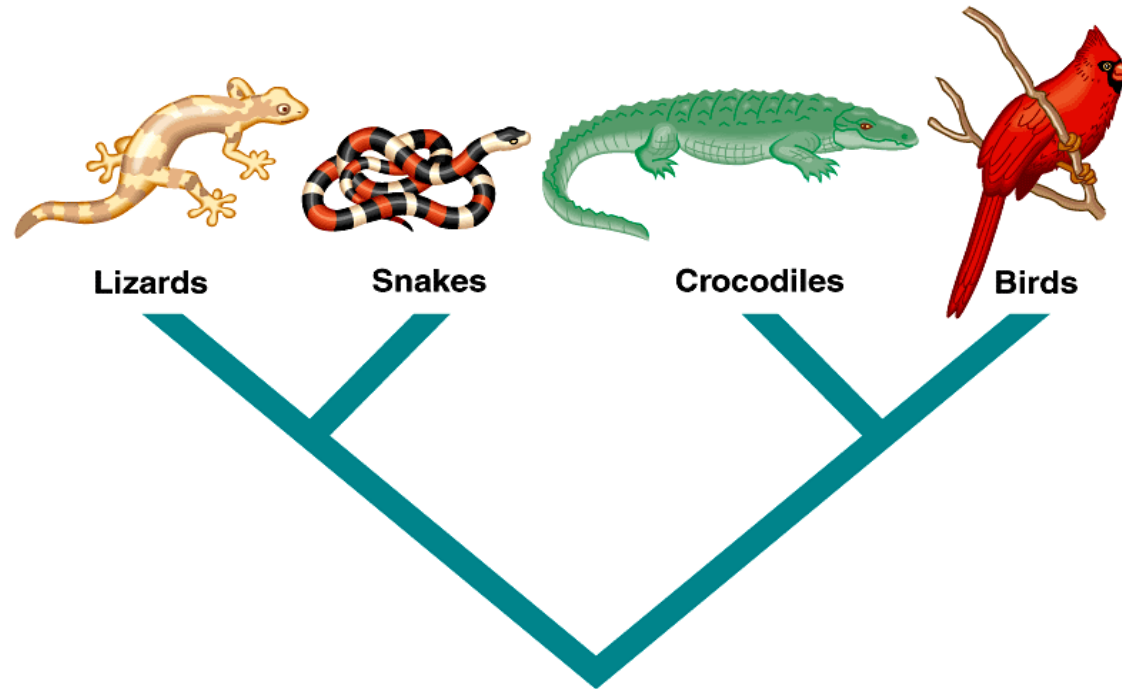


# Today

- This morning
  - What is a phylogenetic tree?
  - How to “read” simple phylogenetic trees
  - How can you make a phylogeny?
  - How can you root a phylogeny?
- **Gene Duplications & orthology**

# So far: one gene, one individual, one species

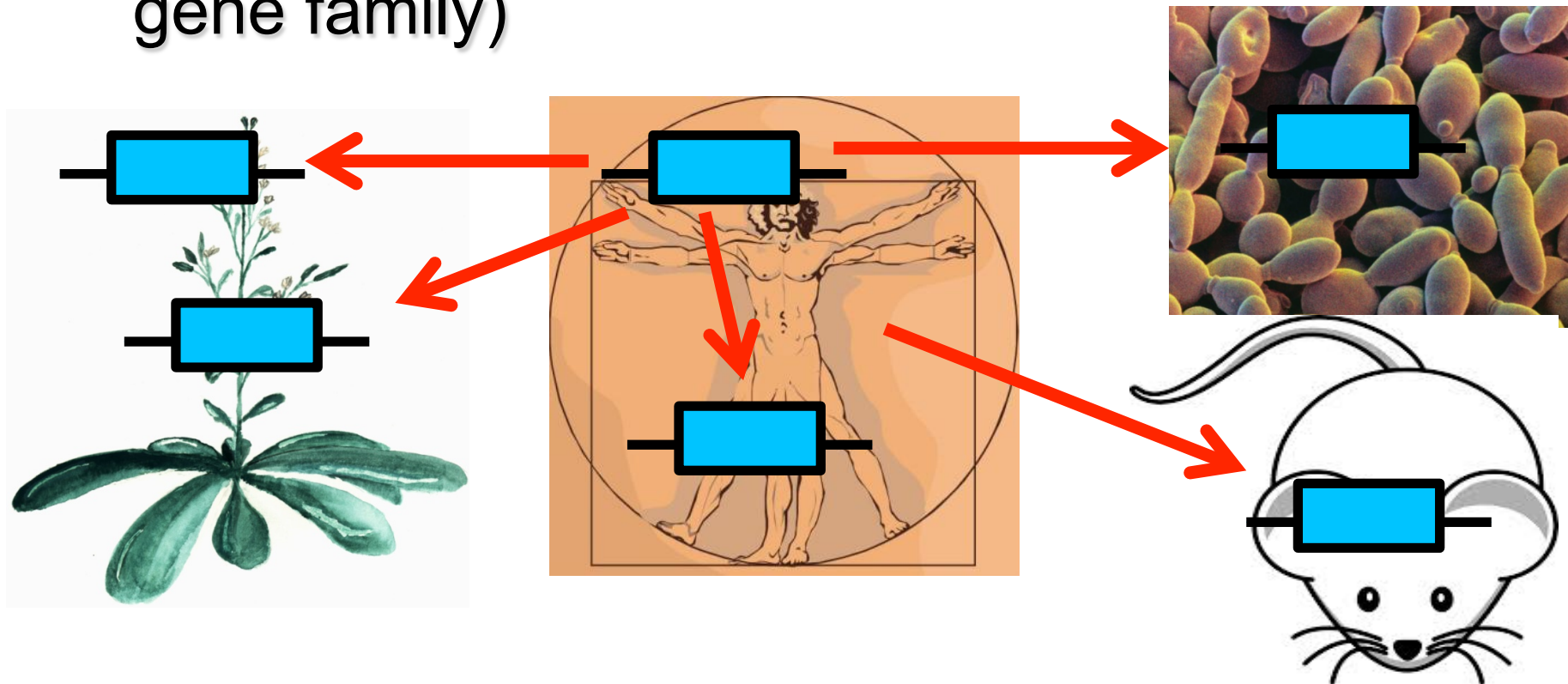


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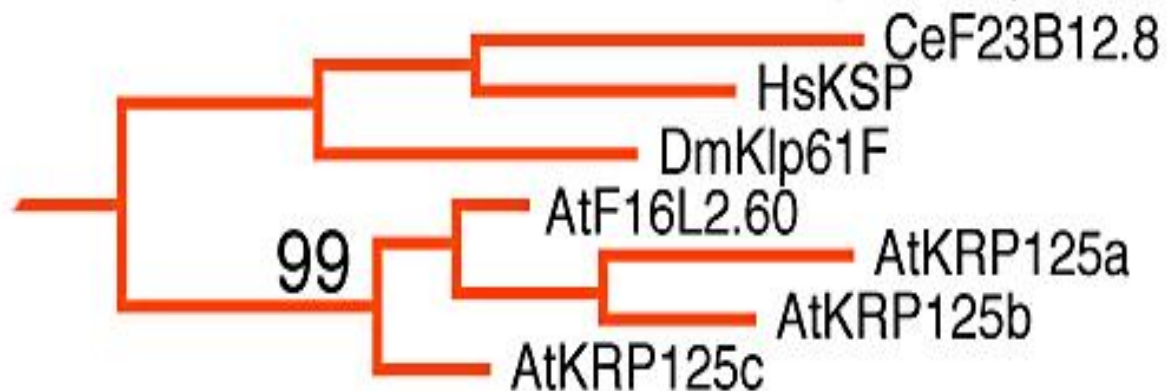
- Biology is more complex
- Not all internal nodes are divergences between species

# General idea of today

- Having all the genomes ...
- What is the **relation** of my gene to *homologous* genes in the same and other organisms (what are the relations within the gene family)

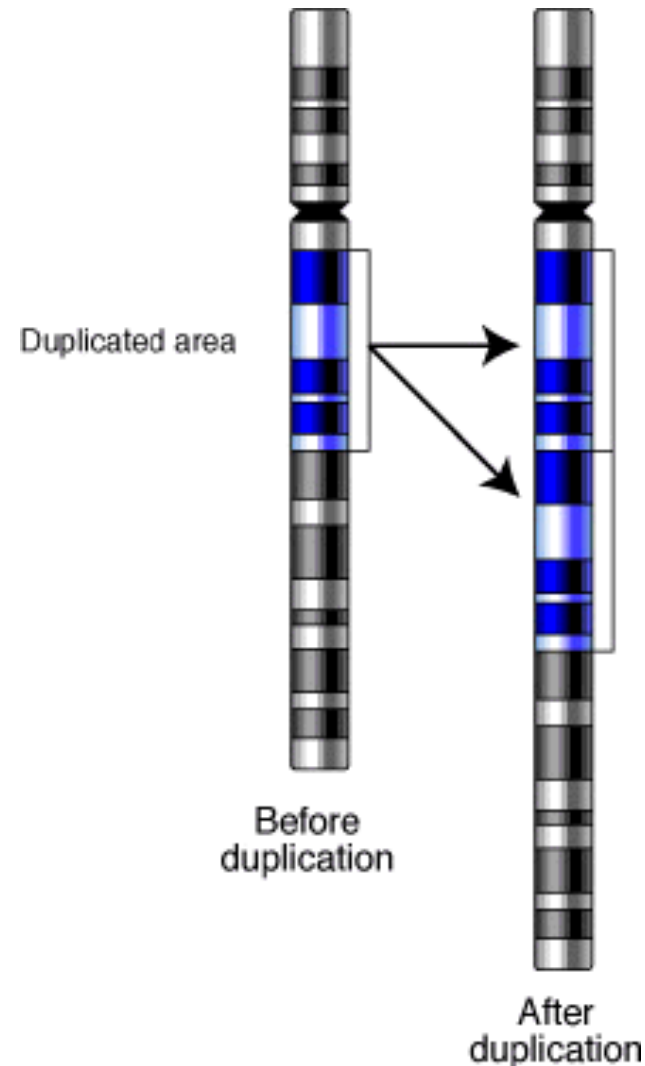


# Not just divergence between species; what is up here?



**Kinase-5:** essential for centrosome separation in mitosis

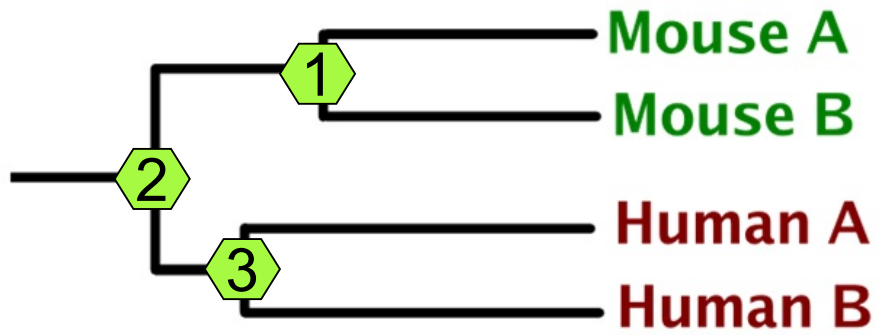
**Gene  
duplication**  
is the duplication  
of a region of DNA  
that contains a  
gene  
(important force in  
evolution of gene  
families / genome  
evolution)



# Two genes per species: how to differentiate between one ancient or two recent duplications?

- Two genes in Human chromosomes ( Human A & Human B) & two genes in mouse chromosomes (Mouse A & Mouse B)

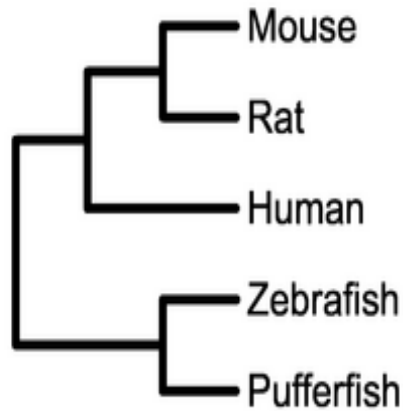
# Duplications, Speciations



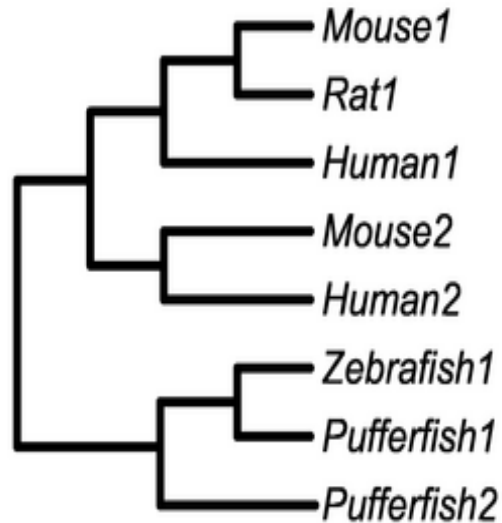
● Speciation    ■ Gene Duplication

# One more genome evolution process / gene family evolution process: what is up here? (besides duplication & speciation)

(a) Species Tree



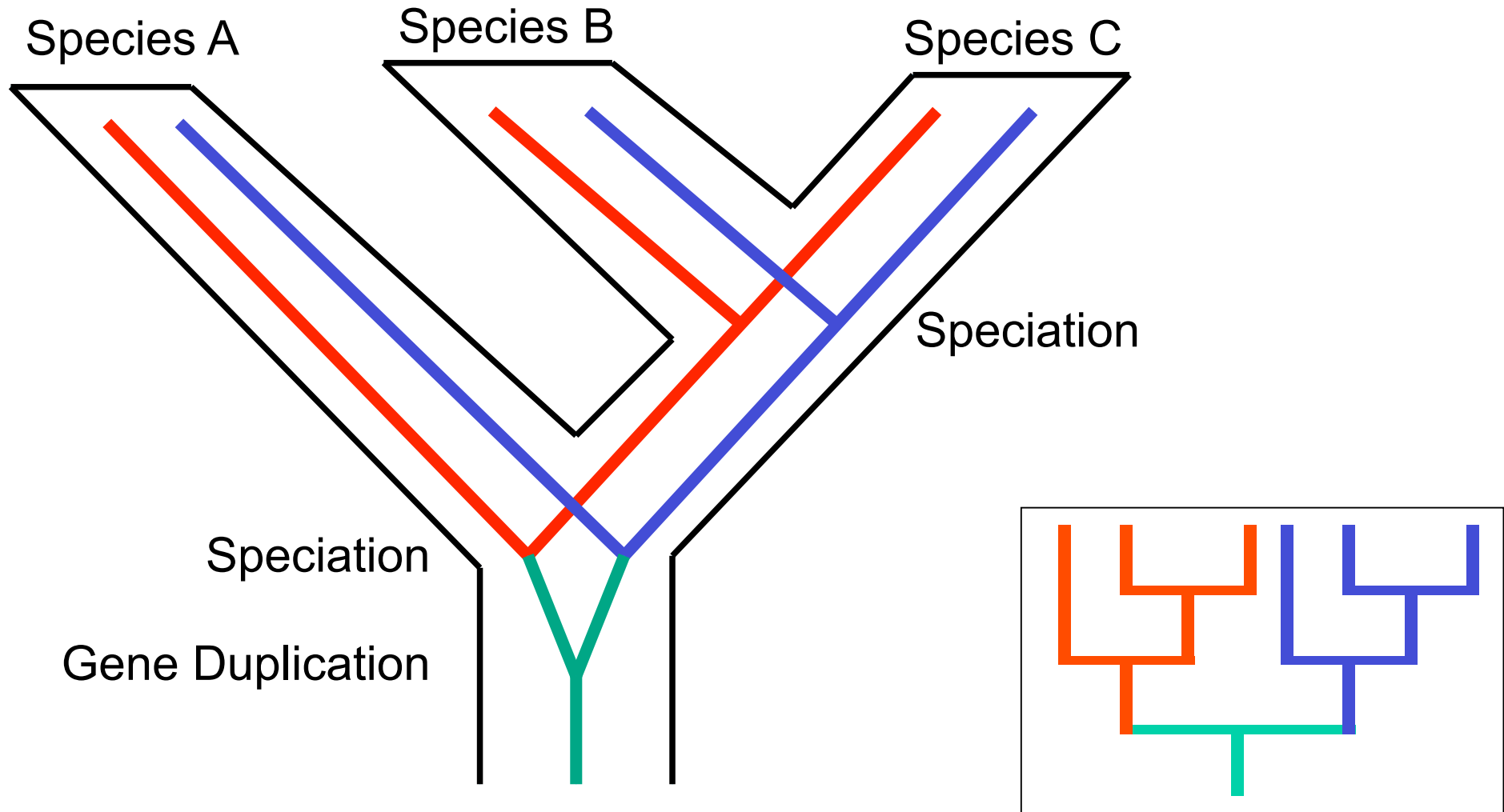
(b) Gene Tree



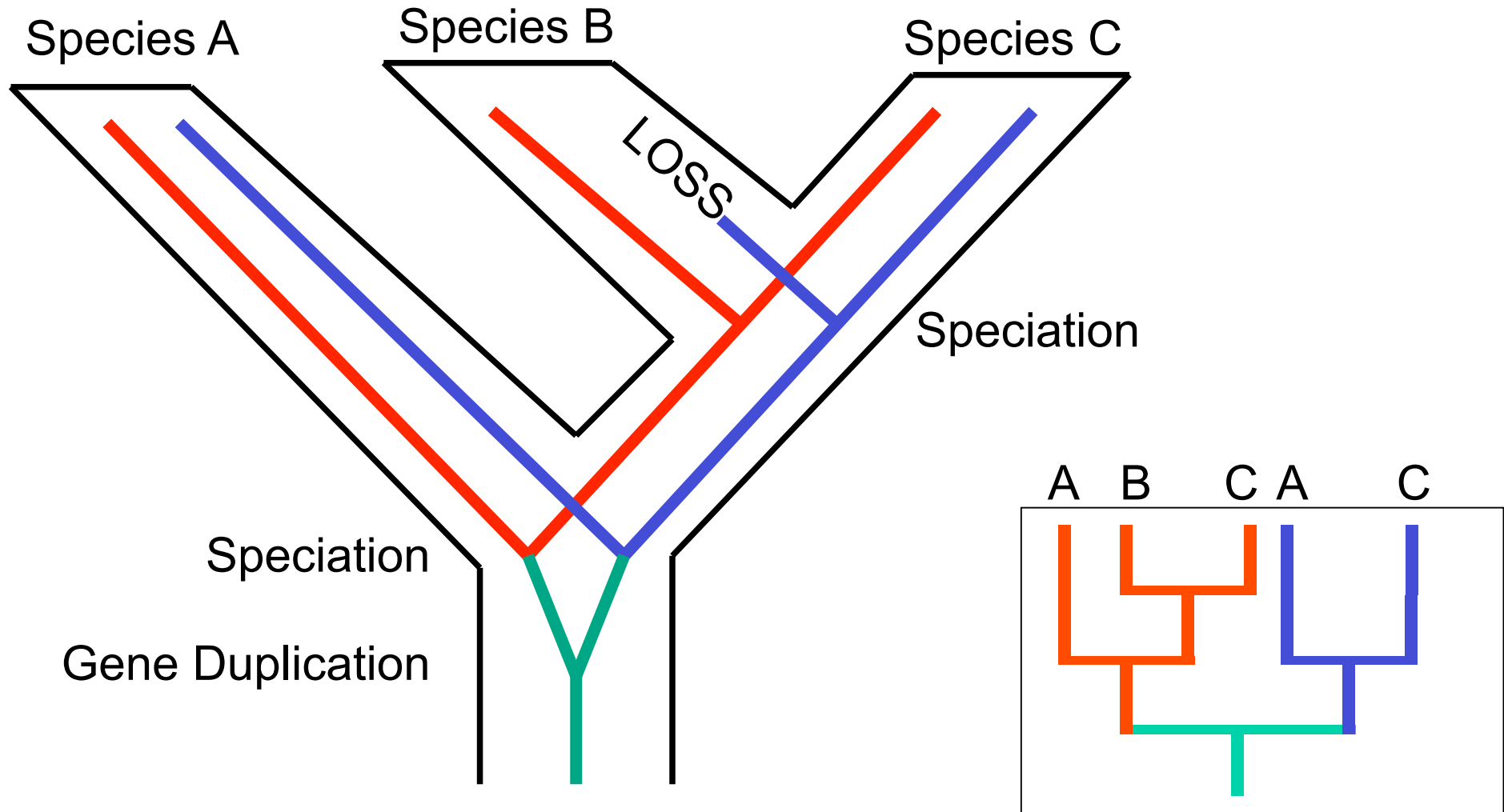
**Gene loss**



# Interpreting the tree: duplications vs speciations, gene tree inside species tree



# Interpreting the tree: duplications vs speciations, gene tree inside species tree loss

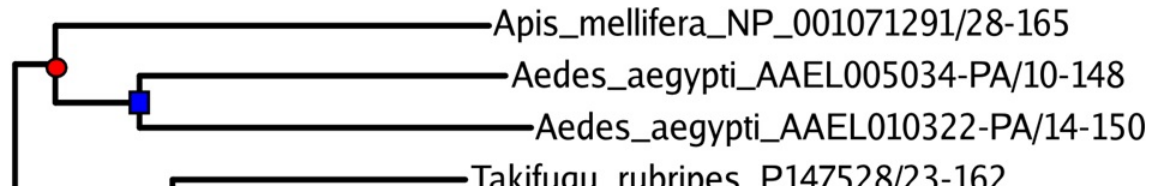


# Blast with a newly sequenced globin from frog

What kind of globin is it?

NEW	gi ...	description	E-value	bit score	U/UG
NEW	gi 56753437 gb AAW24922.1	SJCHGC09035 protein [Schistosoma japo	82.4	1e-14	U
NEW	gi 115913844 ref XP_001199205.1	PREDICTED: similar to polyme...	77.8	3e-13	UG
NEW	gi 32171394 sp Q90W04 NGB_TETNG	Neuroglobin >gi 15387694 emb ...	76.6	7e-13	UG
NEW	gi 71896523 ref NP_001025522.1	neuroglobin [Xenopus tropical...	75.9	1e-12	UG
NEW	gi 22001639 sp Q9M593 HBL_ZEAMP	Non-symbiotic hemoglobin (Hbt...	72.8	1e-11	
NEW	gi 82122237 sp Q575T0 CYGB1_ORYLA	Cytoglobin-1 >gi 62176936 e...	72.4	1e-11	
NEW	gi 74058375 gb AAZ98790.1	hemoglobin 2 [Zea mays]	72.0	2e-11	UG
NEW	gi 32171405 sp P59742 NGB1_ONCMY	Neuroglobin-1 >gi 28569676 e...	71.2	3e-11	
NEW	gi 22001638 sp Q9FY42 HBL_MAIZE	Non-symbiotic hemoglobin (Hbm...	70.9	3e-11	
NEW	gi 62176942 emb CAG25613.1	cytoglobin-1 [Tetraodon nigroviridis	70.9	3e-11	
NEW	gi 77799654 dbj BAE46739.1	nonsymbiotic hemoglobin [Lotus japon	70.9	4e-11	U
NEW	gi 18859087 ref NP_571928.1	neuroglobin [Danio rerio] >gi 12...	70.5	5e-11	UG
NEW	gi 62548111 gb AAZ86687.1	non-symbiotic hemoglobin protein [Gos	69.7	9e-11	U
NEW	gi 22001643 sp Q947C5 HBL1_GOSHI	Non-symbiotic hemoglobin 1 (...	68.9	2e-10	
NEW	gi 78486584 ref NP_001030592.1	neuroglobin [Monodelphis dome...	68.2	3e-10	UG
NEW	gi 47219636 emb CAG02681.1	unnamed protein product [Tetraodon n	68.2	3e-10	
NEW	gi 22001642 sp Q941Q2 HBL2_BRANA	Non-symbiotic hemoglobin 2 (...	67.8	3e-10	
NEW	gi 32171406 sp P59743 NGB2_ONCMY	Neuroglobin-2 >gi 28569678 e...	67.8	3e-10	
NEW	gi 118595771 sp P02206 MYG_HETPO	Myoglobin	67.4	4e-10	
NEW	gi 71895963 ref NP_001026722.1	neuroglobin [Gallus gallus] >...	67.0	5e-10	UG
NEW	gi 23308615 ref NP_694484.1	cytoglobin [Danio rerio] >gi 180...	67.0	6e-10	UG
NEW	gi 118572636 sp Q8UUR3 CYGB1_BRARE	Cytoglobin-1 >gi 63101374 ...	66.6	6e-10	G
NEW	gi 134025076 gb AAI35091.1	Cygb2 protein [Danio rerio]	65.9	1e-09	
NEW	gi 37903656 gb AAP57676.1	non-symbiotic hemoglobin class 1 [Mal	65.9	1e-09	U
NEW	gi 68438057 ref XP_700223.1	PREDICTED: cytoglobin-2 [Danio r...	65.9	1e-09	UG
NEW	gi 30909306 gb AAP37043.1	nonsymbiotic hemoglobin [Raphanus sat	65.1	2e-09	
NEW	gi 33590381 gb AAQ22728.1	non-symbiotic hemoglobin class 1 [Eur	65.1	2e-09	
NEW	gi 15226675 ref NP_179204.1	AHB1 [Arabidopsis thaliana] >gi ...	64.3	4e-09	UG
NEW	gi 22001646 sp Q9FVL0 HBL1_MEDSA	Non-symbiotic hemoglobin 1 (...	63.9	5e-09	
NEW	gi 118572288 sp Q575S9 CYGB2_ORYLA	Cytoglobin-2	63.5	6e-09	
NEW	gi 37903668 gb AAP57677.1	non-symbiotic hemoglobin class 1 [Pyr	63.5	7e-09	
NEW	gi 62176938 emb CAG25611.1	cytoglobin-2 [Oryzias latipes]	63.5	7e-09	U

# Globins



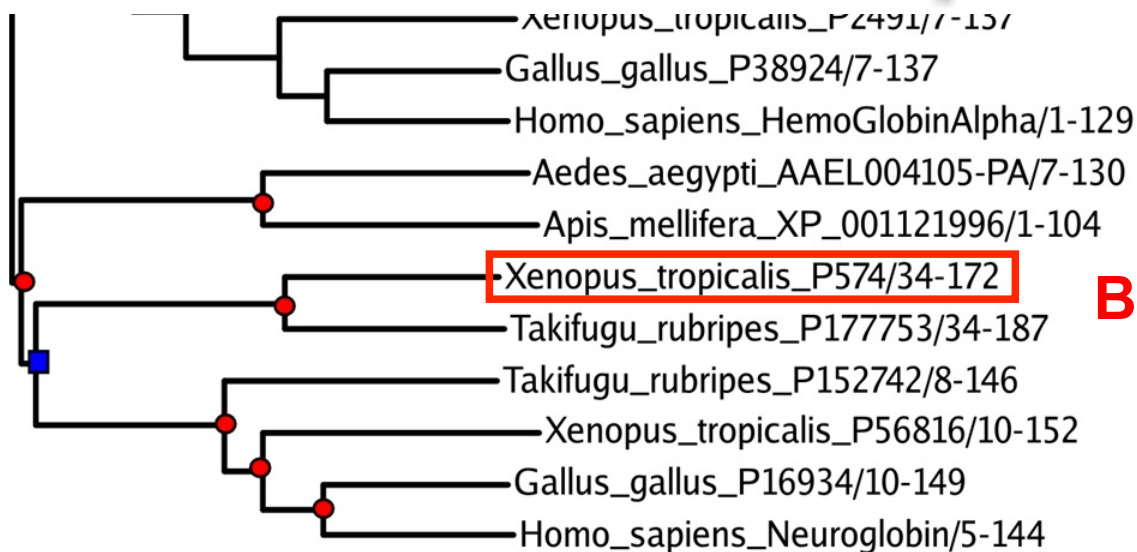
## A Globin Gene of Ancient Evolutionary Origin in Lower Vertebrates: Evidence for Two Distinct Globin Families in Animals

Anja Roesner,\* Christine Fuchs,† Thomas Hankehn,† and Thorsten Burmester\*

\*Institute of Zoology, Johannes Gutenberg University, Mainz, Germany; and †Institute of Molecular Genetics, Johannes-Gutenberg-University, Mainz, Germany

Hemoglobin, myoglobin, neuroglobin, and cytoglobin are four types of vertebrate globins with distinct tissue distributions and functions. Here, we report the identification of a fifth and novel globin gene from fish and amphibians, which has apparently been lost in the evolution of higher vertebrates (Amniota). Because its function is presently unknown, we tentatively call it globin X (GbX). Globin X sequences were obtained from three fish species, the zebrafish

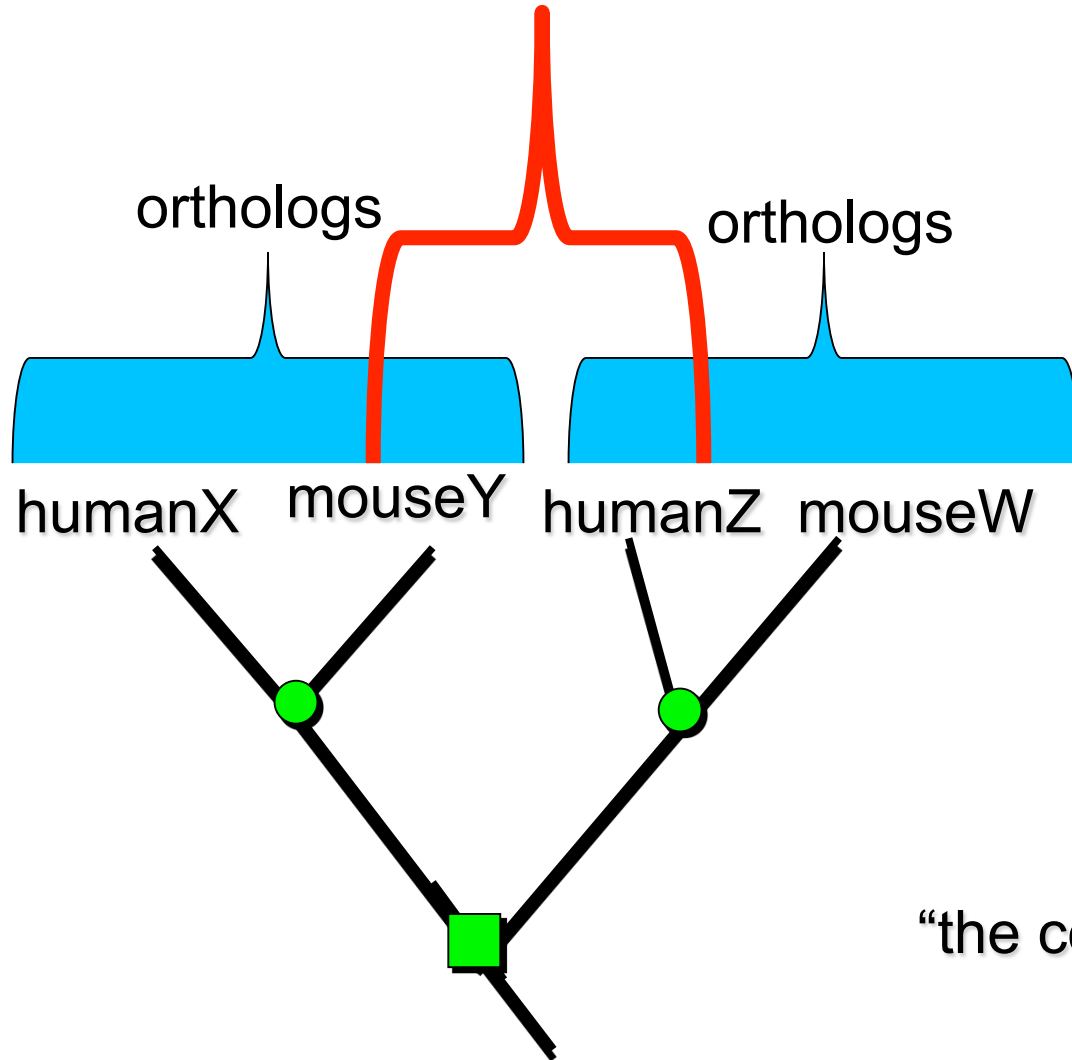
unknown, we tentatively call it globin X (GbX).



α chain / Heme  
(b) Hemoglobin

**Blast query**

NOT orthologous relative to the human-mouse speciation



Fitch 1970

Two genes in two species are orthologous if they derive from one gene in their *last* common ancestor; **This means that the “node” in the tree where they diverge is a speciation node.**

“the corresponding gene”

often have the same function

Genes can diverge by

- Speciation, or
- Duplication

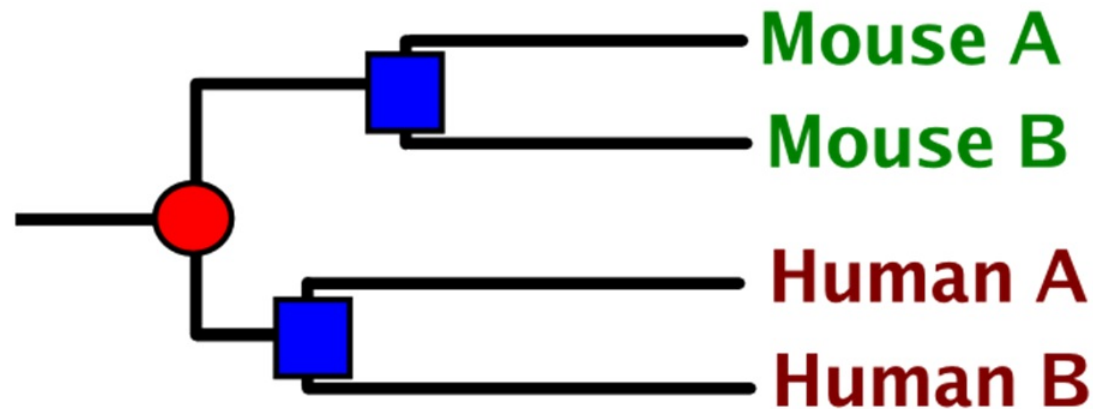
# Retraction in MBE because of duplication / speciation, orthology / paralogy

- <http://retractionwatch.wordpress.com>
- Quite simply, our study targetted specifically a comparative genomics analysis of salmonid species. However, because the whole family went through a relatively recent whole genome duplication event, sorting out paralogs from true orthologs remains a serious challenge. We realised that some targets retained in our analyses were likely to be paralogs, which could cause some biases in our results. We now need to revisit that very carefully using alternative analytical approaches /
- They wanted to compare the sequences of genes across different species, and thought that's what they had done. However, in these species, apparently a lot of genes are duplicated, such that there are two relatively similar copies (call them gene 1a and gene 1b). If you're looking at a copy of a gene in a species, it's difficult to tell whether it's gene 1a or gene 1b. So presumably what happened is that they thought they were looking at gene 1a in both species, but realized they were looking at gene 1a in one species, but gene 1b in another species. This is an easy mistake to make, and could definitely lead to major problems. Though again, without the text of the original article, it's tough to be more precise than that.



# InParalogs (/ Co-orthologs)

(Sonnhammer & Koonin TiG)

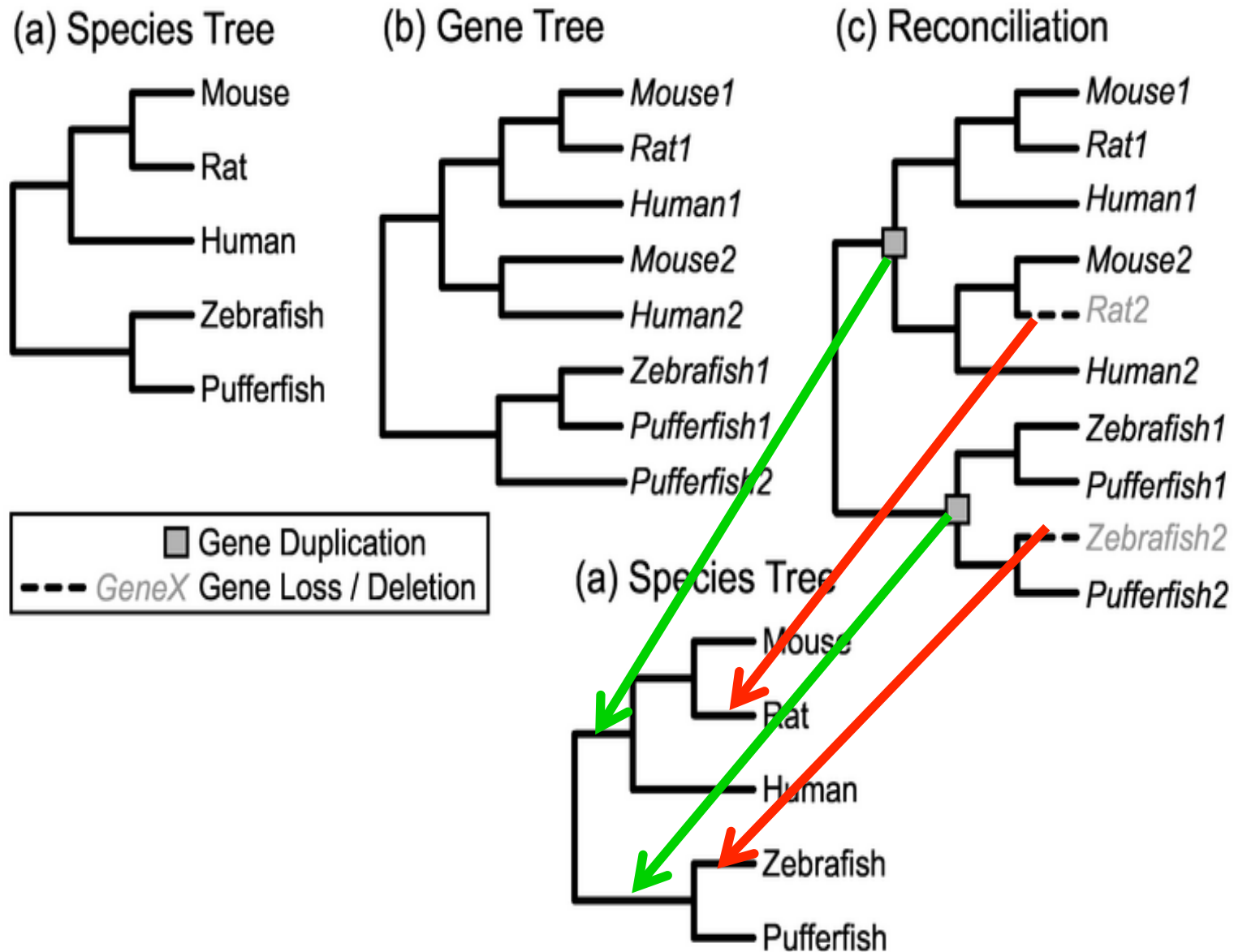


● Speciation    ■ Gene Duplication

If the node where two genes diverged was a speciation than two genes are orthologs; if it was a duplication they are paralogs

2 genes in mouse are both orthologs to two genes in human!!

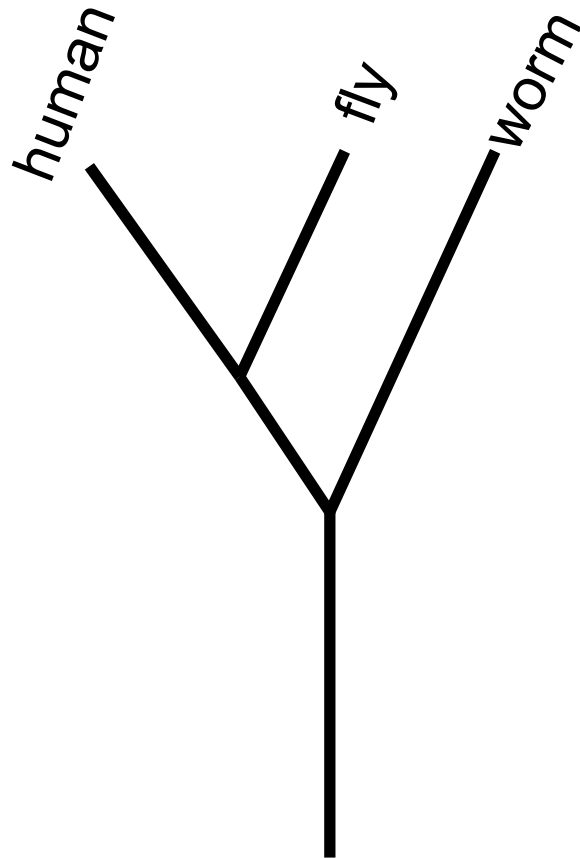
# “Phylogenetic timing of duplicates”



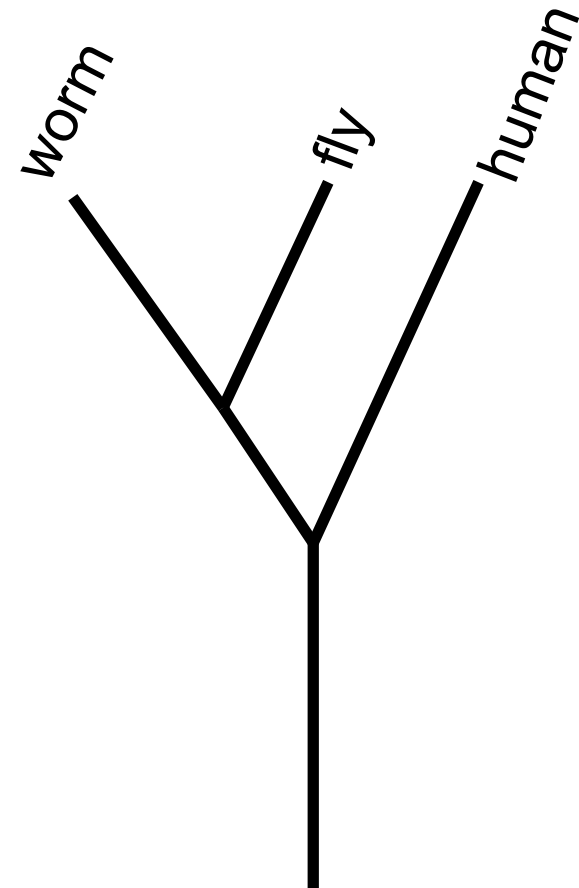


# How to time duplications and detect losses given that single gene trees are often based on too little data to reliably infer their evolutionary history?

Gene tree



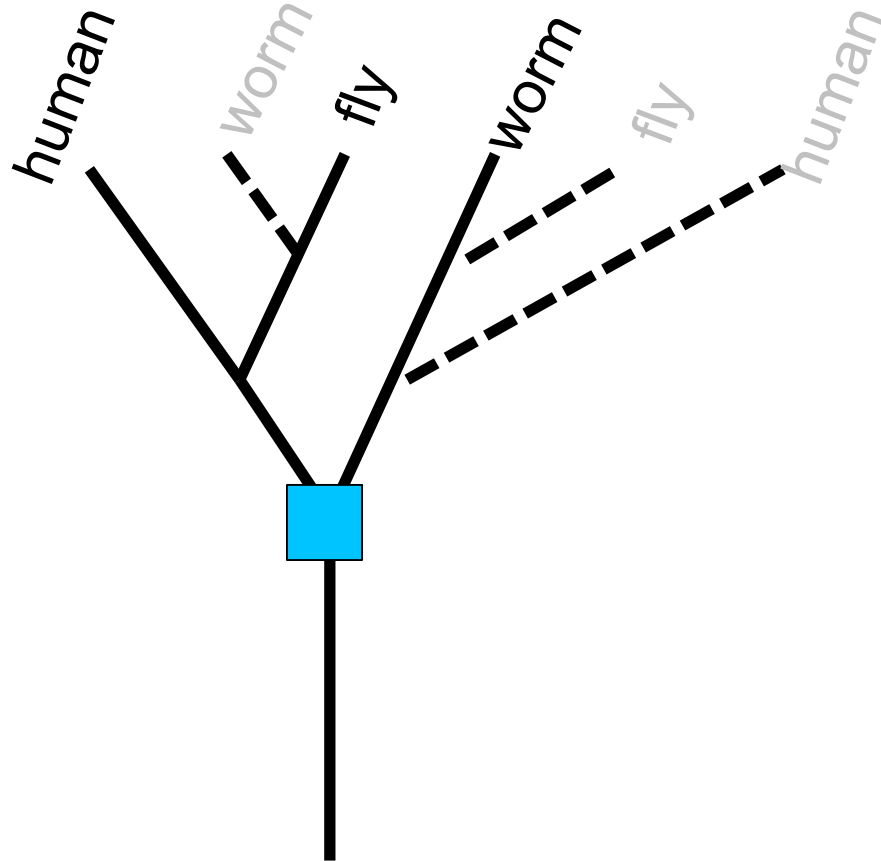
Species tree



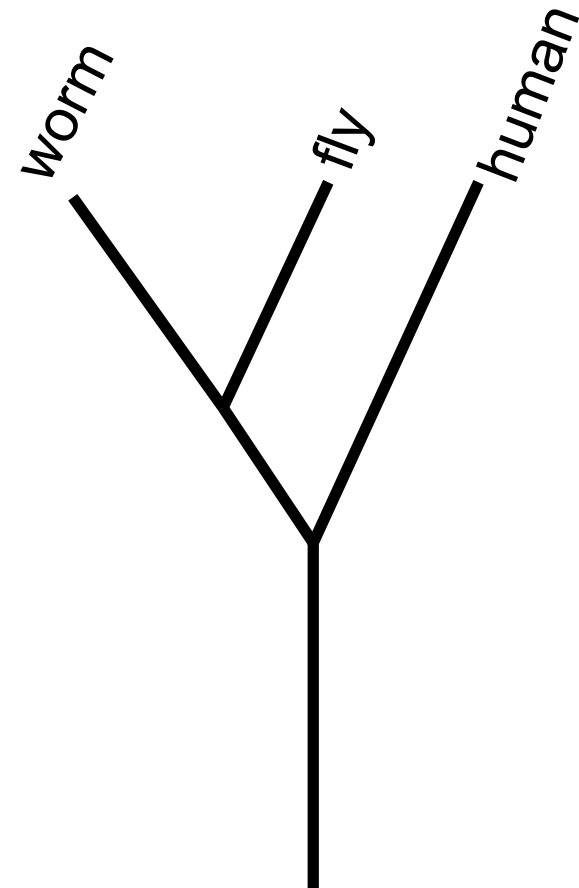
How to time duplications and detect losses given that single gene trees are often based on too little data to reliably infer their evolutionary history?

## Strict reconciliation?

Reconciled Gene tree



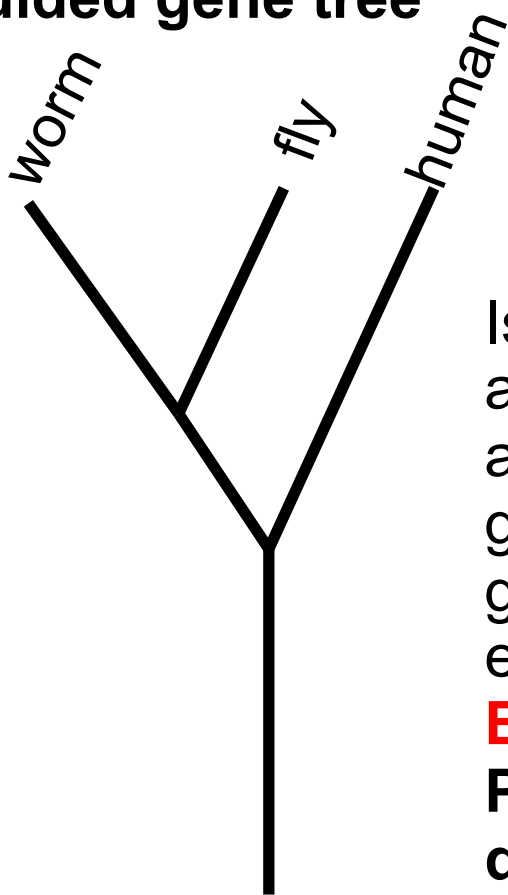
Species tree



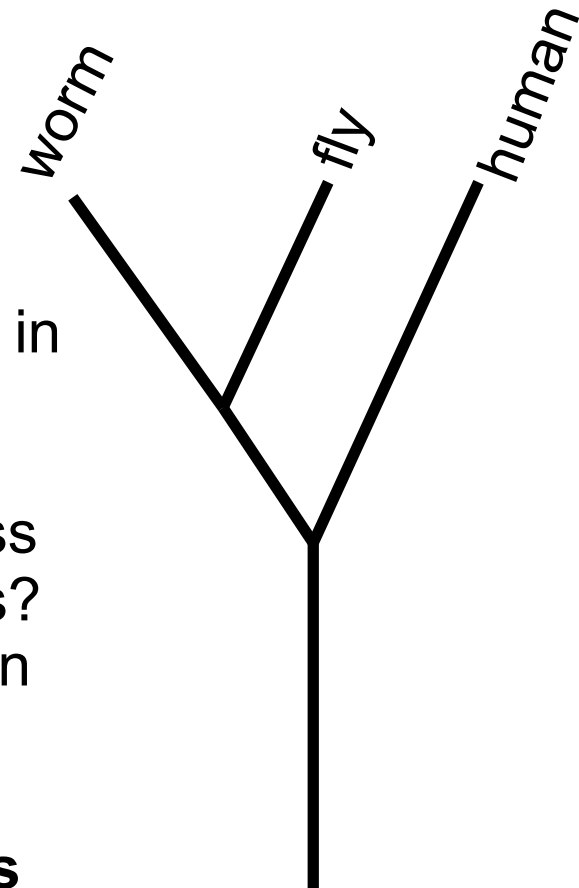
# How to time duplications and detect losses given that single gene trees are often based on too little data to reliably infer their evolutionary history?

## .... Species tree guided tree building

Species tree guided gene tree



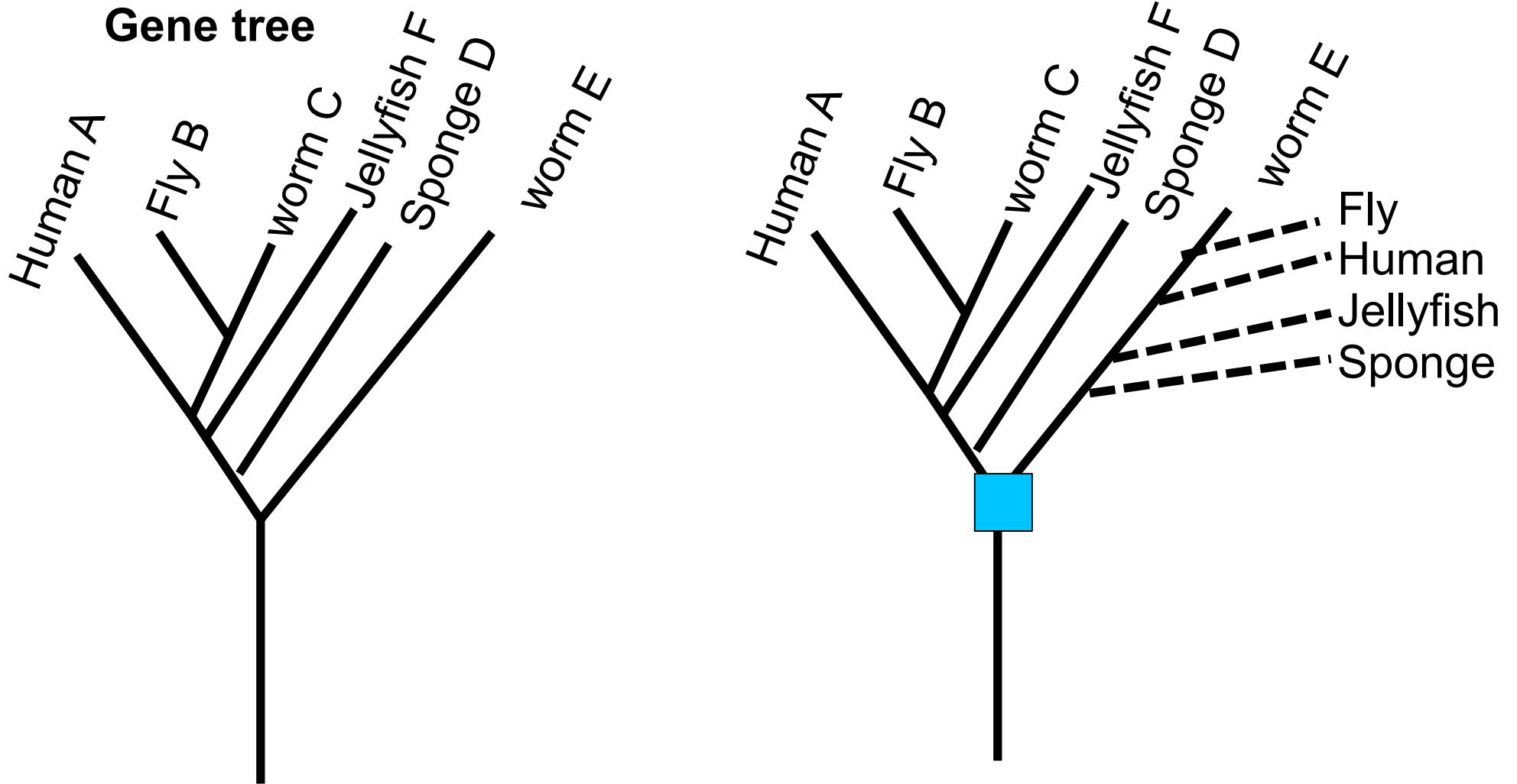
Species tree



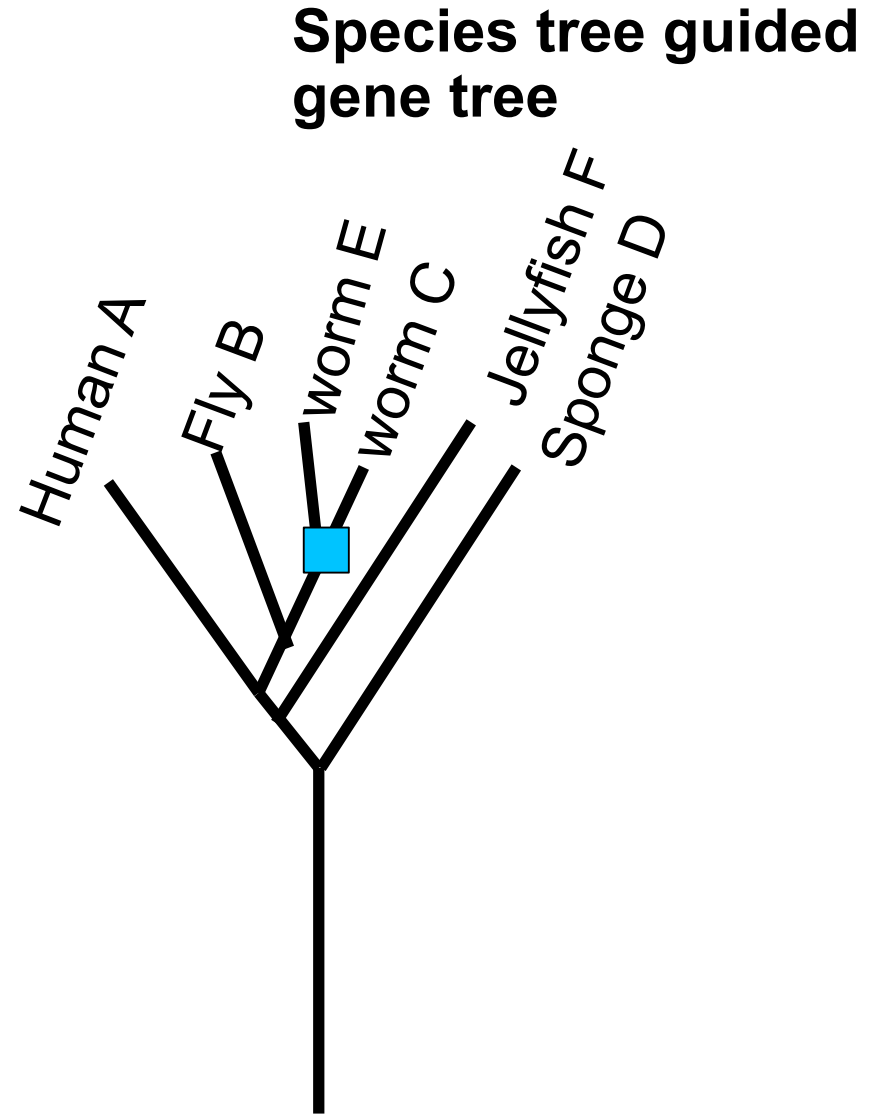
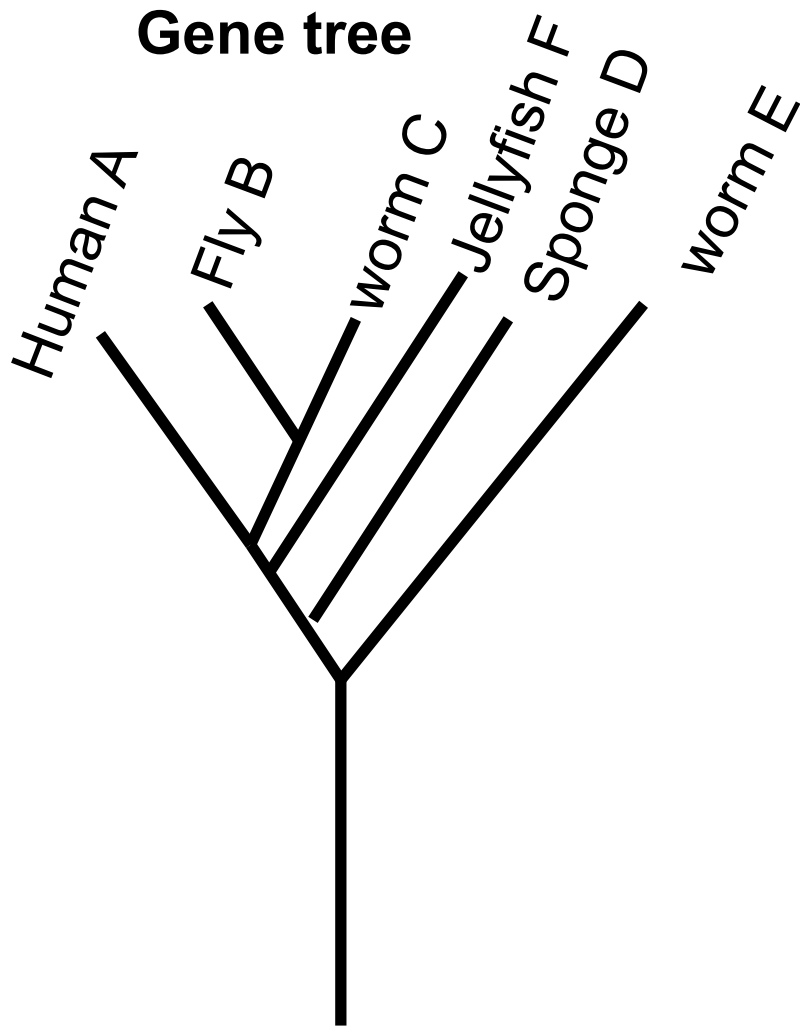
Is there significant signal in aspects of the data (the alignment) to support a gene tree that implies less genome evolution events? e.g. **TreeBEST** as used in **ENSEMBL COMPARA**  
Prevents spurious duplications and losses

# Example of difference between species tree guided reconstruction vs strict tree reconciliation for duplication

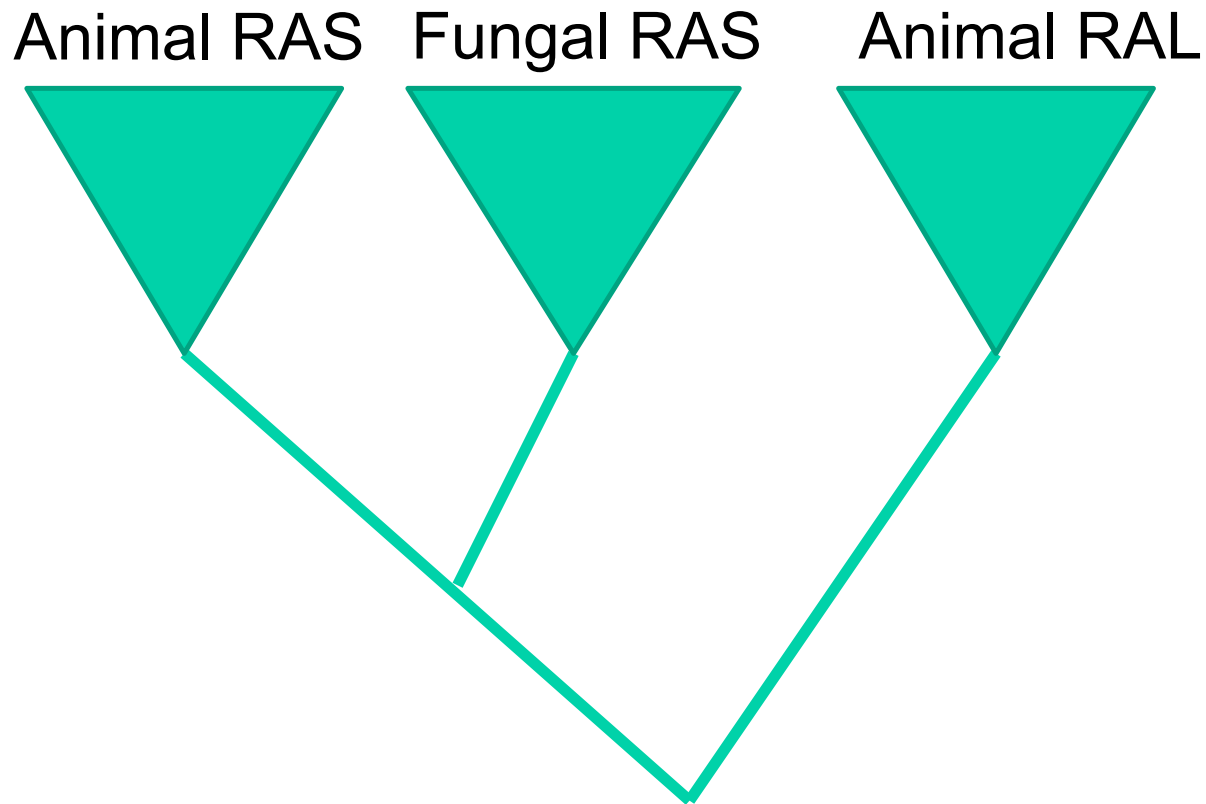
## Strict tree reconciliation



# Example of difference between species tree guided reconstruction vs strict tree reconciliation for duplication

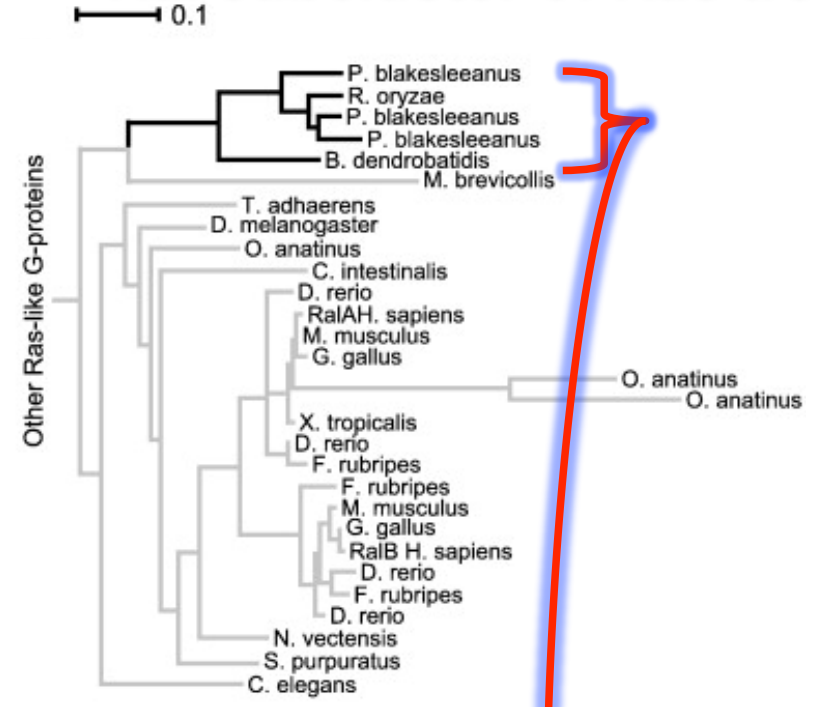
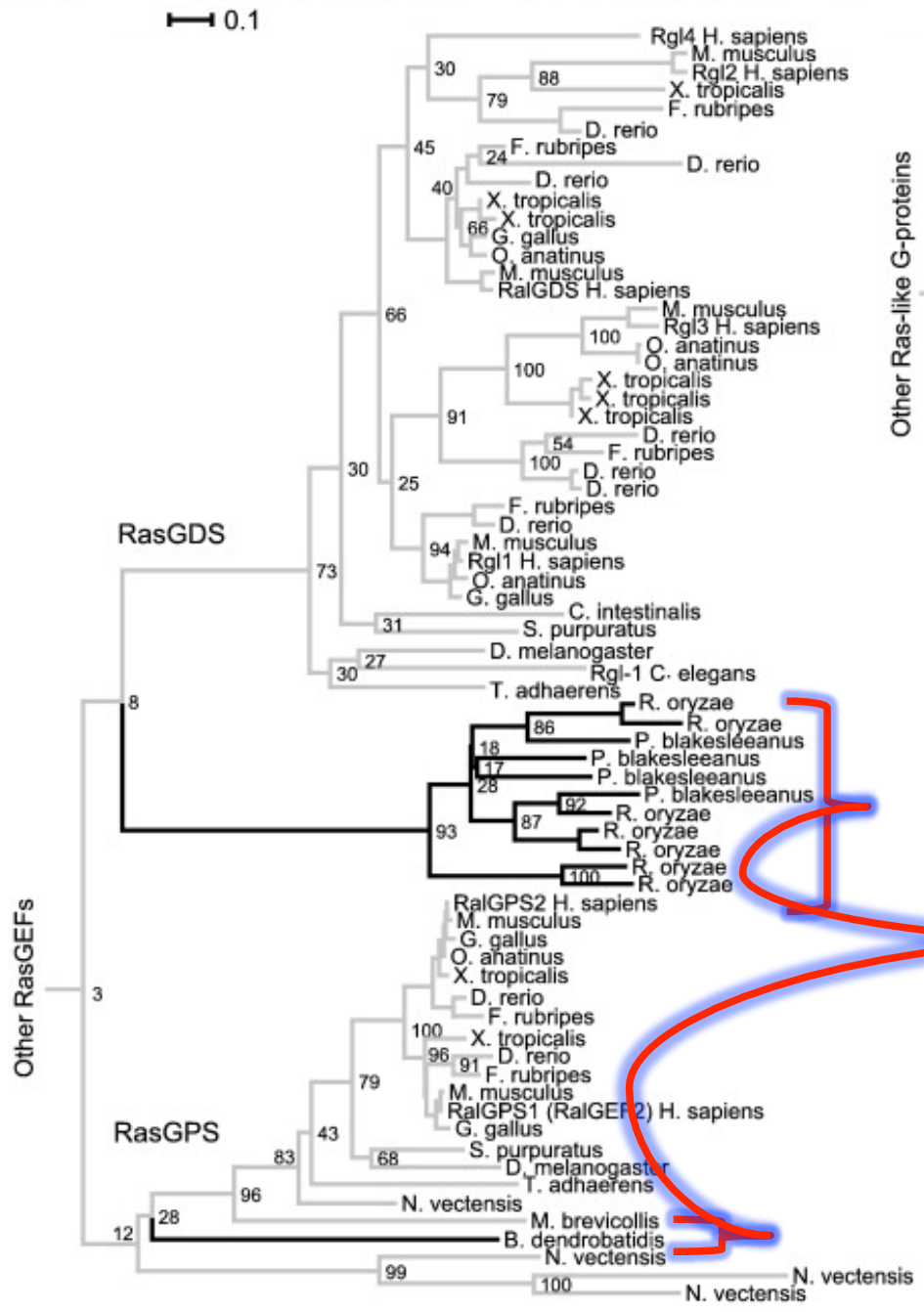


# RAL evolution?



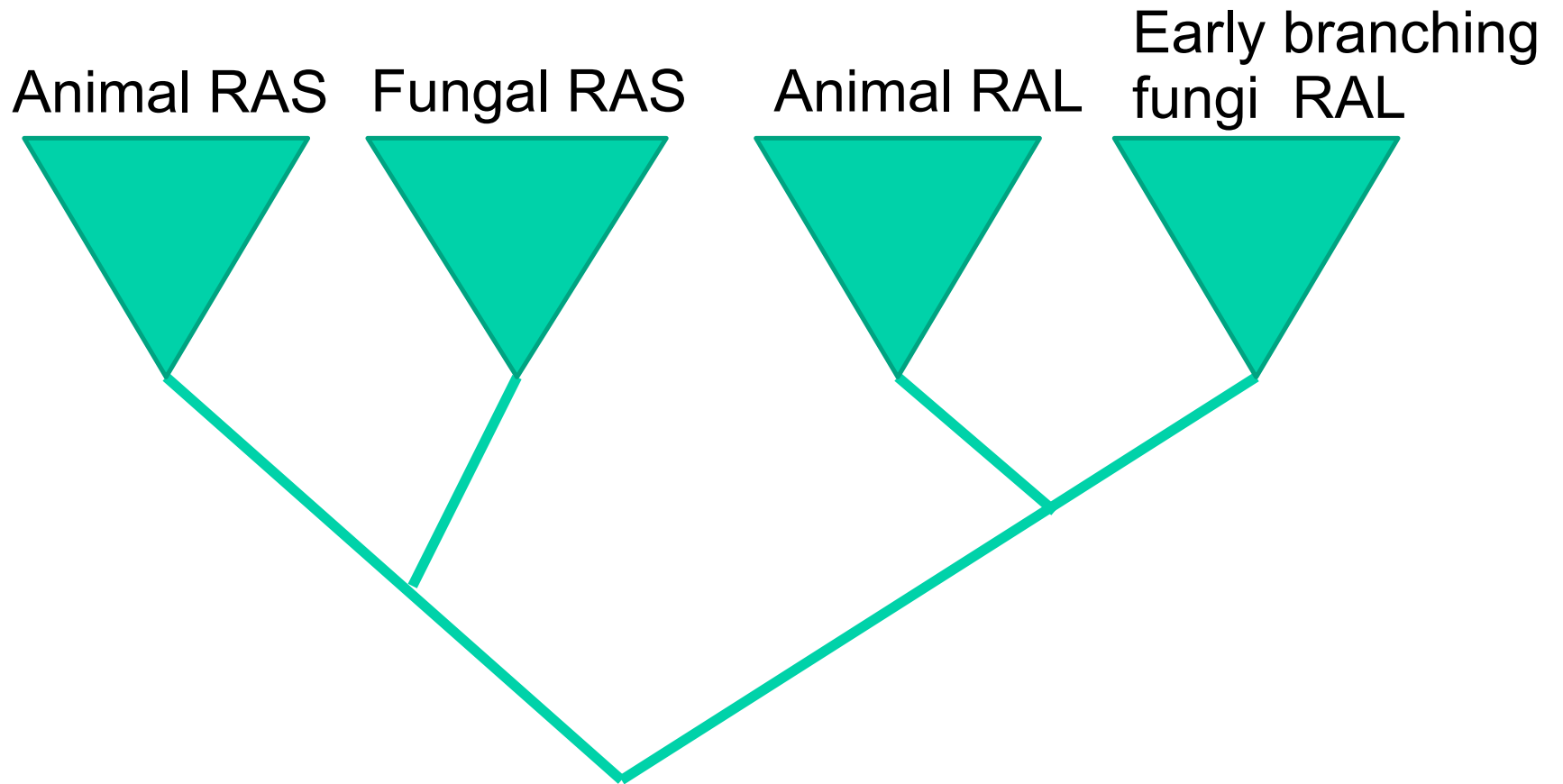
Animal invention and wrong tree ( “consensus” in the RAS field) OR old duplication and loss

# RalGEF subcluster of RasGEF tree    Ral subcluster of Ras tree



*B. dendrobatidis*  
*R. oryzae*  
*P. blakesleeanus*

# RAL evolution?

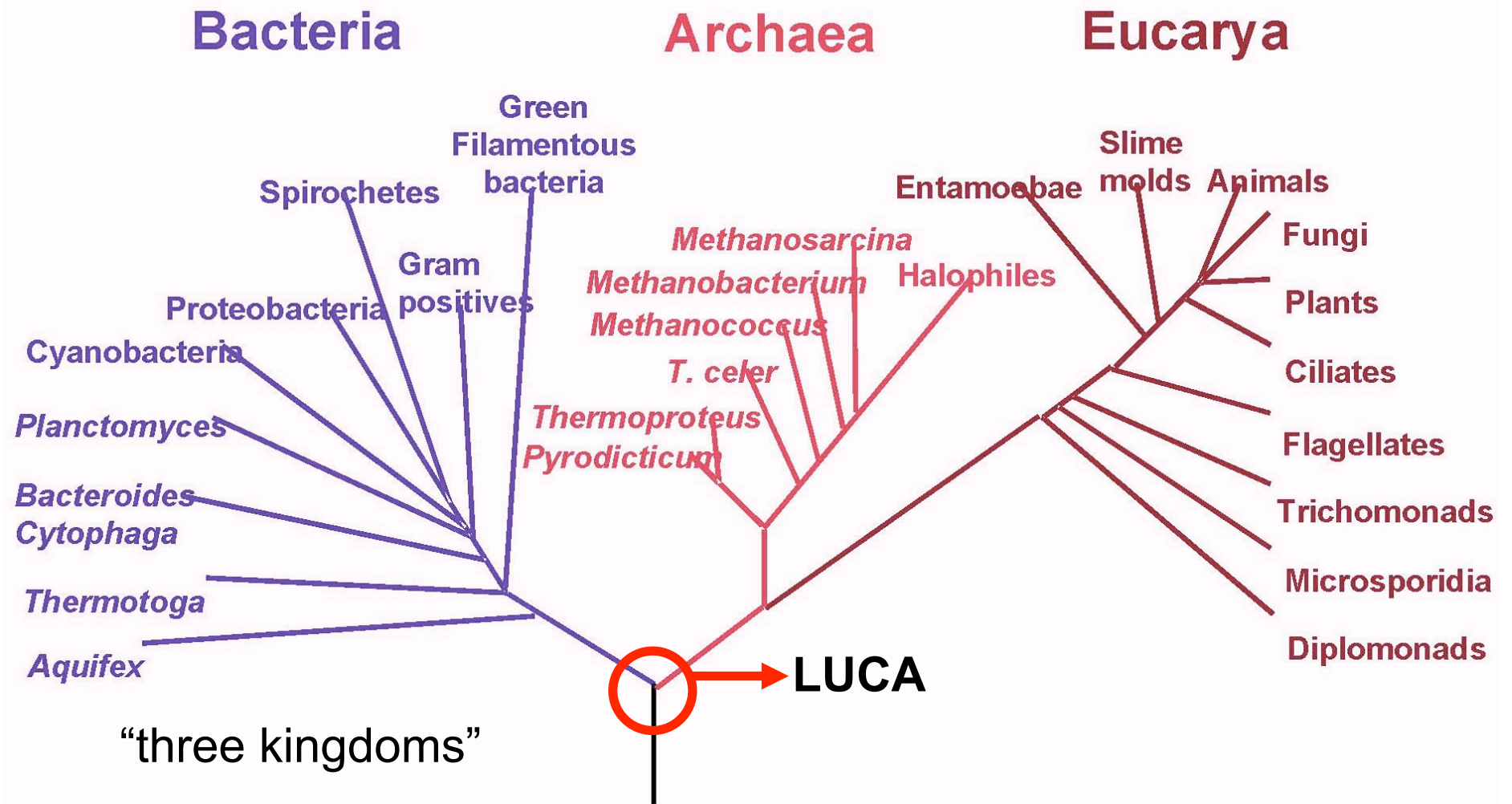


Old duplication and loss. No more OR.



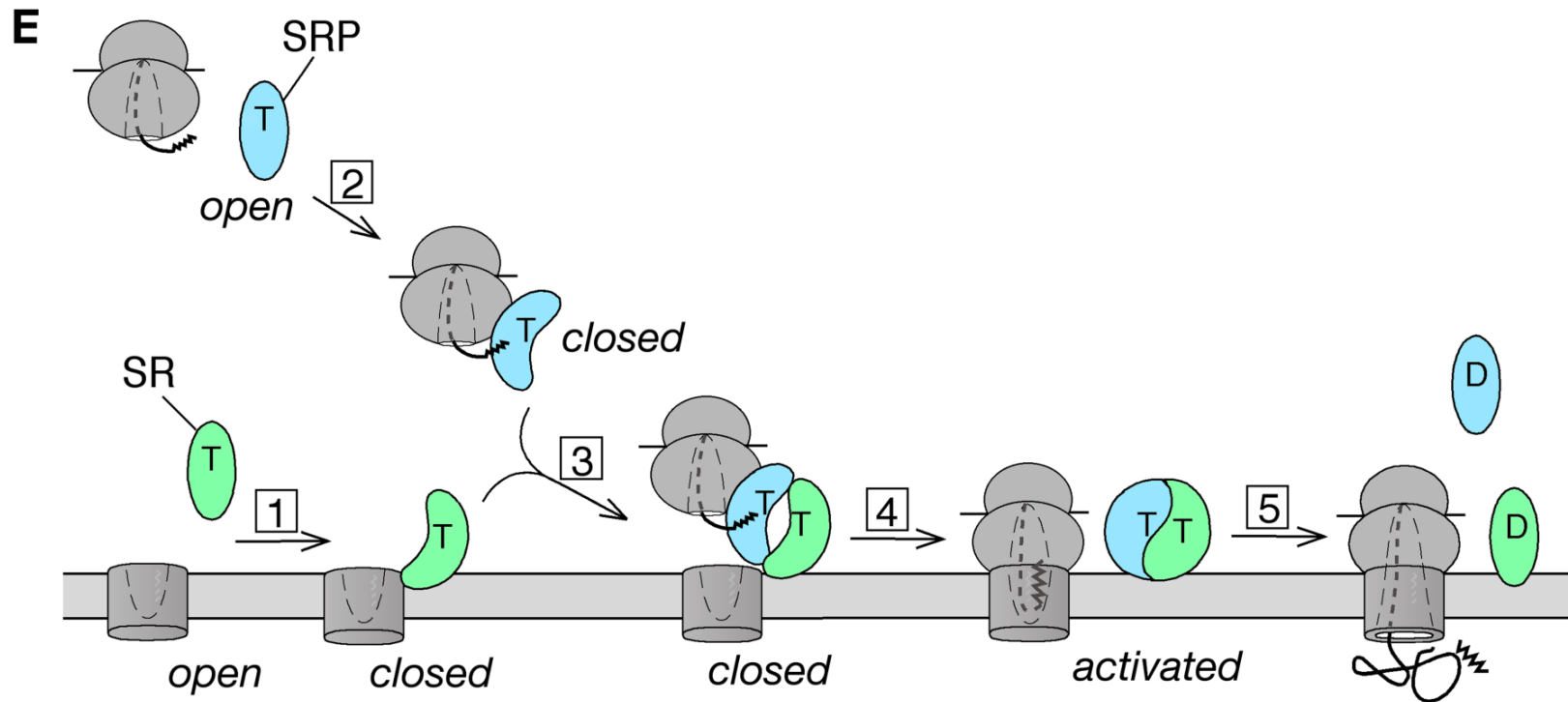
# Rooting 2: via gene duplications: a not unimportant example

## Phylogenetic Tree of Life



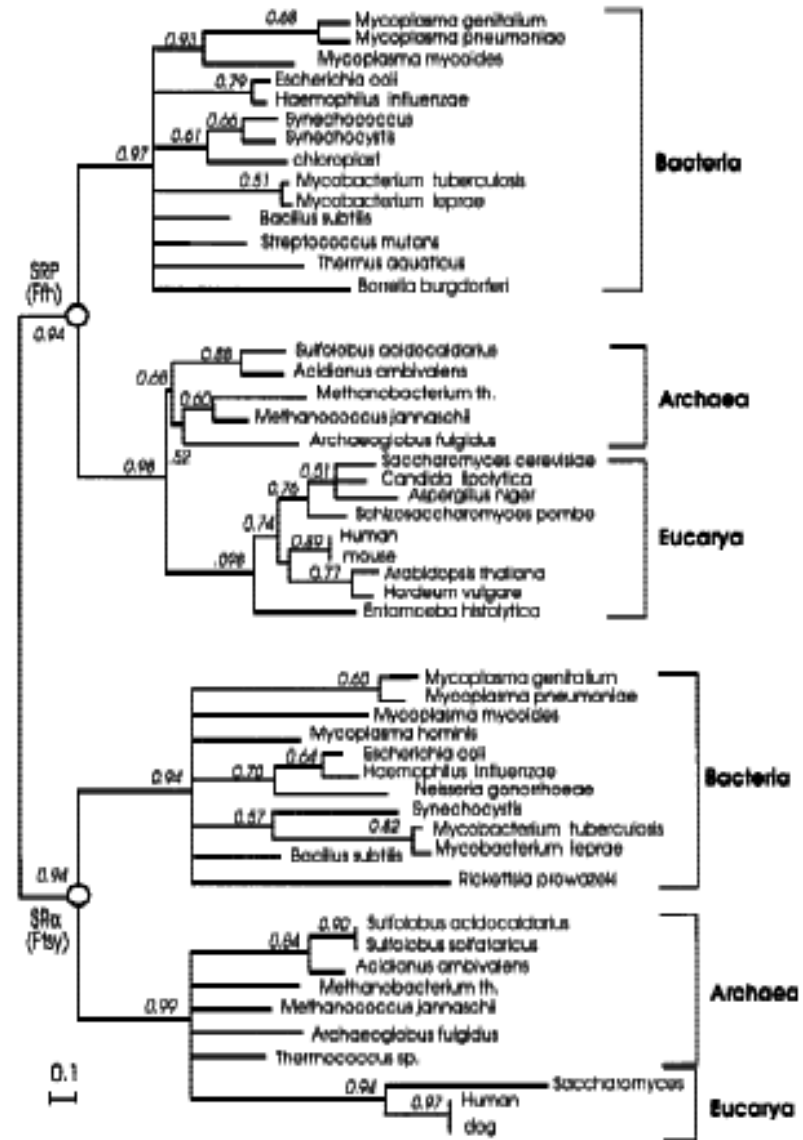
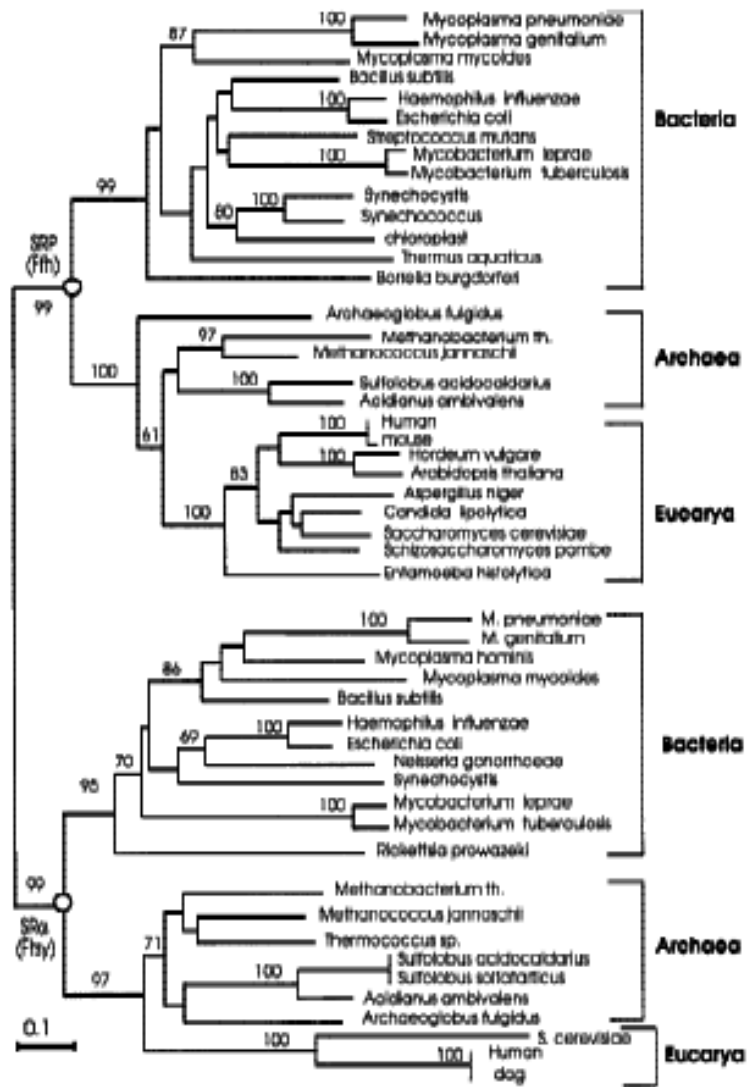
# How to root the tree of life?

## 1: Find paralogs that duplicated before the LUCA



6 found so far

# How to root the tree of life? 2: Make a tree of paralogs that duplicated before the LUCA



A poor alternative, tree reconciliation if e.g. euk vs bac & arch

