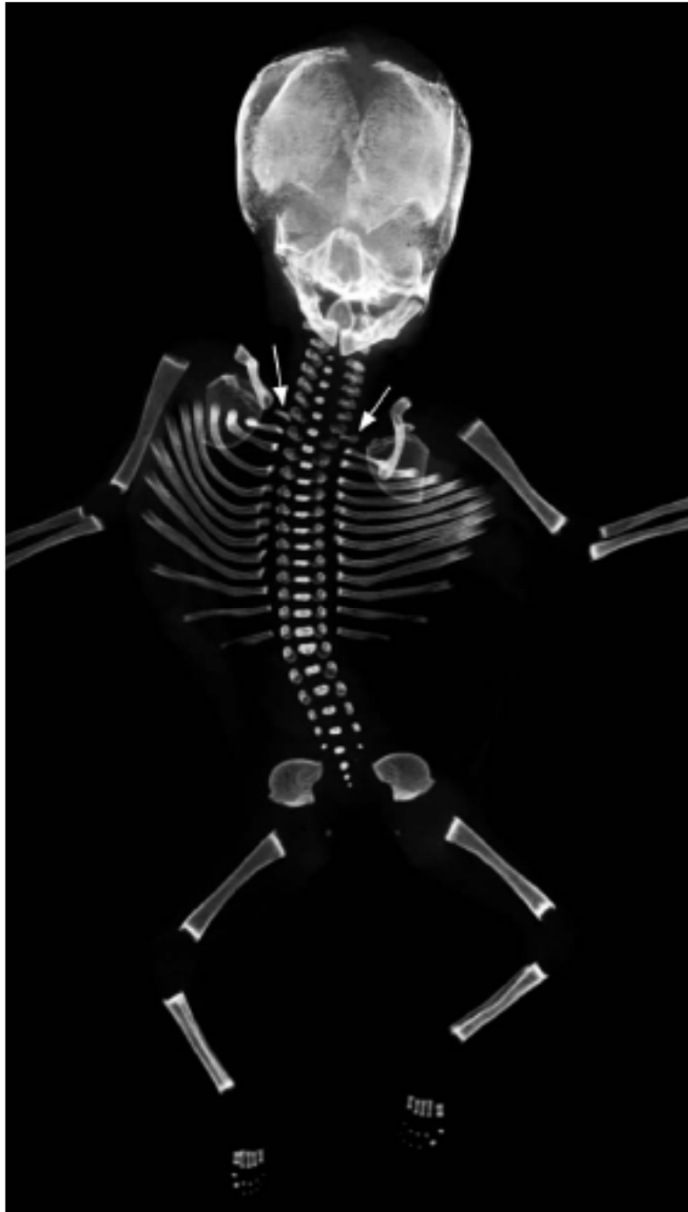




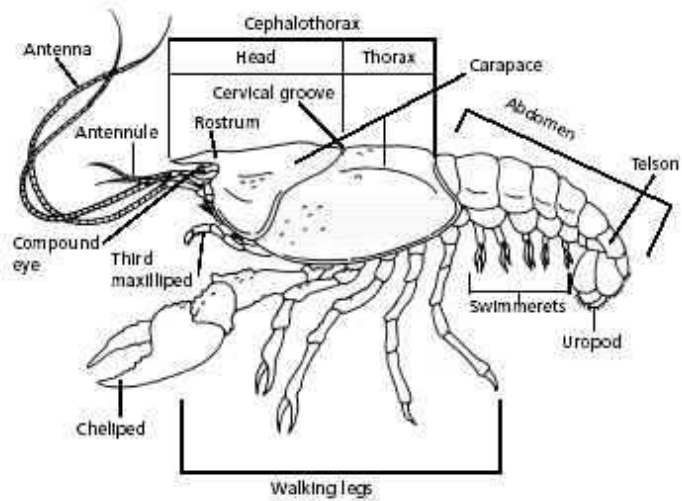


SKELETON OF GIRAFFE.

# Human embryos lacking a cervical vertebra



→ Pleiotropy



**Facilitated variation = positive bias**

(Kirschner and Gerhart)

-compartmentation/uncoupling/modularity





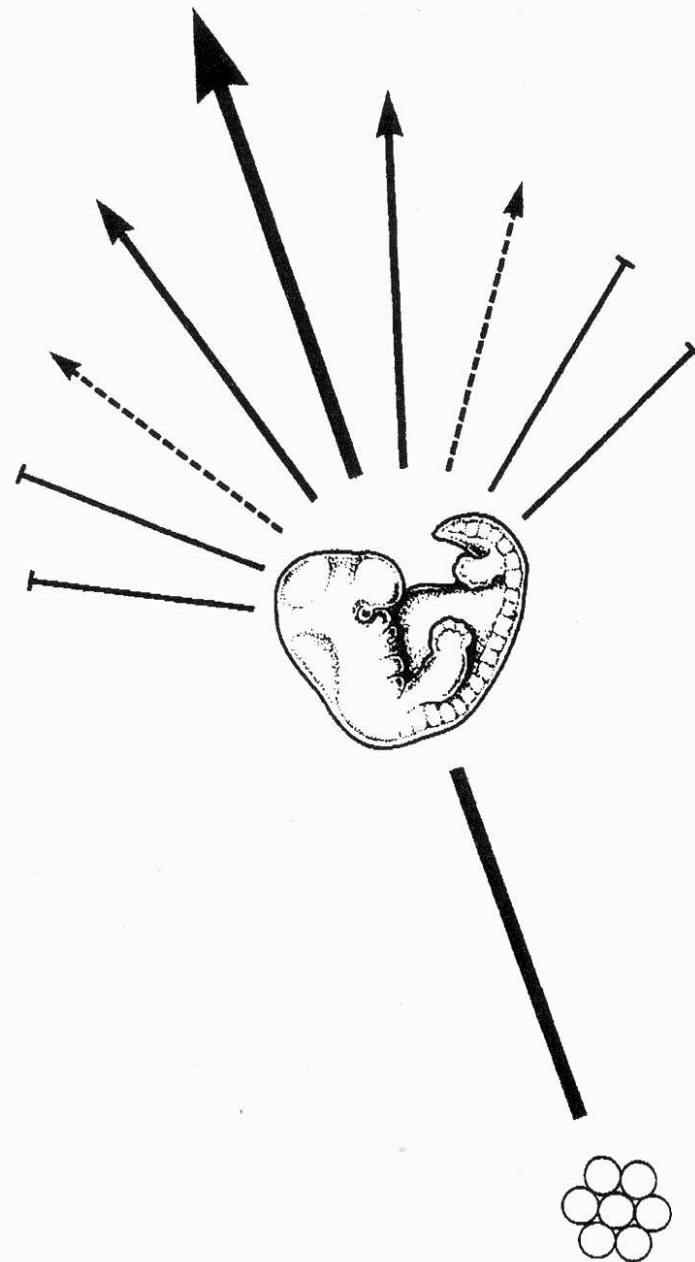


FIGURE 3 Developmental bias, represented by different probabilities of reprogramming an embryo's trajectory in different ways. Large arrow, original trajectory; solid arrow, easy; dashed arrow, difficult; blunt-ending lines, impossible.

Arthur, 2004

# Evolution and development

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Evolution Today

### Instructors



**Menno Schilthuizen**

Prof. Dr.  
Naturalis Biodiversity Center and Leiden University



**Maurijn van der Zee**

Dr.  
Leiden University



**Rutger Vos**

Dr.  
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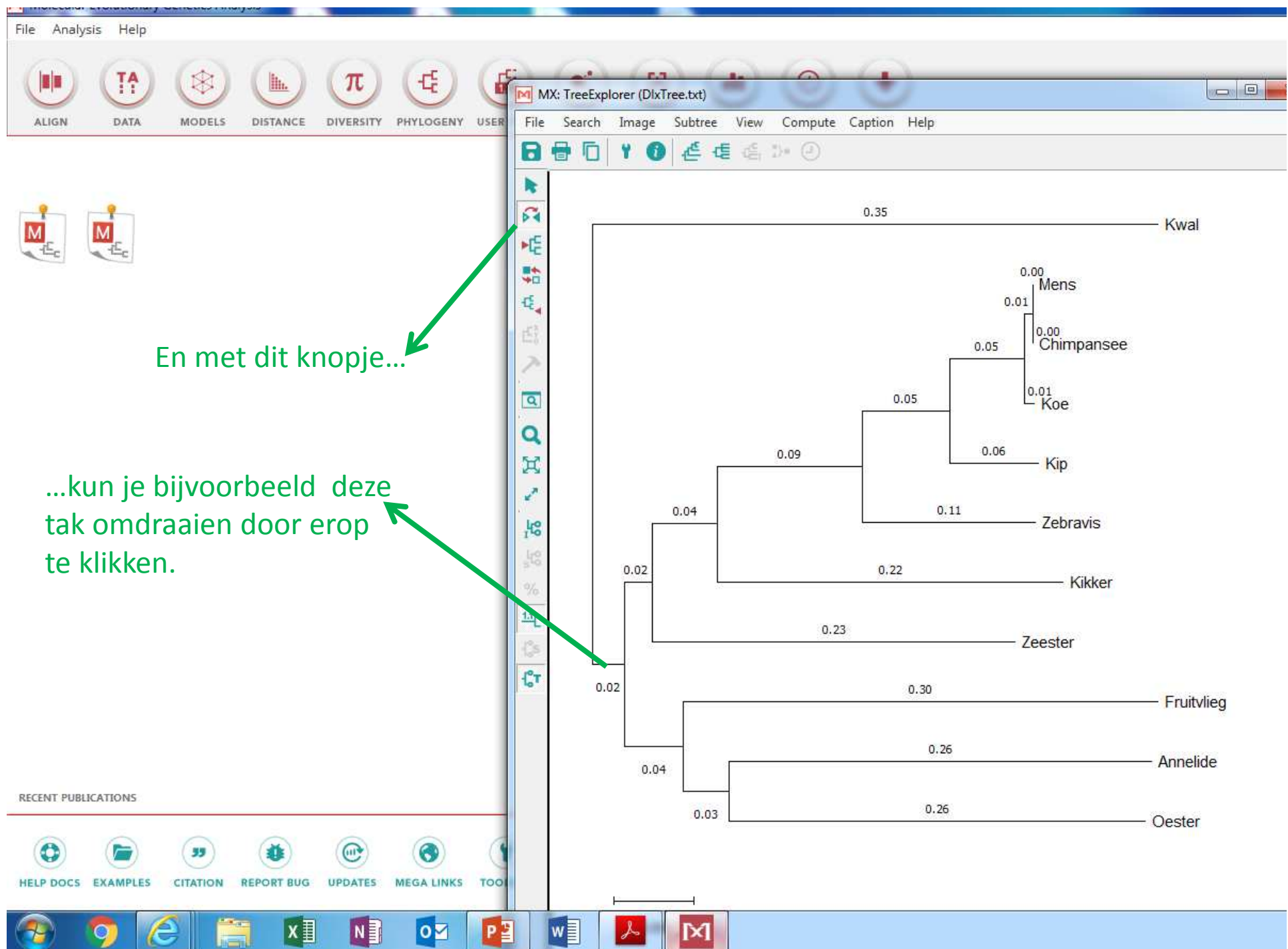


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Molecular Evolutionary Genetics Analysis

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En onder deze optie kun je “Tree” selecteren en daar bijvoorbeeld het aantal pixels van de branch lengths verhogen, om de boom wat uit elkaar te trekken als de taxa te dicht op elkaar staan.

Phylogenetic tree showing relationships between various taxa and their branch lengths:

- Kwal (0.35)
- Fruitvlieg (0.30)
- Annelide (0.26)
- Oester (0.26)
- Mens (0.00)
- Chimpansee (0.01)
- Koe (0.01)
- Kip (0.06)
- Zebravis (0.11)
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- Zeester (0.23)

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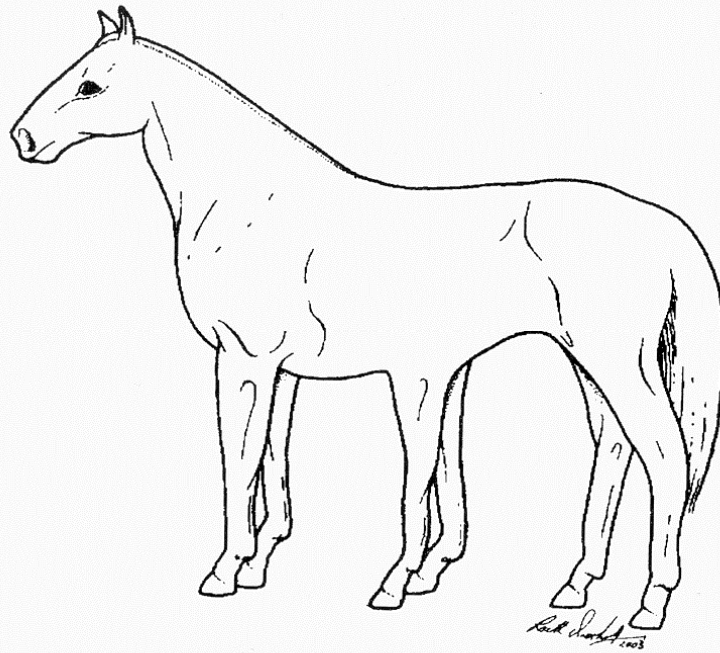


FIGURE 2 The fictitious but potentially viable six-legged horse.

