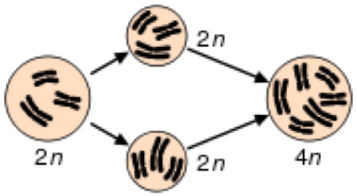
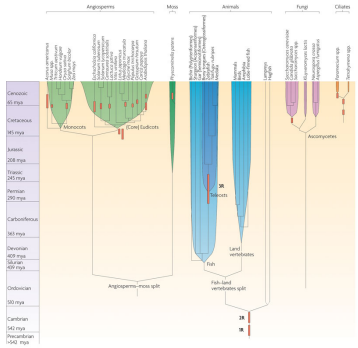
Genome duplications (polyploidy) / ancient genome duplications (paleopolyploidy)/ ancient genome hybridization (allo-paleopolyploidy)



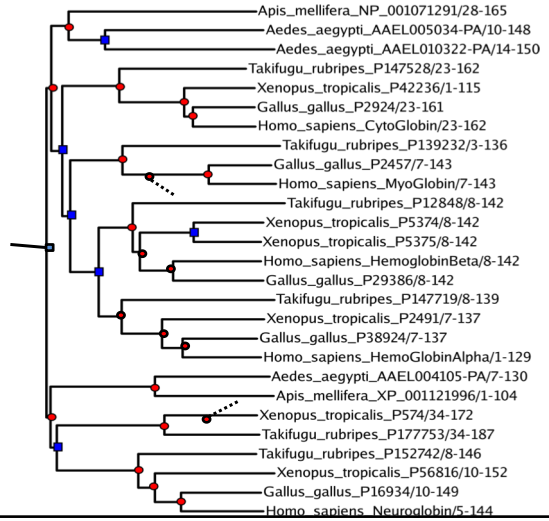
Mechanism? e.g. a diploid cell undergoes failed meiosis, producing diploid gametes, which self-fertilize to produce a tetraploid zygote.

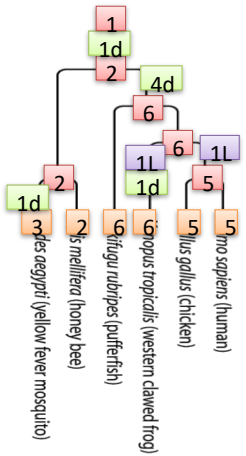
How to detect paleoploidy?



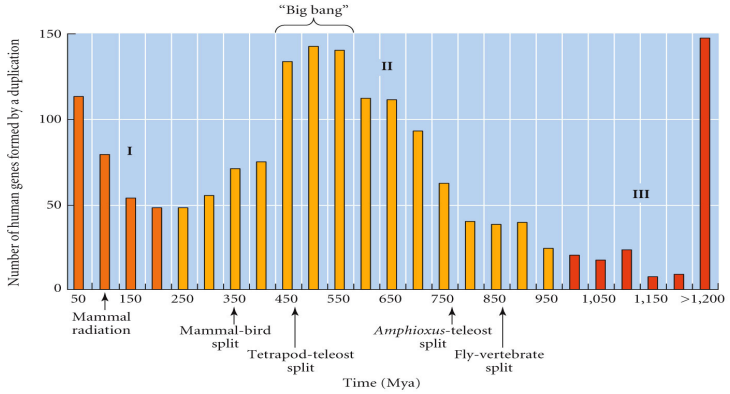
Non-sequitur? How this lecture fits in the course.

- Something to expect in gene trees.
  - If I see two paralogs in human my first guess is that they duplicated at base of vertebrares: provides scenario/search image
- *We want to detective What* has happened, this is generally difficult: here we are clear what happened because of synteny ….
- Some fringe / *in extremis* discussion of paralogy & orthology
- Much more well defined exposition of
  - Again importance of gene loss: provides nice example of expansion contraction / biphasic model of genome evolution
  - Changes in Speed of evolution





Phylogenetic timing of duplicates hints are massive duplications at the base of vertebrates

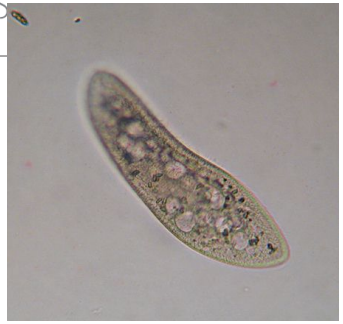


EVOLUTION 2e, Figure 20.19

Paramecium genome duplications

Vol 444|9 November 2006|doi:10.1038/nature05230 nature

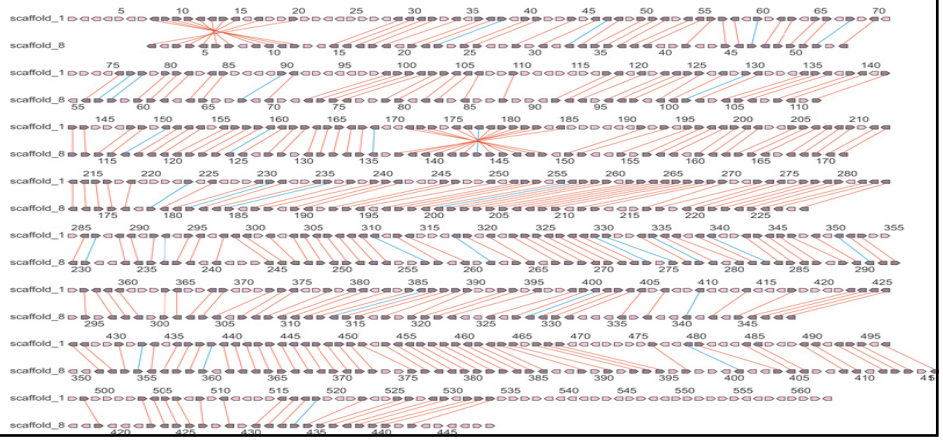
ARTICLES

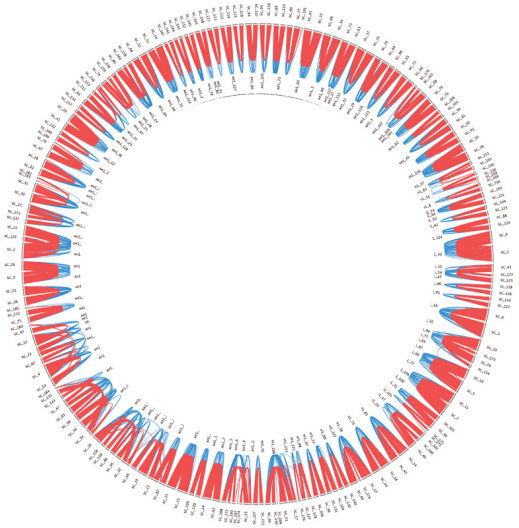


Global trends of whole-genome duplications revealed by the ciliate *Paramecium tetraurelia*

Jean-Marc Aury[1]*, Olivier Jaillon[1]*, Laurent Duret[2], Benjamin Noel[1], Claire Jubin[1], Betina M. Porcel[1], Béatrice Ségurens[1], Vincent Daubin[2], Véronique Anthouard[1], Nathalie Aiach[1], Olivier Arnaiz[3], Alain Billaut[1], Janine Beisson[3], Isabelle Blanc[3], Khaled Bouhouche[4], Francisco Câmara[5], Sandra Duharcourt[4], Roderic Guigo[5], Delphine Gogendeau[3], Michael Katinka[1], Anne-Marie Keller[3], Roland Kissmehl[6], Catherine Klotz[3], France Koll[3], Anne Le Mouël[4], Gersende Lepère[4], Sophie Malinsky[4], Mariusz Nowacki[4], Jacek K. Nowak[7], Helmut Plattner[6], Julie Poulain[1], Françoise Ruiz[3], Vincent Serrano[4], Marek Zagulski[7], Philippe Dessen[8], Mireille Bétermier[3,4], Jean Weissenbach[1], Claude Scarpelli[1], Vincent Schächter[1], Linda Sperling[3], Eric Meyer[4], Jean Cohen[3] & Patrick Wincker[1]

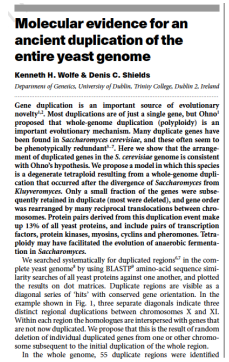
Comparison of two scaffolds originating from a common ancestor at the recent WGD





Whole genome (all scaffolds) can be aligned to itself

Saccharomyces cerevisiae



Molecular evidence for an ancient duplication of the entire yeast genome

Kenneth H. Wolfe & Denis C. Shields

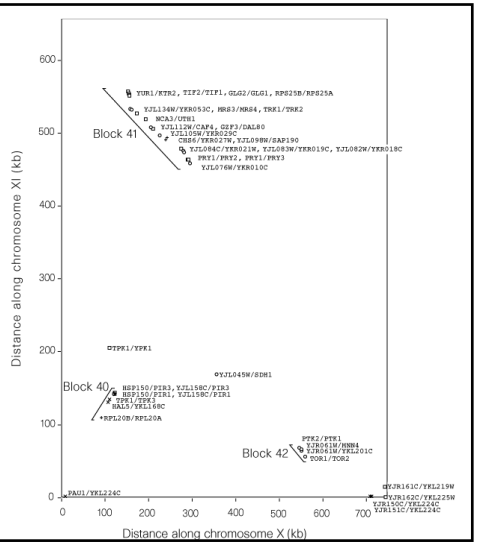
Department of Genetics, University of Dublin, Trinity College, Dublin 2, Ireland

Gene duplication is an important source of evolutionary novelty[1,2]. Most duplications are of just a single gene, but Ohno[1] proposed that whole-genome duplication (polyploidy) is an important evolutionary mechanism. Many duplicate genes have been found in *Saccharomyces cerevisiae*, and these often seem to be phenotypically redundant[3–7]. Here we show that the arrangement of duplicated genes in the *S. cerevisiae* genome is consistent with Ohno's hypothesis. We propose a model in which this species is a degenerate tetraploid resulting from a whole-genome duplication that occurred after the divergence of *Saccharomyces* from *Kluyveromyces*. Only a small fraction of the genes were subsequently retained in duplicate (most were deleted), and gene order was rearranged by many reciprocal translocations between chromosomes. Protein pairs derived from this duplication event make up 13% of all yeast proteins, and include pairs of transcription factors, protein kinases, myosins, cyclins and pheromones. Tetraploidy may have facilitated the evolution of anaerobic fermentation in *Saccharomyces*.

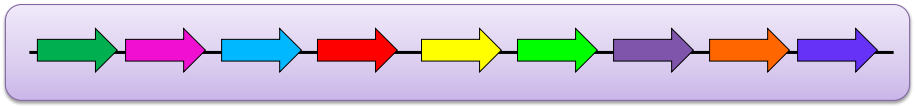
We searched systematically for duplicated regions[8,9] in the complete yeast genome[2] by using BLAST[10] amino-acid sequence similarity searches of all yeast proteins against one another, and plotted the results on dot matrices. Duplicate regions are visible as a diagonal series of 'hits' with conserved gene orientation. In the example shown in Fig. 1, three separate diagonals indicate three distinct regional duplications between chromosomes X and XI. Within each region the homologues are interspersed with genes that are not now duplicated. We propose that this is the result of random deletion of individual duplicated genes from one or other chromosome subsequent to the initial duplication of the whole region.

In the whole genome, 55 duplicate regions were identified

NATURE | VOL 387 | 12 JUNE 1997



Just before genome duplication



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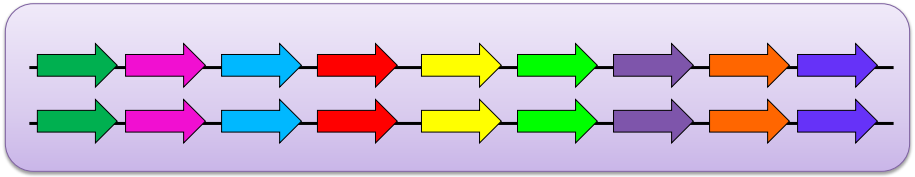
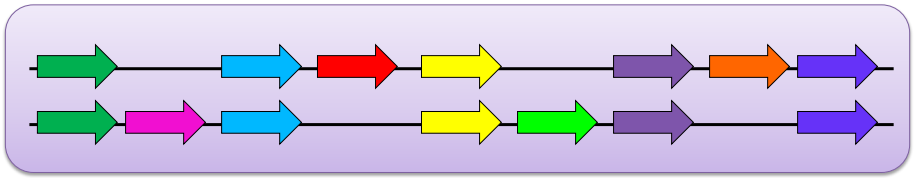
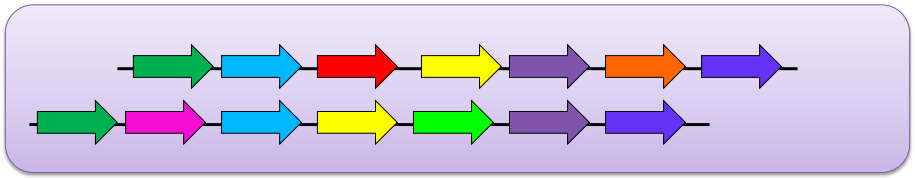
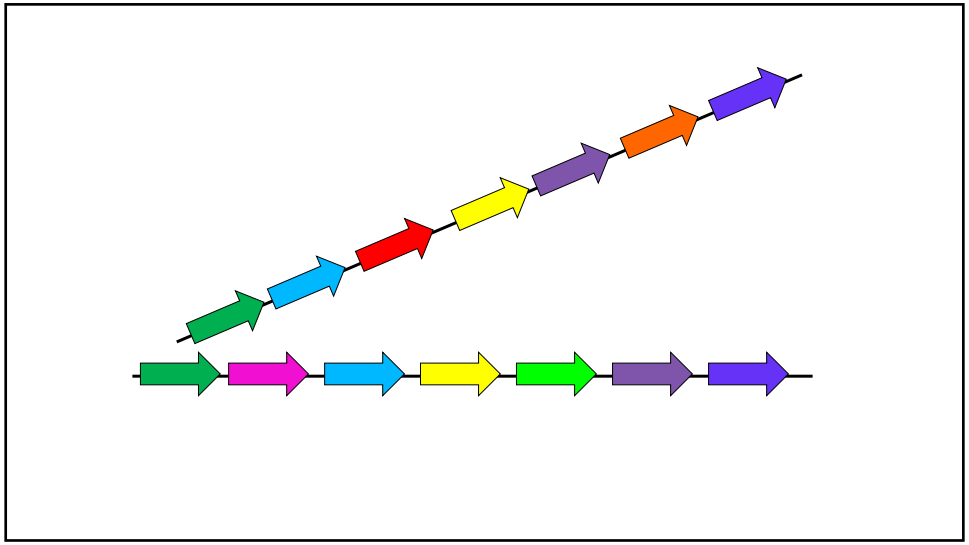


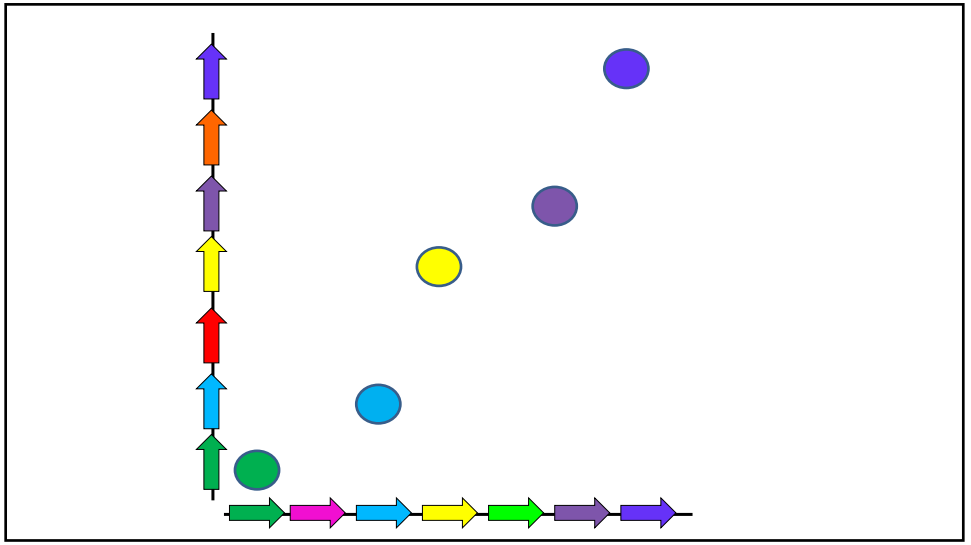
More time after genome duplication



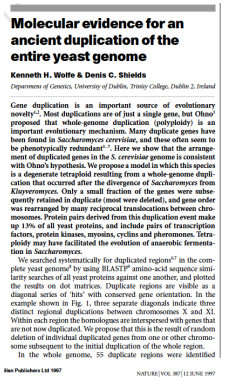
Unaligned view (removing gaps just like in *cerevisiae* has occurred)







Saccharomyces cerevisiae



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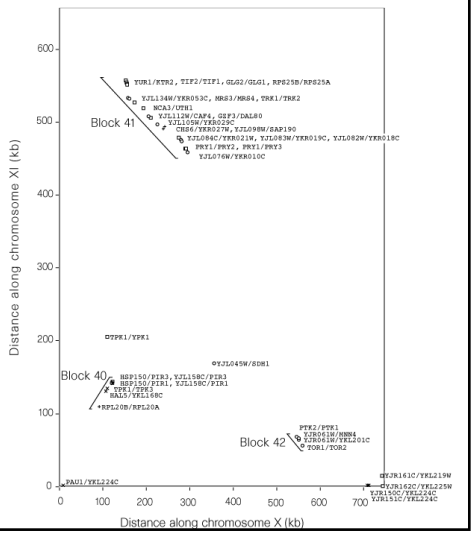
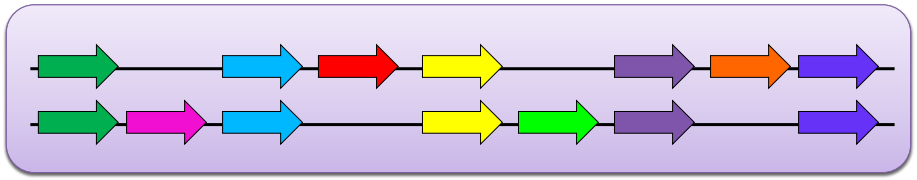


Problem reciprocal gene loss (illustrated with an extreme case); how to solve?



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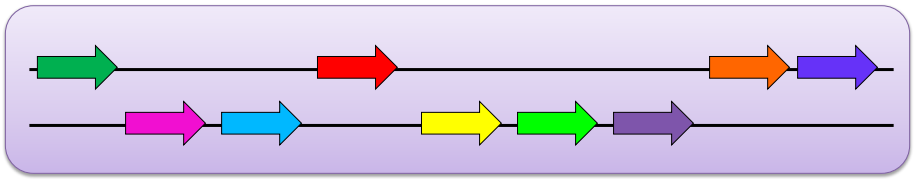
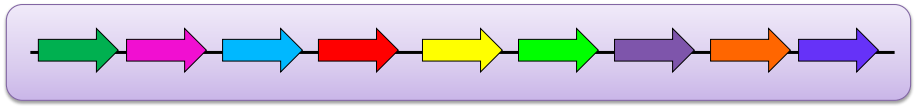
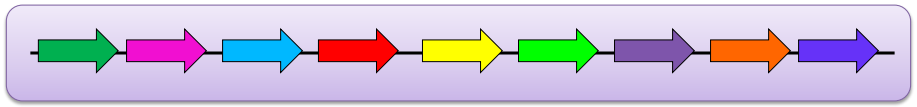


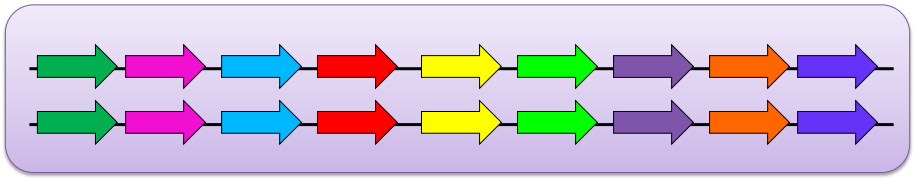
Just before genome duplication



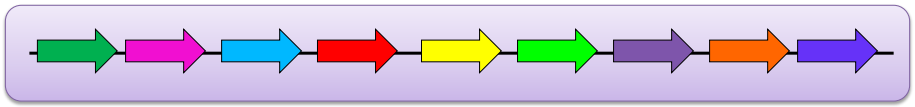
Outgroup!



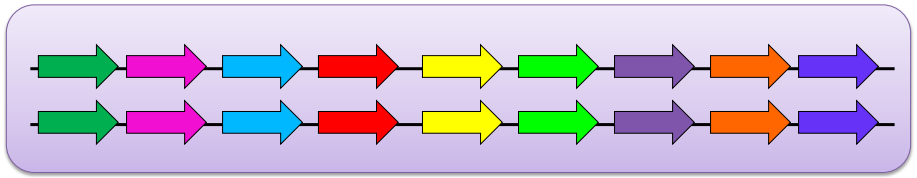
Just after genome duplication



Outgroup



Just after genome duplication



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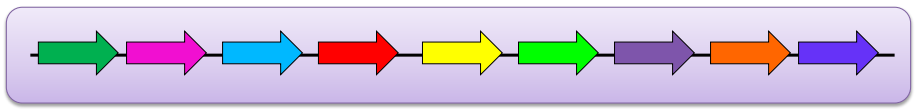
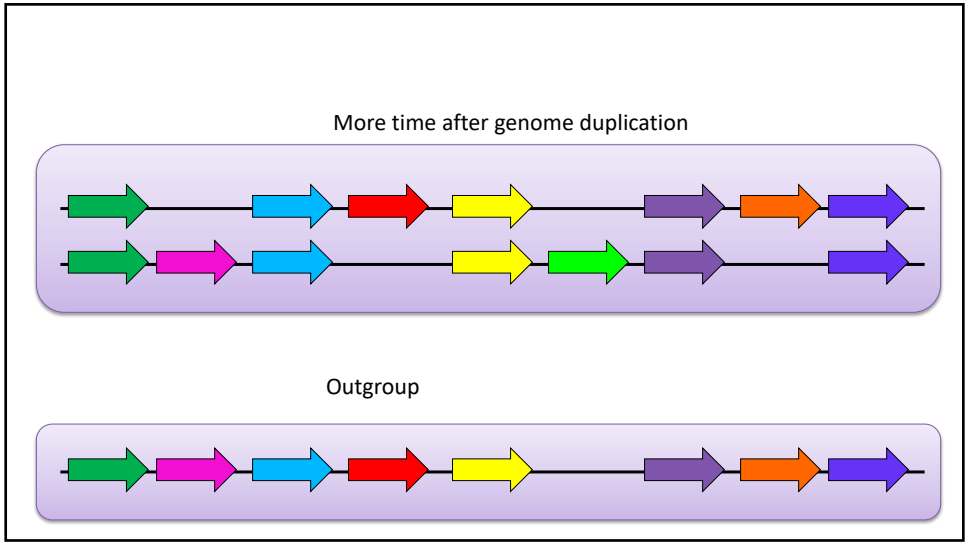
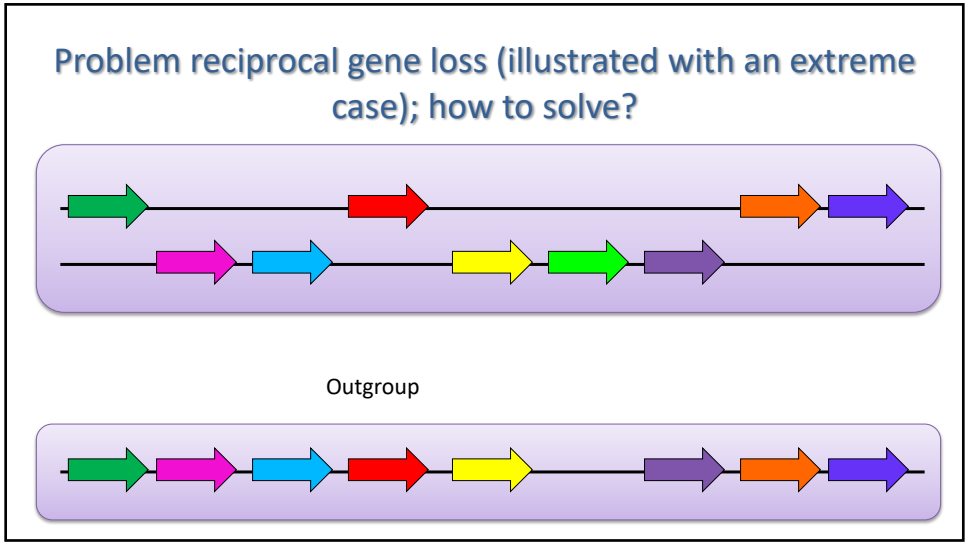
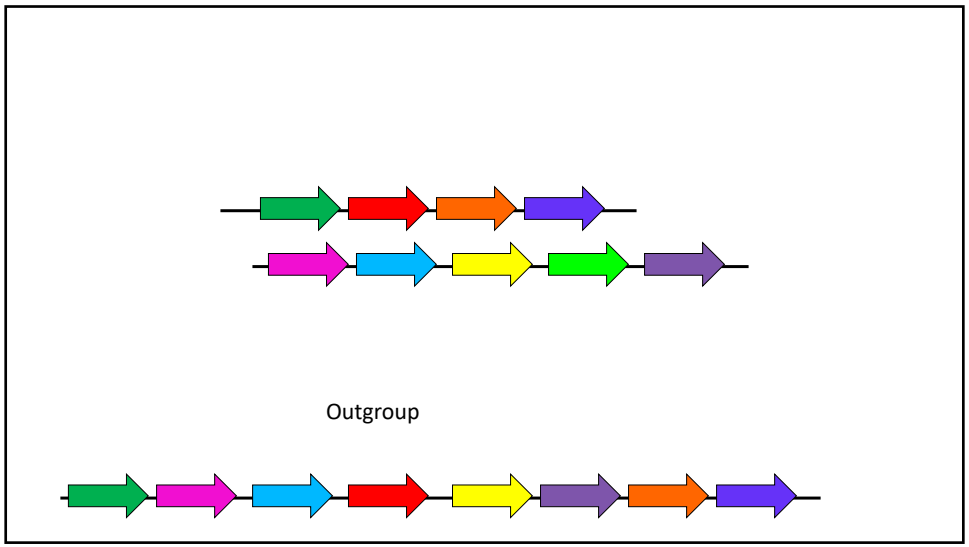



More time after genome duplication
Outgroup


Problem reciprocal gene loss (illustrated with an extreme case); how to solve?
Outgroup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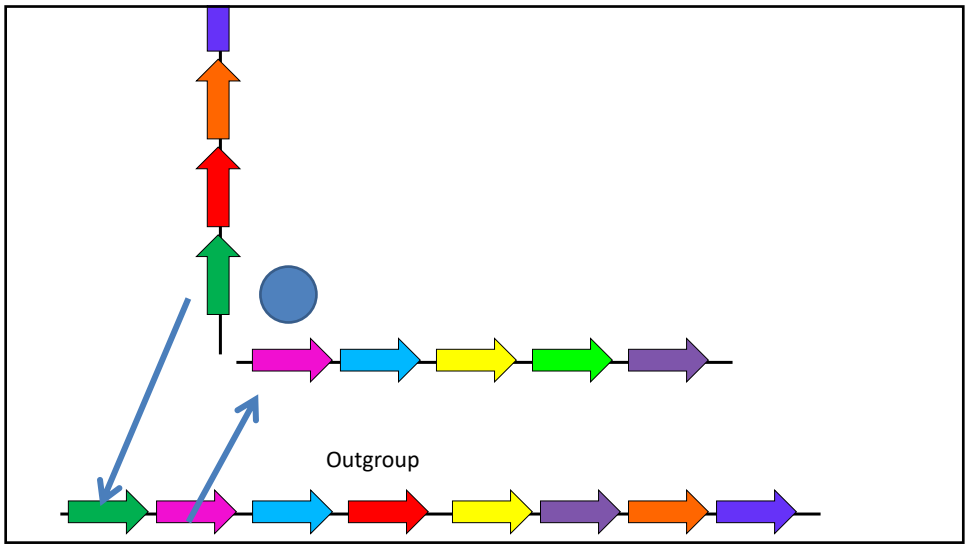
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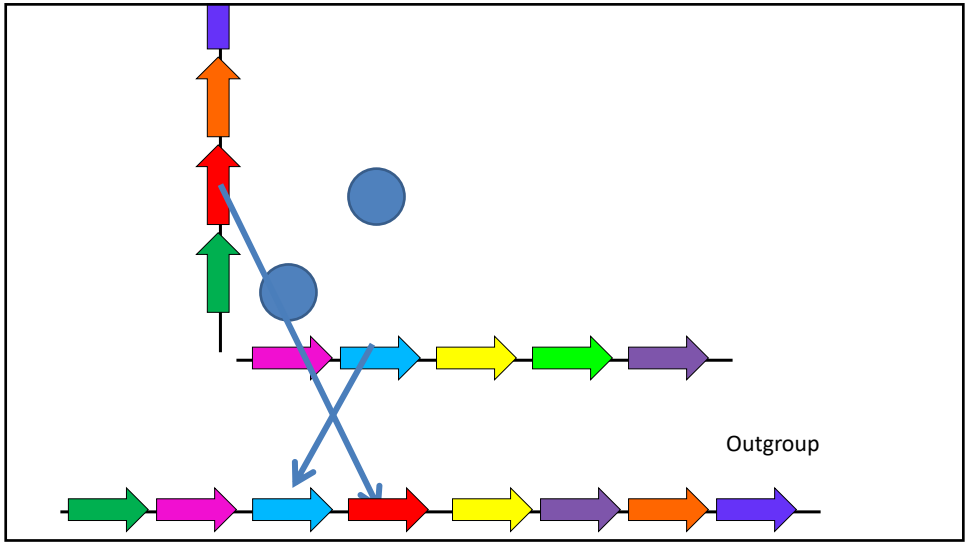
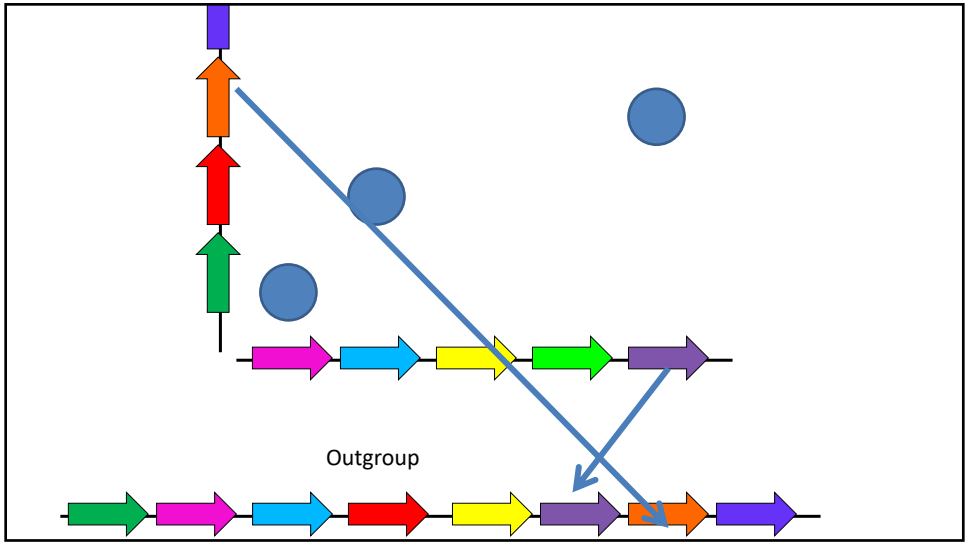
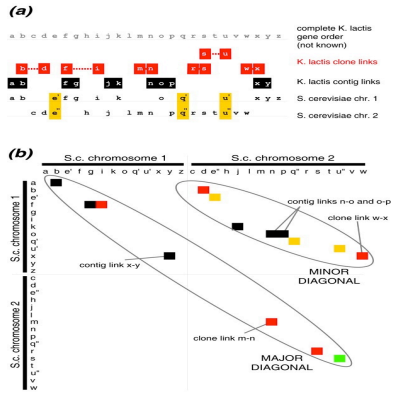
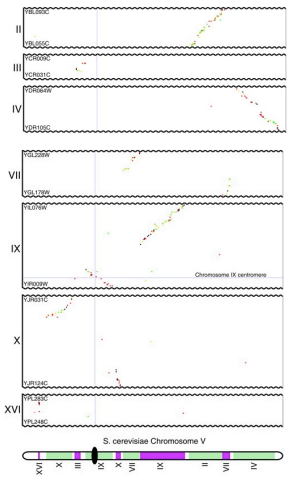


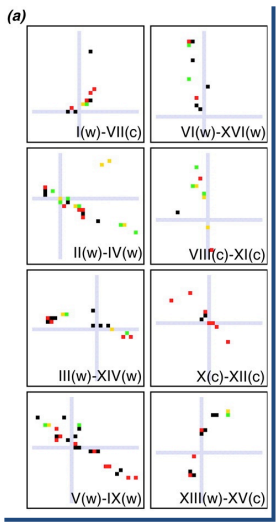


Outgroup genomes allowed full alignment of cerevisiae to itself





Wong et al. 2002 PNAS



Including detection of centromeric resulting from WGD

(b)

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI
I							3									
II				4	1											
III														4		
IV		9					1		1							
V		1	1				1		10							
VI										1						3
VII	7	2		1	1											
VIII											1					
IX					16											
X				1		1						2				
XI							2					1				
XII				1					9	1			1			
XIII											1					6
XIV			6										1			
XV														9		
XVI						4			1							

… maybe it was not a whole genome duplication but a hybridization?

PLOS | BIOLOGY

RESEARCH ARTICLE

Beyond the Whole-Genome Duplication: Phylogenetic Evidence for an Ancient Interspecies Hybridization in the Baker's Yeast Lineage

Marina Marcet-Houben[1,2], Toni Gabaldón[1,2,3]*

1 Centre for Genomic Regulation (CRG), Barcelona, Spain, 2 Universitat Pompeu Fabra (UPF), Barcelona, Spain, 3 Institució Catalana de Recerca i Estudis Avançats (ICREA), Barcelona, Spain

* tgabaldon@crg.es

OPEN ACCESS

Citation: Marcet-Houben M, Gabaldón T (2015)

Abstract

Whole-genome duplications have shaped the genomes of several vertebrate, plant, and fungal lineages. Earlier studies have focused on establishing when these events occurred

Clearer example of allopolyploidy (& genome dominance)

ARTICLE

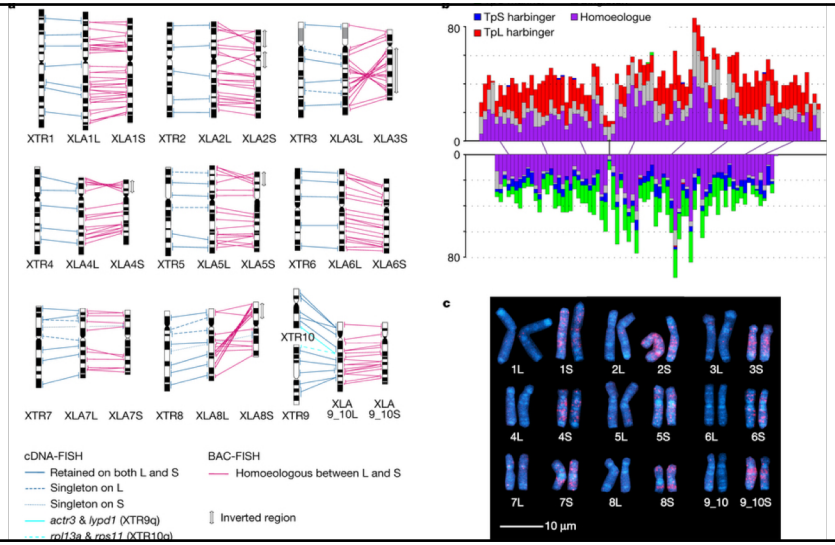
OPEN

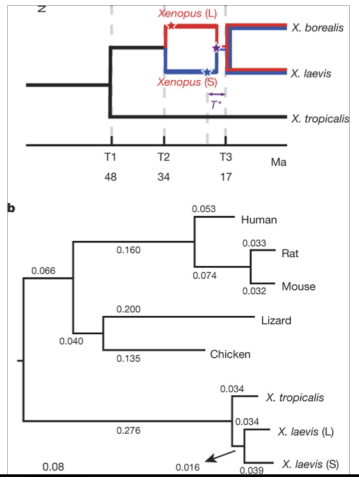
doi:10.1038/nature19840

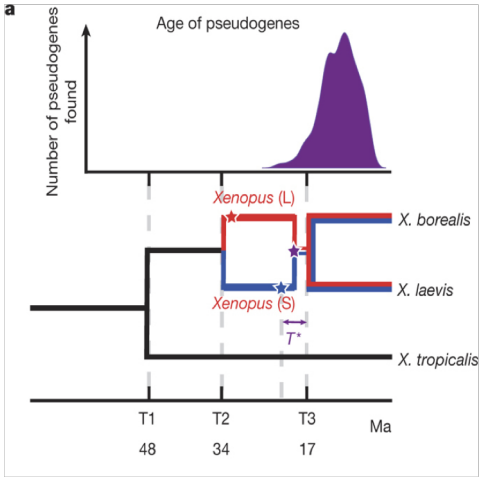
Genome evolution in the allotetraploid frog *Xenopus laevis*

Adam M. Session[1,2]*, Yoshinobu Uno[3]*, Taejoon Kwon[4,5]*, Jarrod A. Chapman[2], Atsushi Toyoda[6], Shuji Takahashi[7], Akimasa Fukui[8], Akira Hikosaka[9], Atsushi Suzuki[7], Mariko Kondo[10], Simon J. van Heeringen[11], Ian Quigley[12], Sven Heinz[13], Hajime Ogino[14], Haruki Ochi[15], Uffe Hellsten[2], Jessica B. Lyons[1], Oleg Simakov[16], Nicholas Putnam[17], Jonathan Stites[17], Yoko Kuroki[18], Toshiaki Tanaka[19], Tatsuo Michiue[20], Minoru Watanabe[21], Ozren Bogdanovic[22], Ryan Lister[22], Georgios Georgiou[11], Sarita S. Paranjpe[11], Ila van Kruijsbergen[11], Shengguang Shu[1], Joseph Carlson[2], Tsutomu Kinoshita[23], Yuko Ohta[24], Shuuji Mawaribuchi[25], Jerry Jenkins[2,26], Jane Grimwood[2,26], Jeremy Schmutz[2,26], Therese Mitros[1], Sahar V. Mozaffari[27], Yutaka Suzuki[28], Yoshikazu Haramoto[29], Takamasa S. Yamamoto[30], Chiyo Takagi[30], Rebecca Heald[31], Kelly Miller[31], Christian Haudenschild[32]†, Jacob Kitzman[33], Takuya Nakayama[34], Yumi Izutsu[35], Jacques Robert[36], Joshua Fortriede[37], Kevin Burns[37], Vaneet Lotay[38], Kamran Karimi[38], Yuuri Yasuoka[39], Darwin S. Dichmann[1], Martin F. Flajnik[24], Douglas W. Houston[40], Jay Shendure[33], Louis DuPasquier[41], Peter D. Vize[38], Aaron M. Zorn[37], Michihiko Ito[42], Edward M. Marcotte[4], John B. Wallingford[4], Yuzuru Ito[29], Makoto Asashima[29], Naoto Ueno[30,43], Yoichi Matsuda[3], Gert Jan C. Veenstra[44], Asao Fujiyama[6,44,45], Richard M. Harland[1], Masanori Taira[46] & Daniel S. Rokhsar[1,2,16]

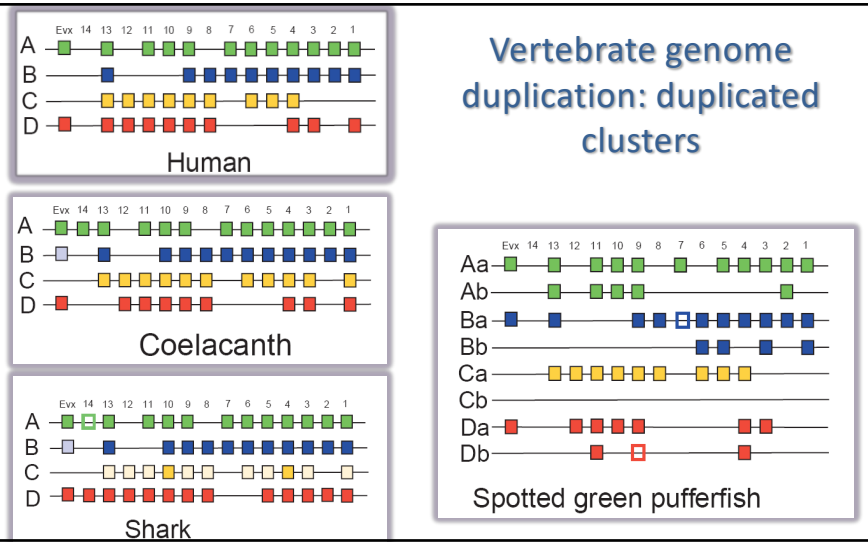
To explore the origins and consequences of tetraploidy in the African clawed frog, we sequenced the *Xenopus laevis* genome and compared it to the related diploid *X. tropicalis* genome. We characterize the allotetraploid origin of *X. laevis* by partitioning its genome into two homoeologous subgenomes, marked by distinct families of 'fossil' transposable elements. On the basis of the activity of these elements and the age of hundreds of unitary pseudogenes, we estimate that the two diploid progenitor species diverged around 34 million years ago (Ma) and combined to form an allotetraploid around 17–18 Ma. More than 56% of all genes were retained in two homoeologous copies. Protein function, gene expression, and the amount of conserved flanking sequence all correlate with retention rates. The subgenomes have evolved asymmetrically, with one chromosome set more often preserving the ancestral state and the other experiencing more gene loss, deletion, rearrangement, and reduced gene expression.

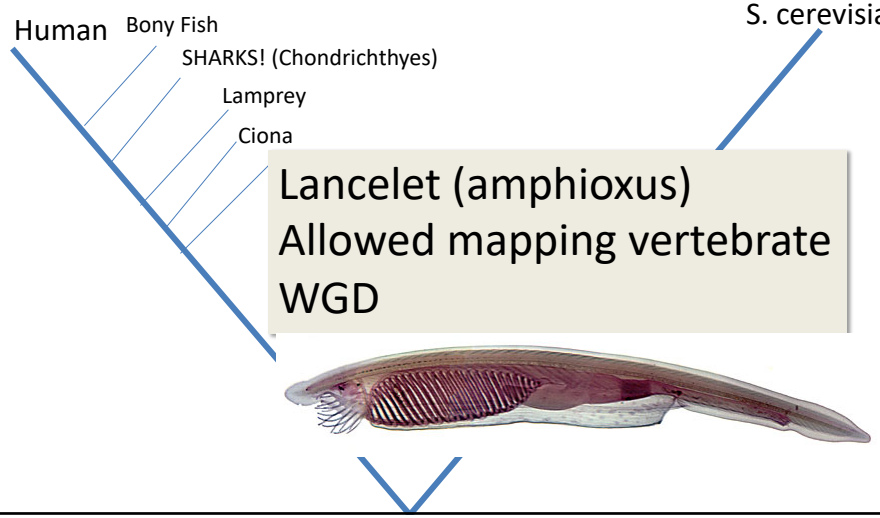


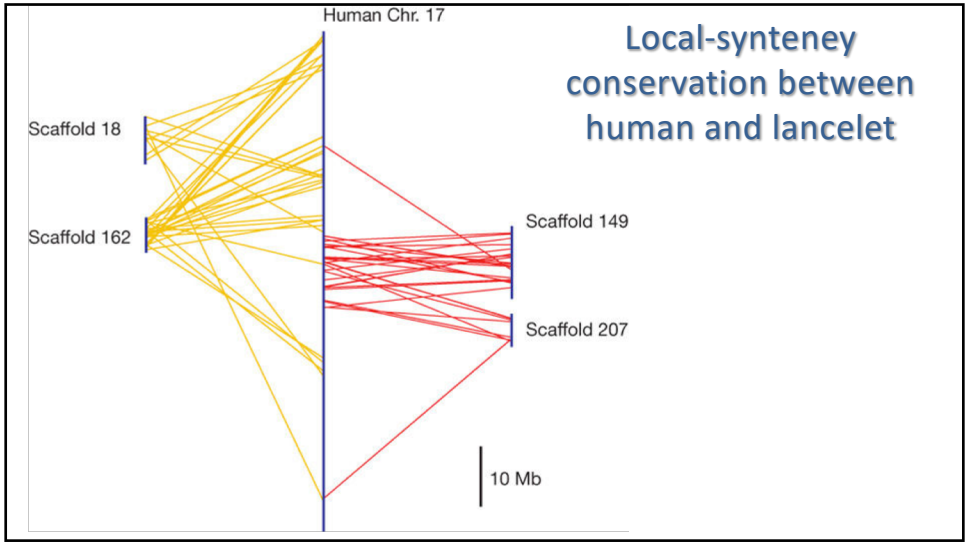




Vertebrate genome duplication: duplicated clusters

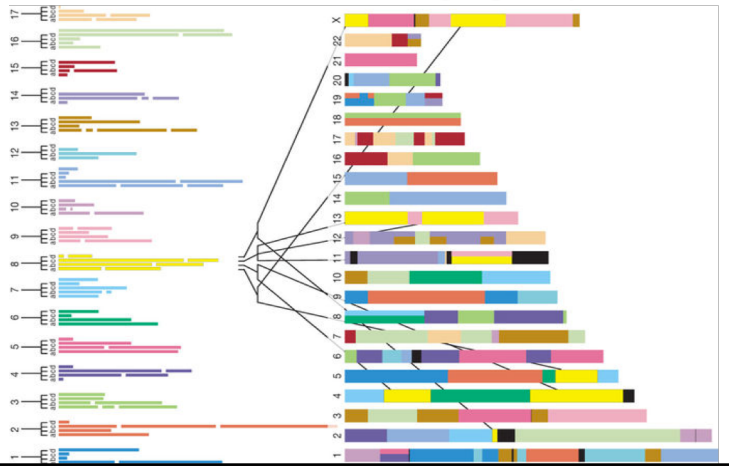




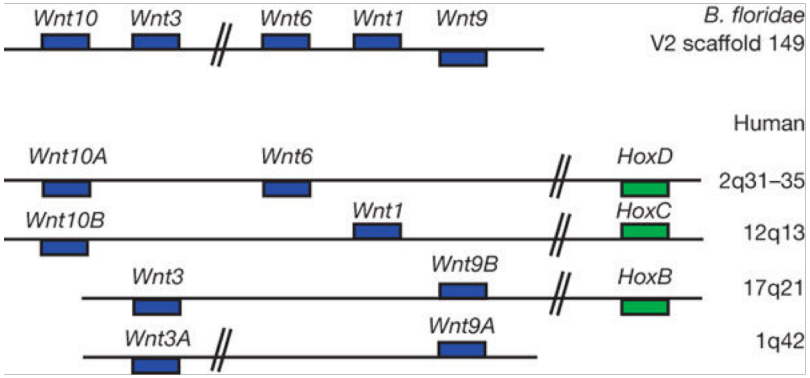


Local-synteney conservation between human and lancelet

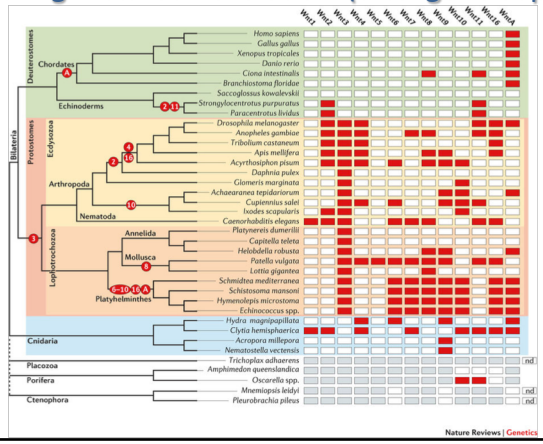
Chordate linkage groups



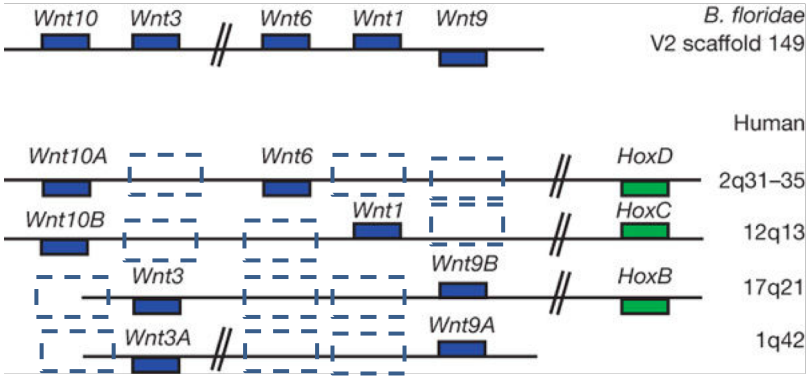
Duplicated wnt “clusters” detected via lancelet outgroup



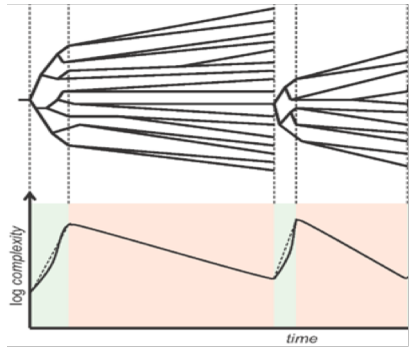
wingless (Wnt) : a paradigmatic example of the pervasiveness of gene loss during metazoan evolution. (after gene duplication)



Wnt example of gene loss after WGD

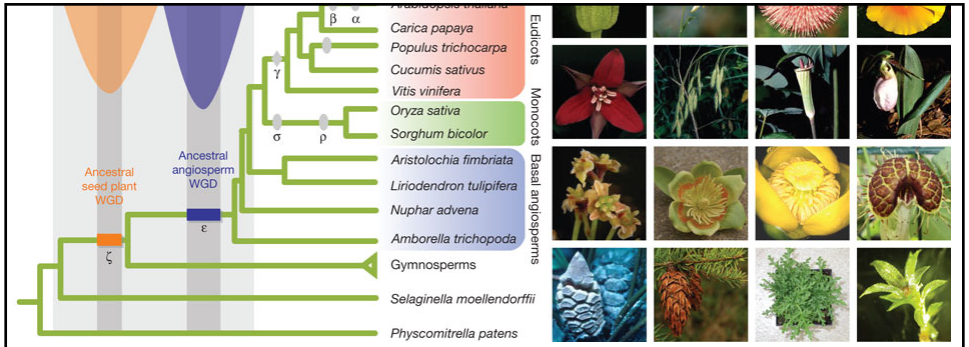


WNT



Tandem duplications at base of animals

WGD at base of vertebrates

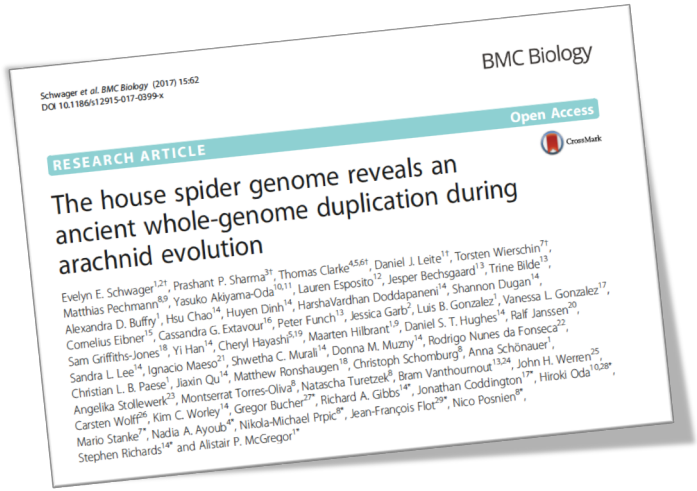


All from gene trees!!!

Nature. 2011 Apr 10. [

Ancestral polyploidy in seed plants and angiosperms.

Jiao Y, Wickett NJ, Ayyampalayam S, Chanderbali AS, Landherr L, Ralph PE, Tomsho LP, Hu Y, Liang H, Soltis PS, Soltis DE, Clifton SW, Schlarbaum SE, Schuster SC, Ma H, Leebens-Mack J, Depamphilis CW.



BMC Biology

Schwager et al. BMC Biology (2017) 15:62
DOI 10.1186/s12915-017-0399-x

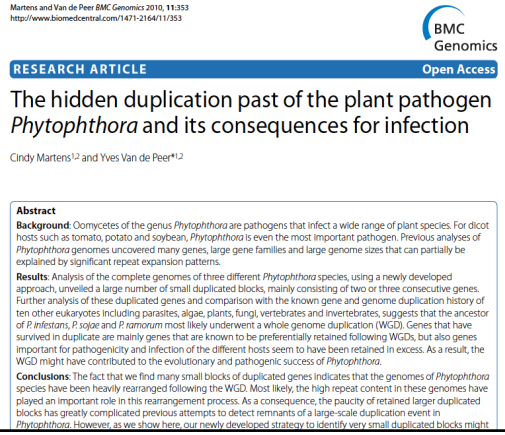
Open Access

RESEARCH ARTICLE

The house spider genome reveals an ancient whole-genome duplication during arachnid evolution

Evelyn E. Schwager[1,2†], Prashant P. Sharma[3†], Thomas Clarke[4,5,6†], Daniel J. Leite[1†], Torsten Wierschin[7†], Matthias Pechmann[8,9], Yasuko Akiyama-Oda[10,11], Lauren Esposito[12], Jesper Bechsgaard[13], Trine Bilde[13], Alexandra D. Buffry[1], Hsu Chao[14], Huyen Dinh[14], HarshaVardhan Doddapaneni[14], Shannon Dugan[14], Cornelius Eibner[15], Cassandra G. Extavour[16], Peter Funch[13], Jessica Garb[2], Luis B. Gonzalez[1], Vanessa L. Gonzalez[17], Sam Griffiths-Jones[18], Yi Han[14], Cheryl Hayashi[5,19], Maarten Hilbrant[19], Daniel S. T. Hughes[14], Ralf Janssen[20], Sandra L. Lee[14], Ignacio Maeso[21], Shwetha C. Murali[14], Donna M. Muzny[14], Rodrigo Nunes da Fonseca[22], Christian L. B. Paese[1], Jiaxin Qu[14], Matthew Ronshaugen[18], Christoph Schomburg[8], Anna Schönauer[1], Angelika Stollewerk[23], Montserrat Torres-Oliva[8], Natascha Turetzek[8], Bram Vanthournout[13,24], John H. Werren[25], Carsten Wolff[26], Kim C. Worley[14], Gregor Bucher[27*], Richard A. Gibbs[14*], Jonathan Coddington[17*], Hiroki Oda[10,28*], Mario Stanke[7*], Nadia A. Ayoub[4*], Nikola-Michael Prpic[8*], Jean-François Flot[29*], Nico Posnien[8*], Stephen Richards[14*] and Alistair P. McGregor[1*]

Is it always genome duplication?



Martens and Van de Peer *BMC Genomics* 2010, **11**:353
http://www.biomedcentral.com/1471-2164/11/353

BMC Genomics

RESEARCH ARTICLE Open Access

The hidden duplication past of the plant pathogen *Phytophthora* and its consequences for infection

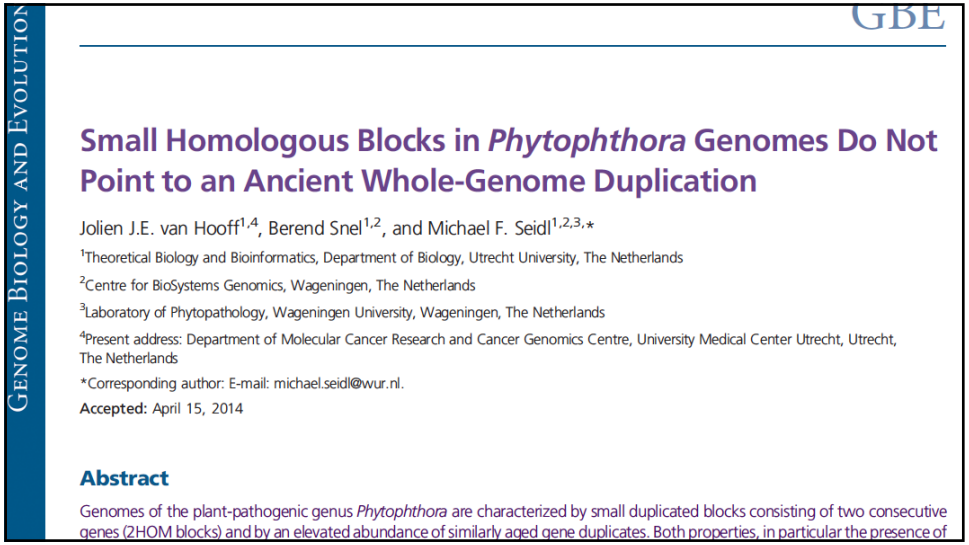
Cindy Martens[1,2] and Yves Van de Peer*[1,2]

Abstract

Background: Oomycetes of the genus *Phytophthora* are pathogens that infect a wide range of plant species. For dicot hosts such as tomato, potato and soybean, *Phytophthora* is even the most important pathogen. Previous analyses of *Phytophthora* genomes uncovered many genes, large gene families and large genome sizes that can partially be explained by significant repeat expansion patterns.

Results: Analysis of the complete genomes of three different *Phytophthora* species, using a newly developed approach, unveiled a large number of small duplicated blocks, mainly consisting of two or three consecutive genes. Further analysis of these duplicated genes and comparison with the known gene and genome duplication history of ten other eukaryotes including parasites, algae, plants, fungi, vertebrates and invertebrates, suggests that the ancestor of *P. infestans*, *P. sojae* and *P. ramorum* most likely underwent a whole genome duplication (WGD). Genes that have survived in duplicate are mainly genes that are known to be preferentially retained following WGDs, but also genes important for pathogenicity and infection of the different hosts seem to have been retained in excess. As a result, the WGD might have contributed to the evolutionary and pathogenic success of *Phytophthora*.

Conclusions: The fact that we find many small blocks of duplicated genes indicates that the genomes of *Phytophthora* species have been heavily rearranged following the WGD. Most likely, the high repeat content in these genomes have played an important role in this rearrangement process. As a consequence, the paucity of retained larger duplicated blocks has greatly complicated previous attempts to detect remnants of a large-scale duplication event in *Phytophthora*. However, as we show here, our newly developed strategy to identify very small duplicated blocks might



GENOME BIOLOGY AND EVOLUTION

GBE

Small Homologous Blocks in *Phytophthora* Genomes Do Not Point to an Ancient Whole-Genome Duplication

Jolien J.E. van Hooff[1,4], Berend Snel[1,2], and Michael F. Seidl[1,2,3,*]

[1]Theoretical Biology and Bioinformatics, Department of Biology, Utrecht University, The Netherlands

[2]Centre for BioSystems Genomics, Wageningen, The Netherlands

[3]Laboratory of Phytopathology, Wageningen University, Wageningen, The Netherlands

[4]Present address: Department of Molecular Cancer Research and Cancer Genomics Centre, University Medical Center Utrecht, Utrecht, The Netherlands

*Corresponding author: E-mail: michael.seidl@wur.nl.

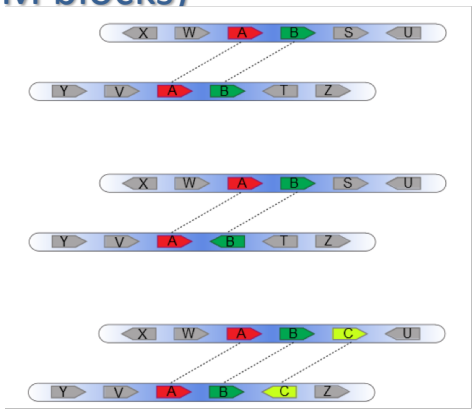
Accepted: April 15, 2014

Abstract

Genomes of the plant-pathogenic genus *Phytophthora* are characterized by small duplicated blocks consisting of two consecutive genes (2HOM blocks) and by an elevated abundance of similarly aged gene duplicates. Both properties, in particular the presence of

Phytophthoras have many paralogous blocks (HOM blocks)

2HOM block with conserved orientation



2HOM block with unconserved orientation

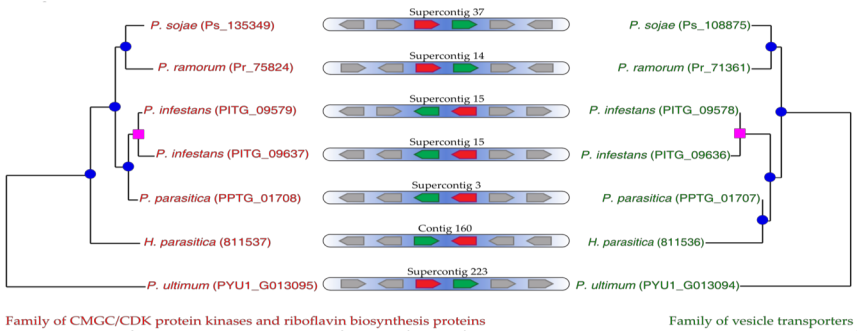
2HOM block being part of a 3HOM block

Adapted from: C Martens and Y van de Peer BMC Genomics (2010)

HOM block features do not point to a WGD

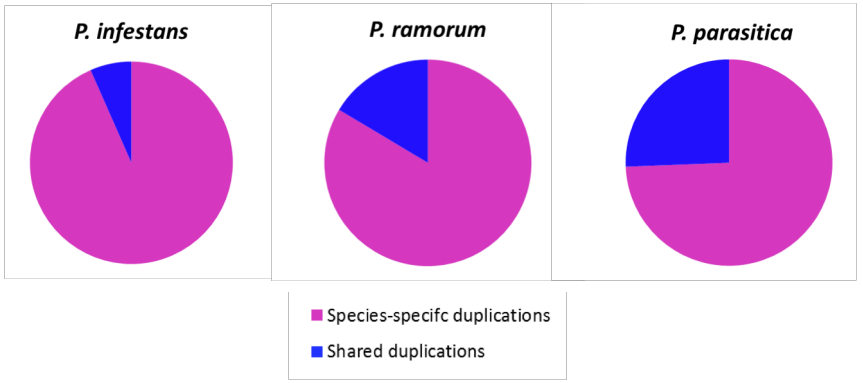
Species	2HOM blocks	TE-filtered			
		Full set	> 2 copies	Same scaffold	2 copies, different scaffolds
P. infestans	253	86	14	25	55
P. ramorum	128	31	1	16	15
P. sojae	207	35	4	15	18

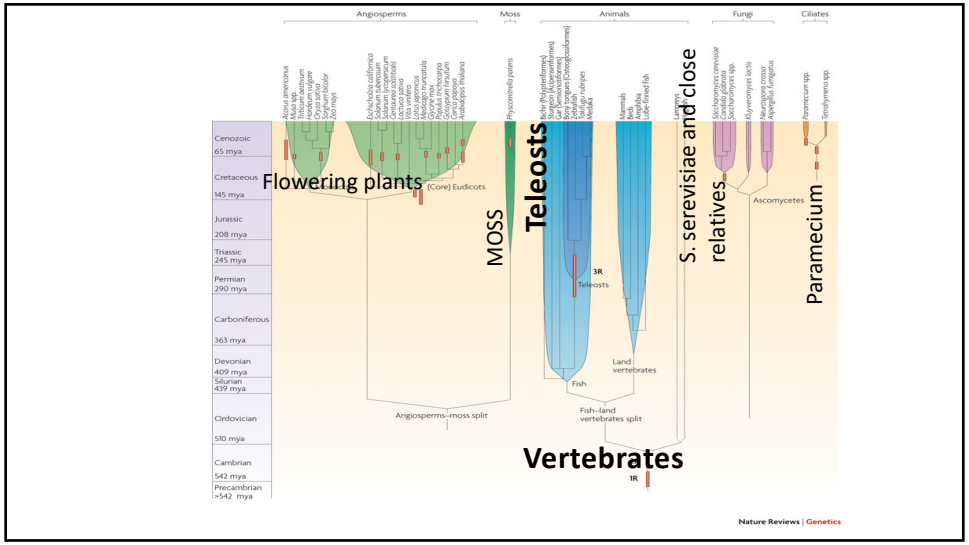
majority originated from recent species-specific duplications



E.g: in *P. infestans*, 132 out of 146 (90%) blocks analysed is species-specific, so cannot result from a WGD in the *Phytophthora* ancestor

Individual duplications are even more often species-specific



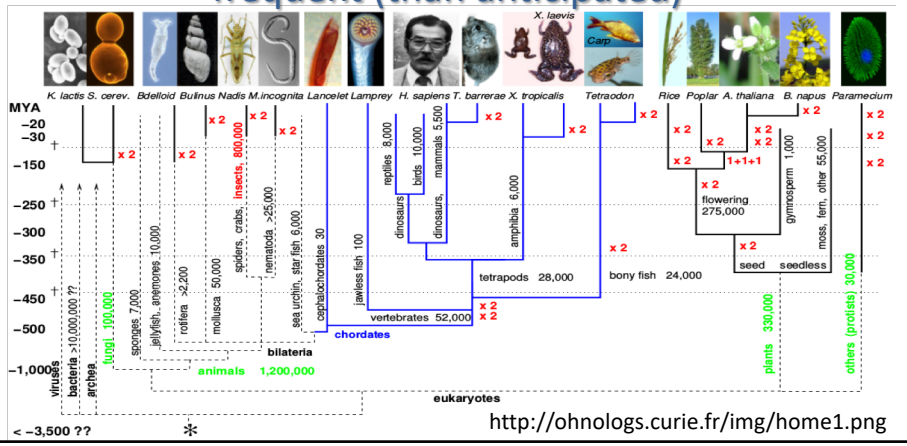


Biology (2016), http://dx.doi.org/10.1016/j.cub.2016.04.038
Current Biology
Report

Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication

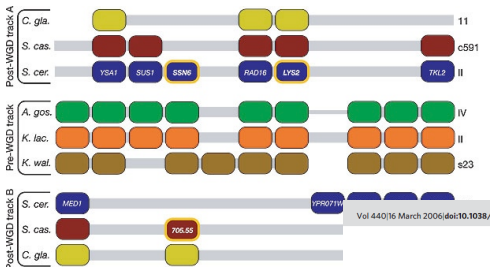
Luis M. Corrochano,[1,*] Alan Kuo,[2] Marina Marcet-Houben,[3,4] Silvia Polaino,[5] Asaf Salamov,[2] José M. Villalobos-Escobedo,[6] Jane Grimwood,[2,7] M. Isabel Álvarez,[8] Javier Avalos,[1] Diane Bauer,[2] Ernesto P. Benito,[8,9] Isabelle Benoit,[10] Gertraud Burger,[11] Lola P. Camino,[1] David Cánovas,[1] Enrique Cerdá-Olmedo,[1] Jan-Fang Cheng,[2] Angel Domínguez,[8] Marek Eliás,[12] Arturo P. Eslava,[8] Fabian Glaser,[13] Gabriel Gutiérrez,[1] Joseph Heitman,[14] Bernard Henrissat,[15,16] Enrique A. Iturriaga,[8] B. Franz Lang,[11] José L. Lavín,[17] Soo Chan Lee,[14] Wenjun Li,[14] Erika Lindquist,[2] Sergio López-García,[18] Eva M. Luque,[1] Ana T. Marcos,[1] Joel Martin,[2] Kevin McCluskey,[19]

Genome duplications turn out to be (much) more frequent (than anticipated)



http://ohnologs.curie.fr/img/home1.png

Reconstructed map of genome duplications allows unprecedented mapping of evolutionary history of genes in genomes

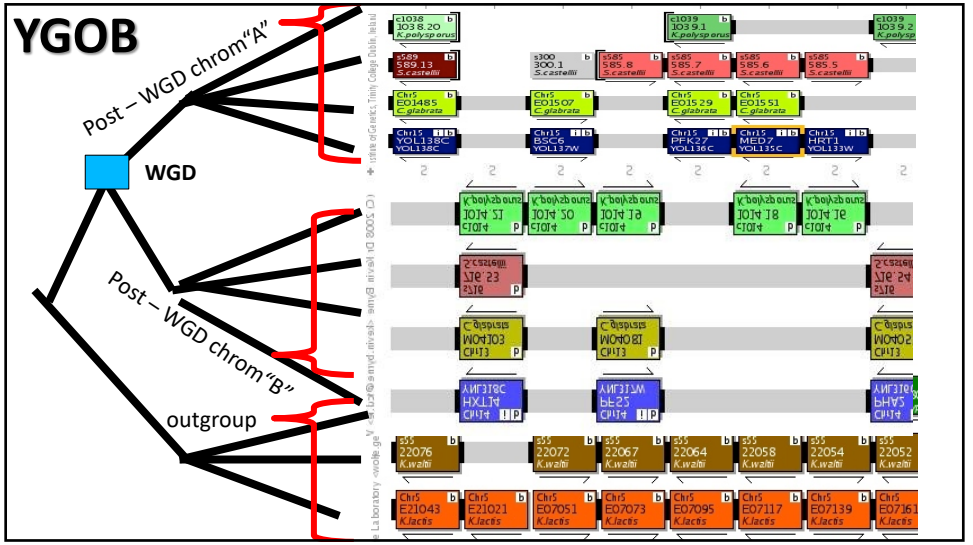


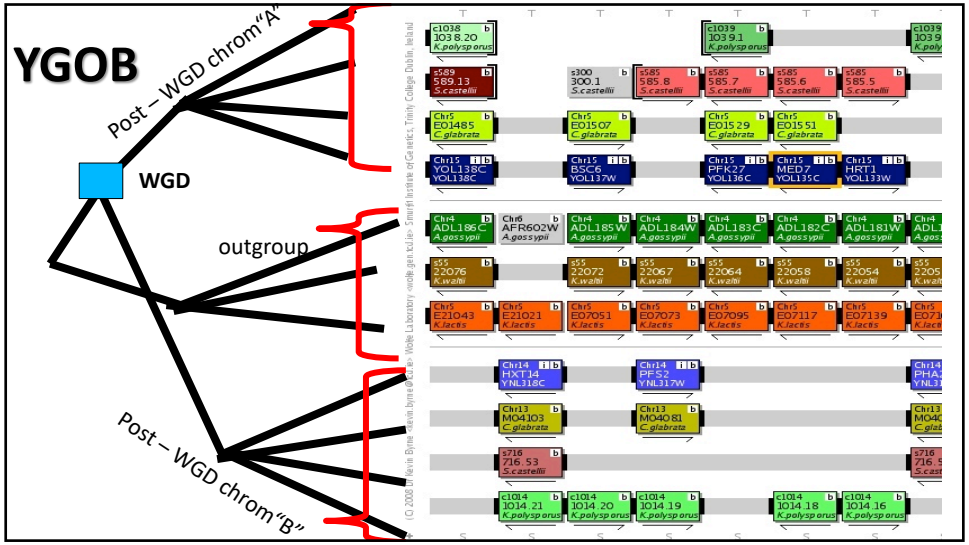
Vol 440|16 March 2006|doi:10.1038/nature04562 nature

LETTERS

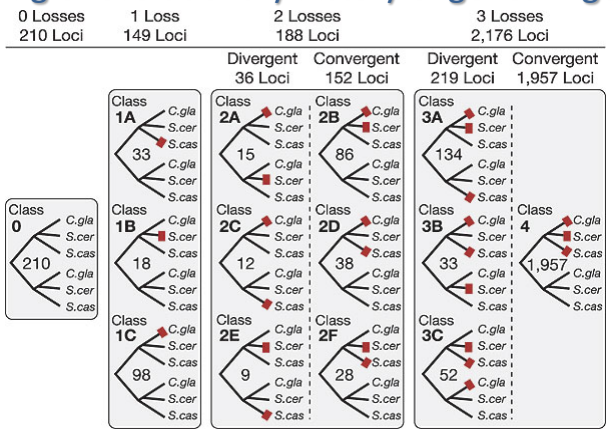
Multiple rounds of speciation associated with reciprocal gene loss in polyploid yeasts

Devin R. Scannell[1]*, Kevin P. Byrne[1]*, Jonathan L. Gordon[1], Simon Wong[1] & Kenneth H. Wolfe[1]

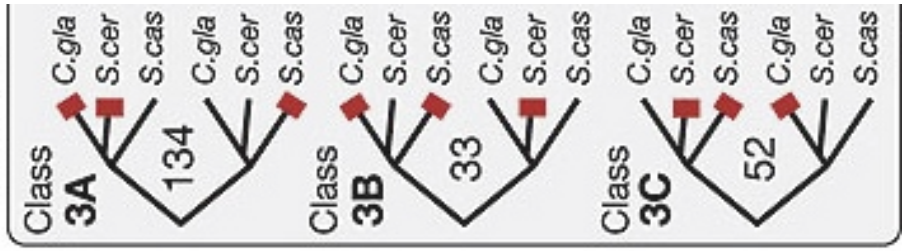




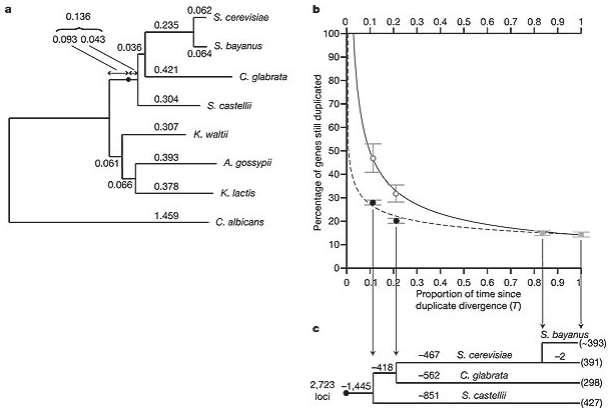
Reconstruction of genome duplications allows unprecedented mapping of evolutionary history of genes in genomes



Reconstructed map of genome duplications allows unprecedented mapping of evolutionary history of genes in genomes: “pseudo-orthology”



Major fate is gene loss



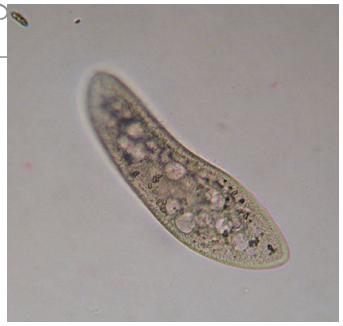
Paramecium genome duplications

Vol 444|9 November 2006|doi:10.1038/nature05230 nature

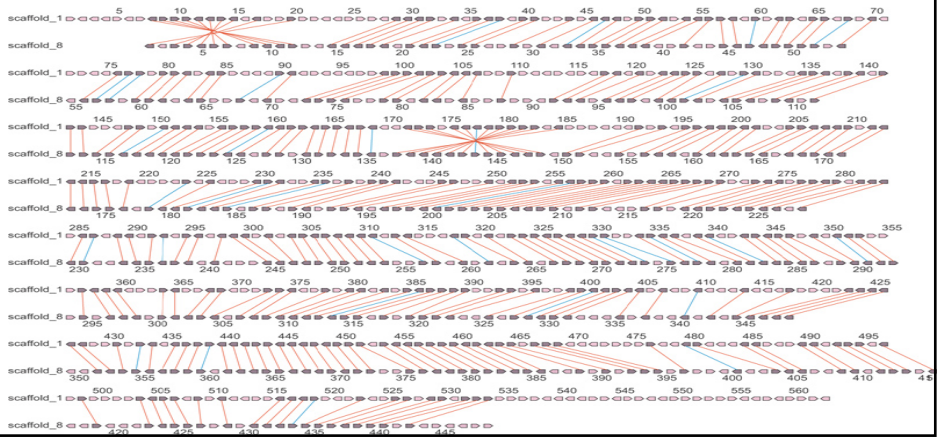
ARTICLES

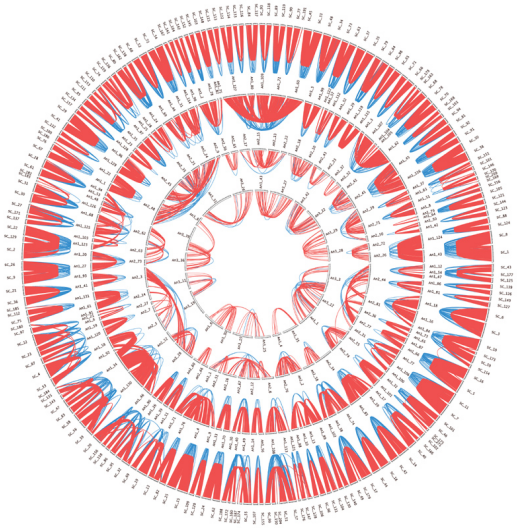
Global trends of whole-genome duplications revealed by the ciliate *Paramecium tetraurelia*

Jean-Marc Aury[1]*, Olivier Jaillon[1]*, Laurent Duret[2], Benjamin Noel[1], Claire Jubin[1], Betina M. Porcel[1], Béatrice Ségurens[1], Vincent Daubin[2], Véronique Anthouard[1], Nathalie Aiach[1], Olivier Arnaiz[3], Alain Billaut[1], Janine Beisson[3], Isabelle Blanc[3], Khaled Bouhouche[4], Francisco Câmara[5], Sandra Duharcourt[4], Roderic Guigo[5], Delphine Gogendeau[3], Michael Katinka[1], Anne-Marie Keller[3], Roland Kissmehl[6], Catherine Klotz[3], France Koll[3], Anne Le Mouël[4], Gersende Lepère[4], Sophie Malinsky[4], Mariusz Nowacki[4], Jacek K. Nowak[7], Helmut Plattner[6], Julie Poulain[1], Françoise Ruiz[3], Vincent Serrano[4], Marek Zagulski[7], Philippe Dessen[8], Mireille Bétermier[3,4], Jean Weissenbach[1], Claude Scarpelli[1], Vincent Schächter[1], Linda Sperling[3], Eric Meyer[4], Jean Cohen[3] & Patrick Wincker[1]



Comparison of two scaffolds originating from a common ancestor at the recent WGD





In *paramecium* 3 or 4 WGD

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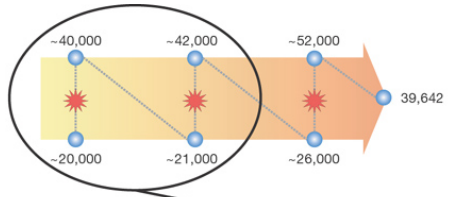
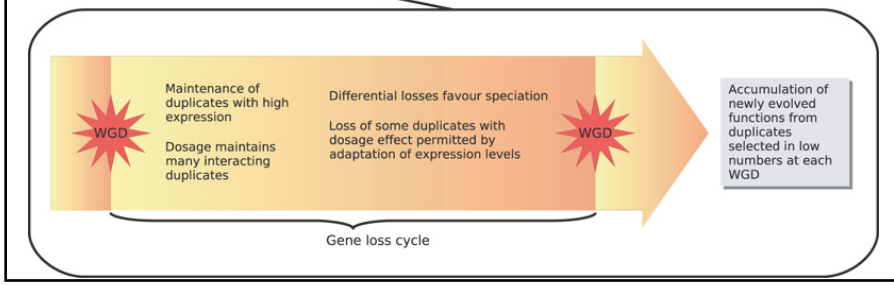
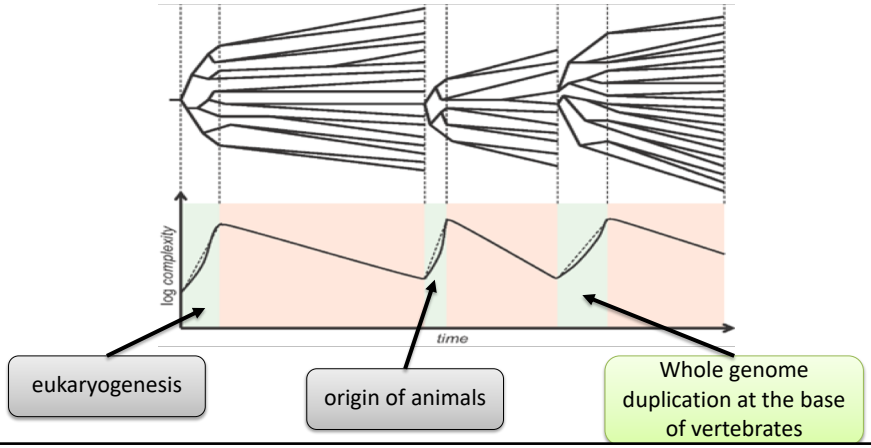
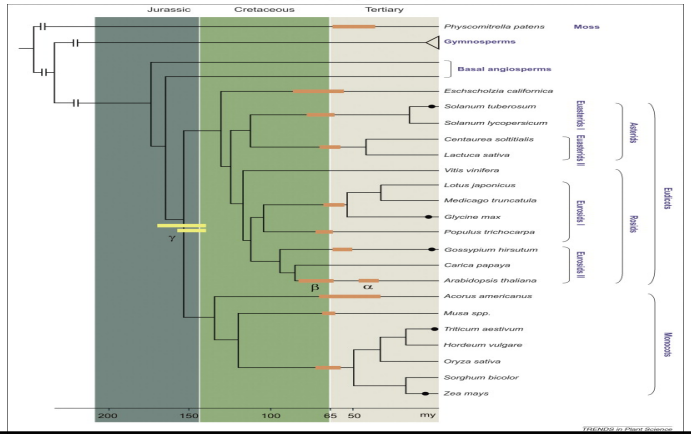


Massive gene loss

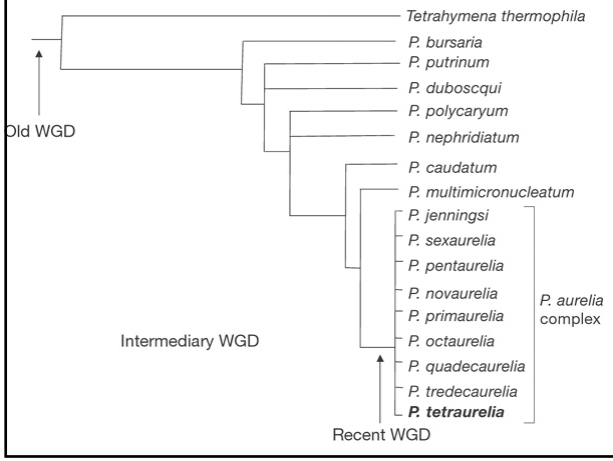




WGD's sometimes correlate to (adaptive) radiation?

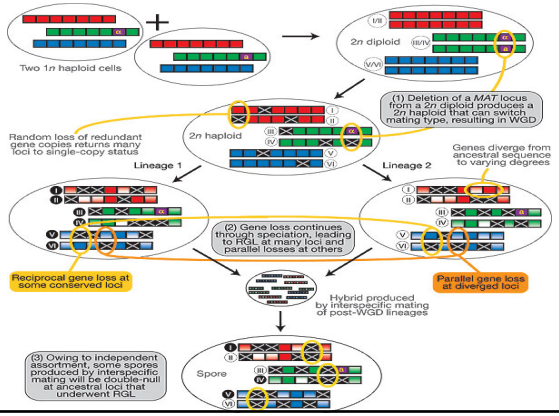


Correlation to (adaptive) radiation?

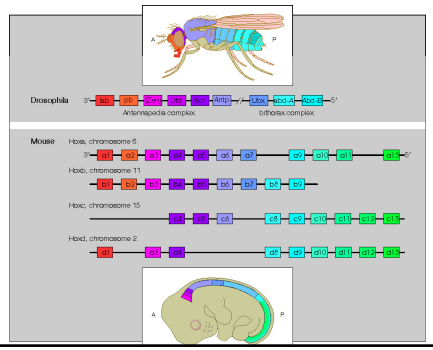


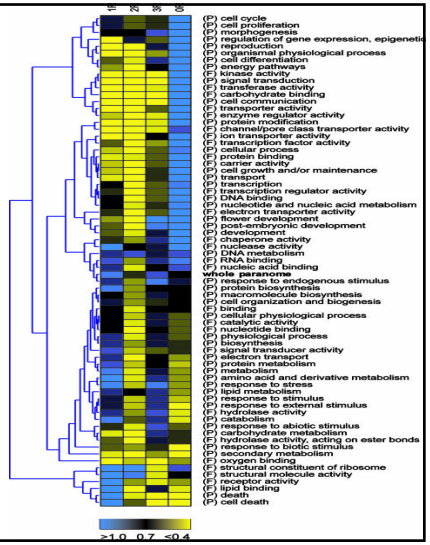
- Vertebrates
- Flowering plants
- Teleosti most species rich group of vertebrates
- Yeasts

Explanations for adaptive radiation? Incompatibility at essential loci



Explanations for adaptive radiation? Regulatory innovations





Non-sequitur? How this lecture fits in the course.

- Something to expect in gene trees.
  - If I see two paralogs in human my first guess is that they duplicated at base of vertebrares: provides scenario/search image
- *We want to detective What* has happened, this is generally difficult: here we are clear what happened because of synteny ….
- Some fringe / *in extremis* discussion of paralogy & orthology
- Much more well defined exposition of
  - Again importance of gene loss: provides nice example of expansion contraction / biphasic model of genome evolution
  - Changes in Speed of evolution