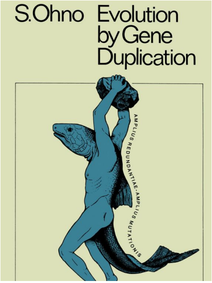
# Repetición y Evolución Genómica

# Susumu Ohno, 1970

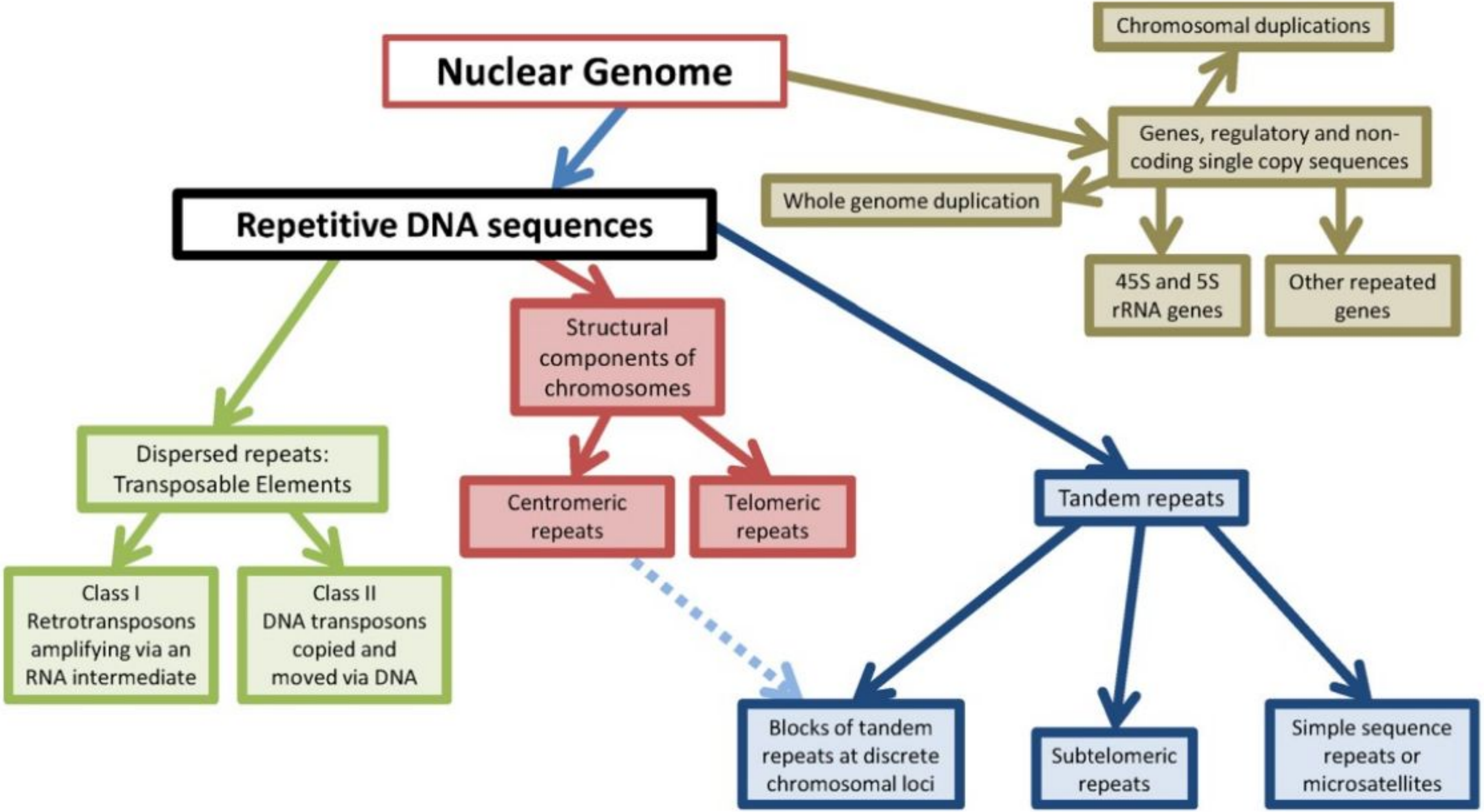



Gene duplication emerged as the major force of evolution. Only when a redundant gene locus is created by duplication is it permitted to accumulate formerly *forbidden* mutations and emerge as a new gene locus with a hitherto unknown function.

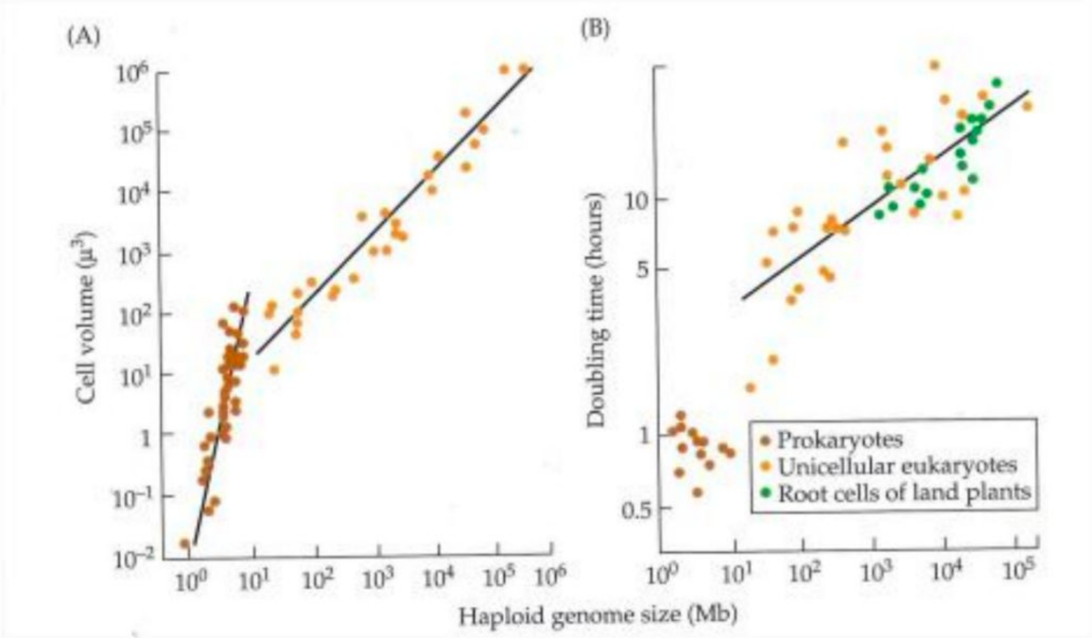
We have written two short reviews (OHNO *et al.*, 1968; OHNO, 1969) stressing the role gene duplication played in vertebrate evolution. This theme is expanded herein by reconstructing the process of evolution which produced man and other mammals from primitive fish of 300 million years ago.

In this golden age of biology, a book faces the danger of becoming obsolete before its publication. It is my belief that in order to avoid early obsolescence, the author, judging on the basis of the scant evidence available, is obliged to anticipate future developments and paint a picture with broad strokes of his brush. This I have done rather freely in this book.

# Una taxonomía de la repetición



# ADN egoísta y de relleno...




- Selfish DNA (Doolitle and Sapienza, Orgel and Crick)'80

Aumento del tamaño genómico por expansión de EM

- Bulk DNA (Commoner, Benett, Cavalier-Smith)'60 '70

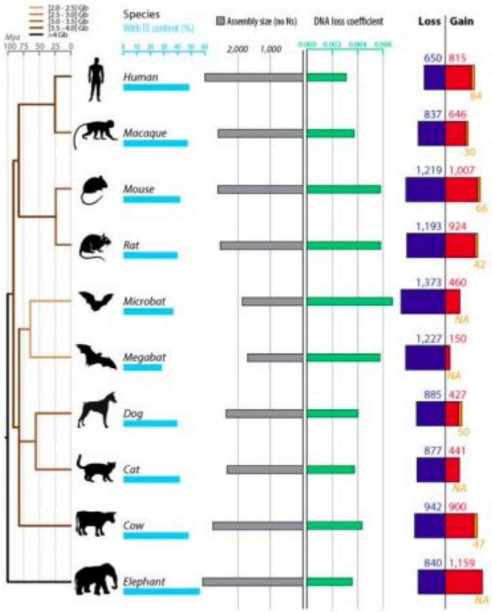
Aumento del tamaño producto directo de la selección natural
- Volumen nuclear
- Tamaño celular
- Tasa de división celular

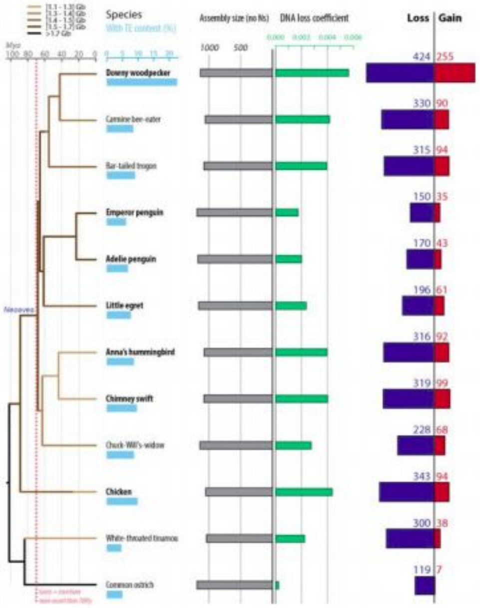
# Dynamics of genome size evolution in birds and mammals

Aurélie Kapusta[a], Alexander Suh[b], and Cédric Feschotte[a,1]

[a]Department of Human Genetics, University of Utah School of Medicine, Salt Lake City, UT 84112; and [b]Department of Evolutionary Biology, Evolutionary Biology Centre, Uppsala University, SE-752 36 Uppsala, Sweden

# Eucariotas - Animales



Current Biology
Dispatches
CellPress

# Genome Size Evolution: Small Transposons with Large Consequences

Alexander Suh
Department of Evolutionary Biology, Evolutionary Biology Centre (EBC), Science for Life Laboratory, Uppsala University, SE-752 36, Uppsala, Sweden
Correspondence: alexander.suh@ebc.uu.se
https://doi.org/10.1016/j.cub.2019.02.032

Transposable elements (TEs) heavily influence genome size variation between organisms. A new study on larvacean tunicates now shows that even non-autonomous TEs — small TEs that parasitize the enzymatic machinery of large, autonomous TEs — can have a large impact on genome size.

Blommaert *et al. BMC Genomics* (2019) 20:466
https://doi.org/10.1186/s12864-019-5859-y
BMC Genomics
RESEARCH ARTICLE Open Access

# Small, but surprisingly repetitive genomes: transposon expansion and not polyploidy has driven a doubling in genome size in a metazoan species complex

J. Blommaert[1], S. Riss[1], B. Hecox-Lea[2], D. B. Mark Welch[2] and C. P. Stelzer[1*]

genes
MDPI

*Review*

# Genome Size Diversity and Its Impact on the Evolution of Land Plants

Jaume Pellicer *, Oriane Hidalgo, Steven Dodsworth and Ilia J. Leitch
Department of Comparative Plant and Fungal Biology, Royal Botanic Gardens, Kew TW9 3DS, UK; o.hidalgo@kew.org (O.H.); s.dodsworth@kew.org (S.D.); i.leitch@kew.org (I.J.L.)
* Correspondence: j.pellicer@kew.org; Tel.: +44-208-332-5337

Received: 10 January 2018; Accepted: 5 February 2018; Published: 14 February 2018

Current Biology
Report
CellPress

# Massive Changes of Genome Size Driven by Expansions of Non-autonomous Transposable Elements

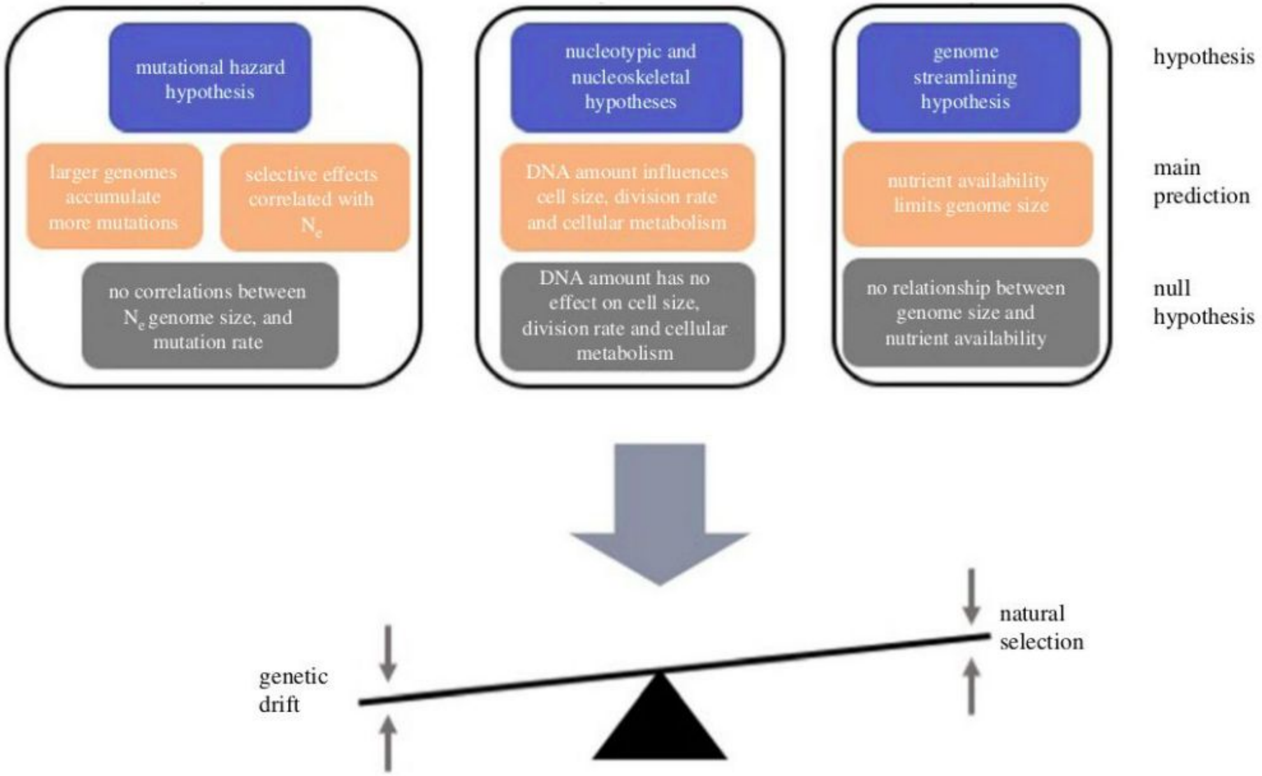
Magali Naville,[1,5] Simon Henriet,[2,5] Ian Warren,[1] Sara Sumic,[2] Magnus Reeve,[2,4] Jean-Nicolas Volff,[1,*] and Daniel Chourrout[2,3,6,*]

Genome size evolution: towards new model systems for old questions

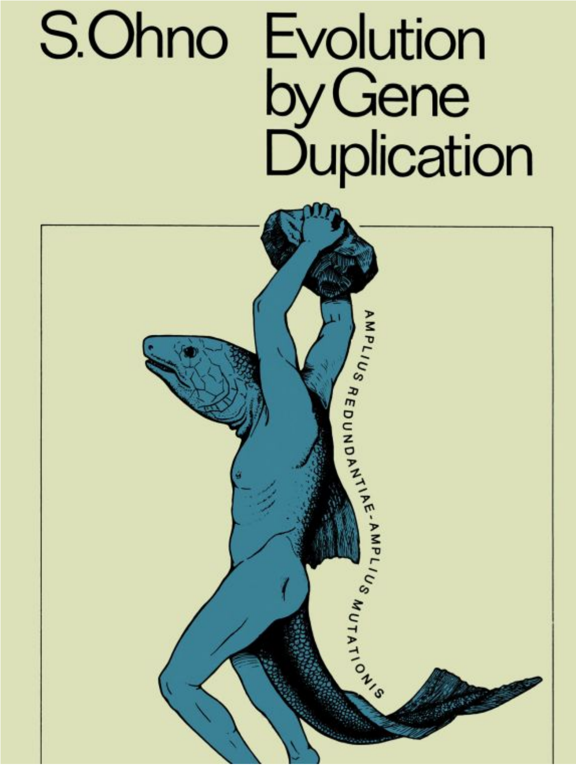
Julie Blommaert

Department of Organismal Biology, Uppsala University, Uppsala, Sweden

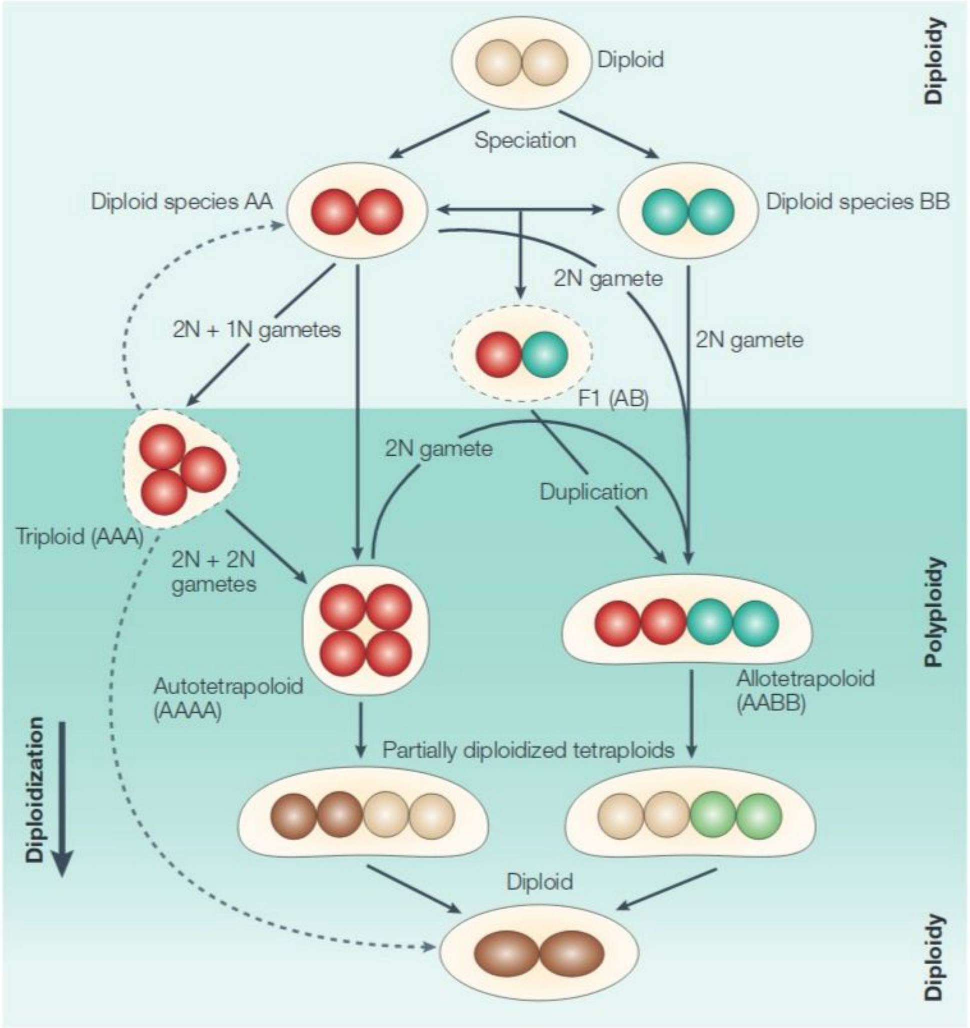
# Hipótesis evolutivas



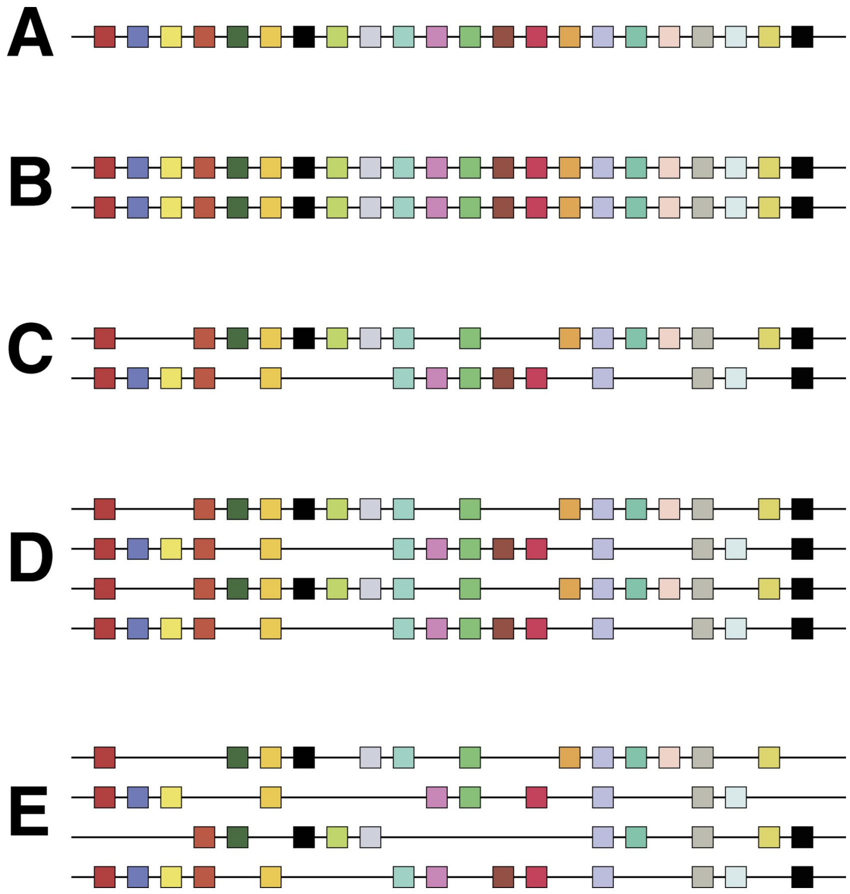
# Susumu Ohno, 1970



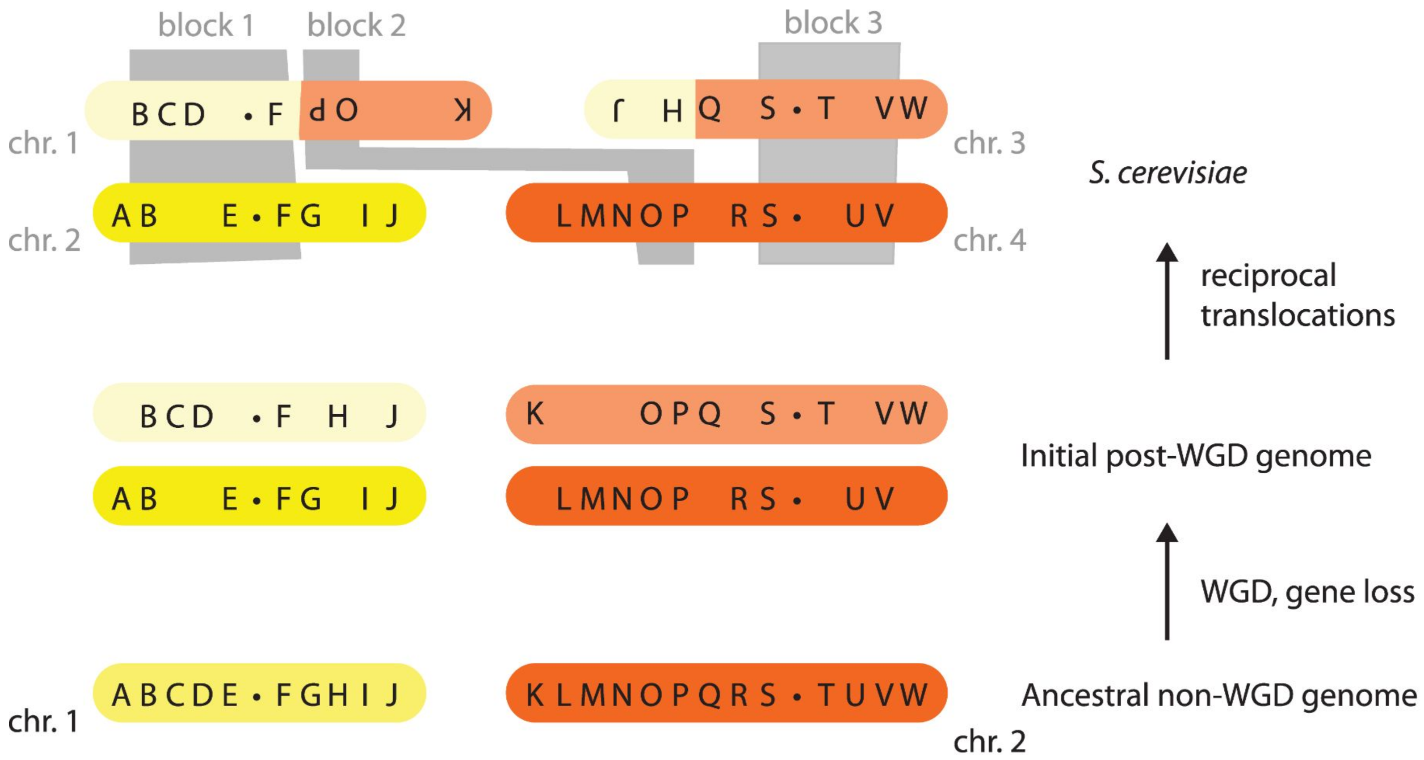
# Polyploidy and WGD



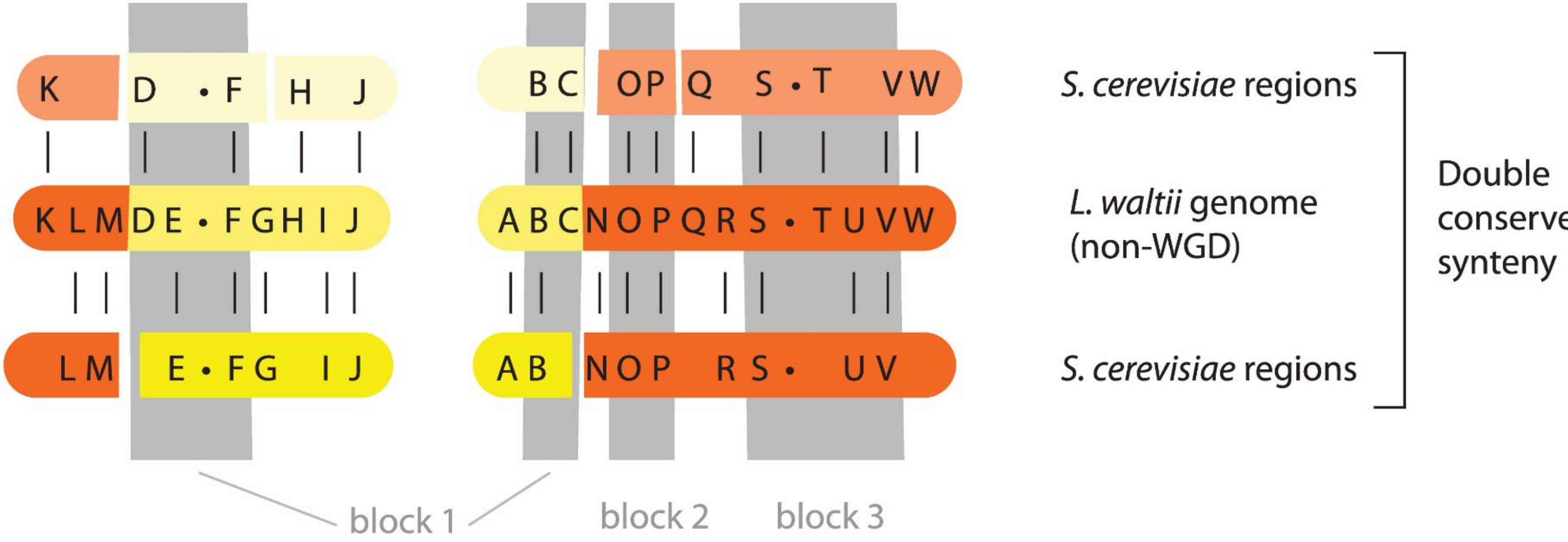
# Detecting WGD



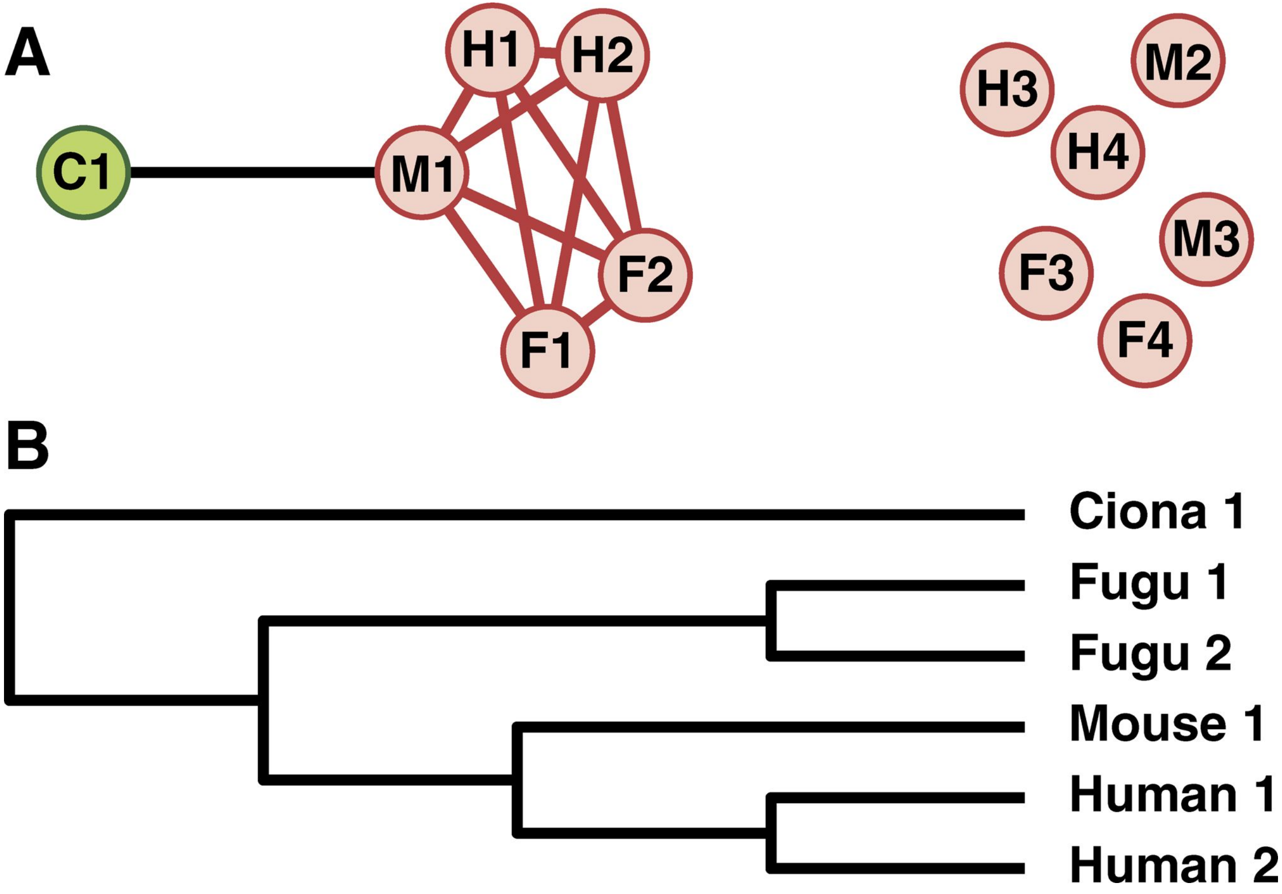
# Detecting WGD



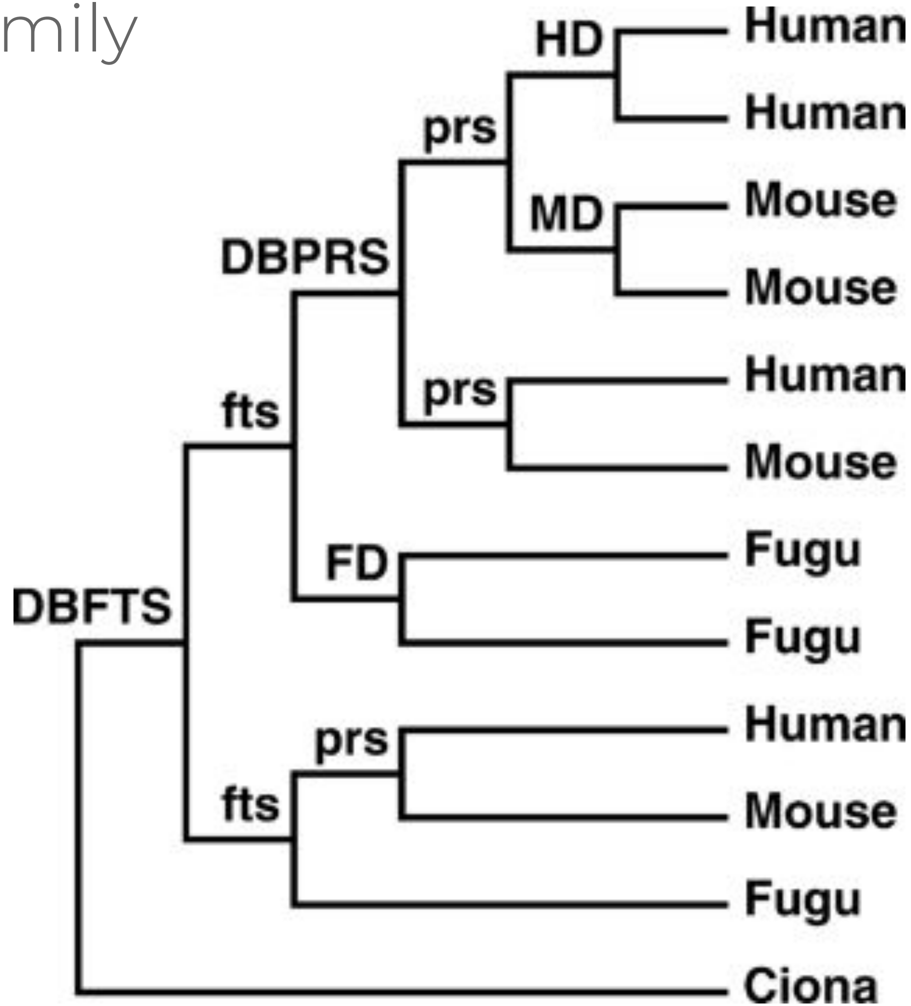
# Detecting WGD



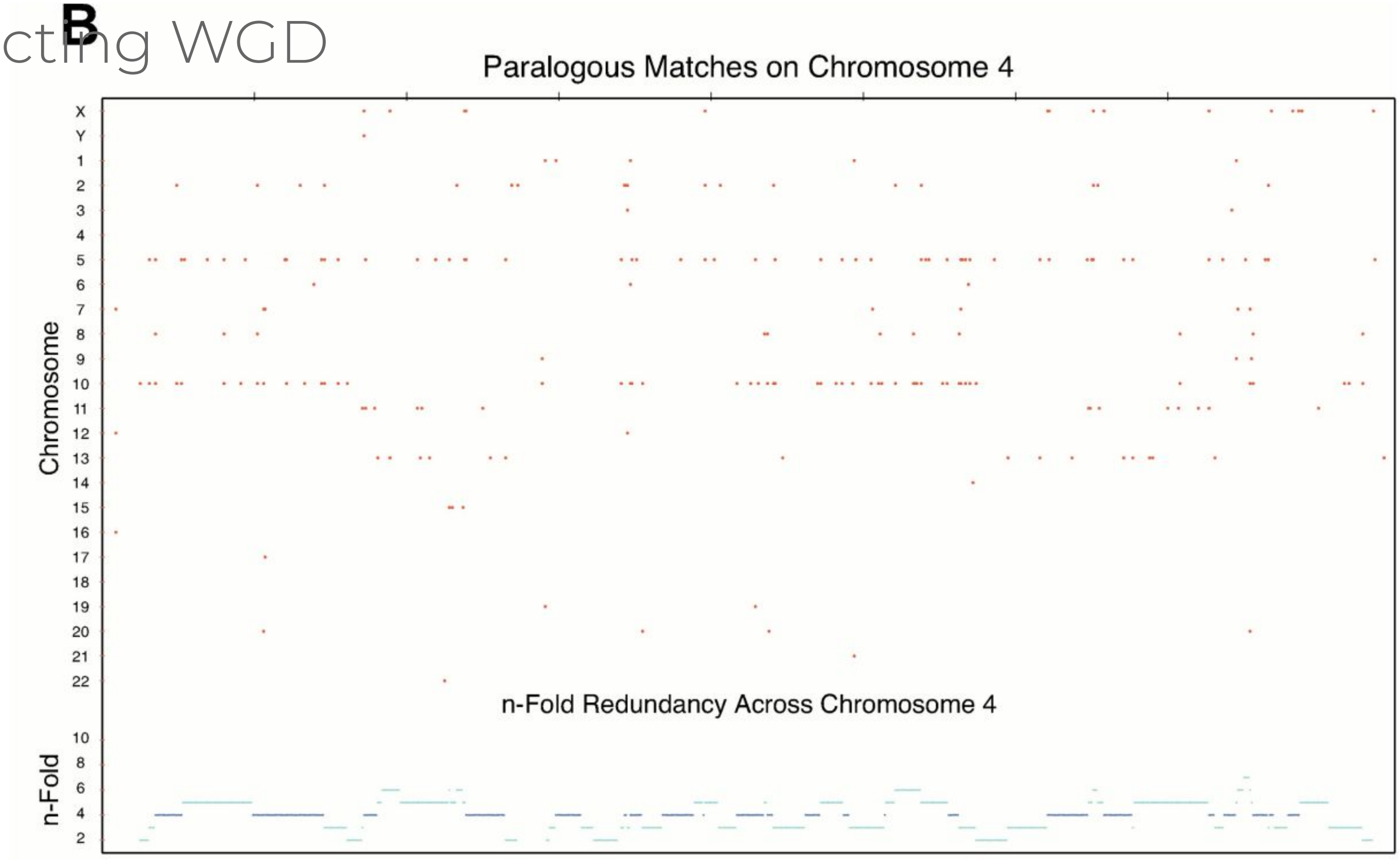
# Detecting WGD



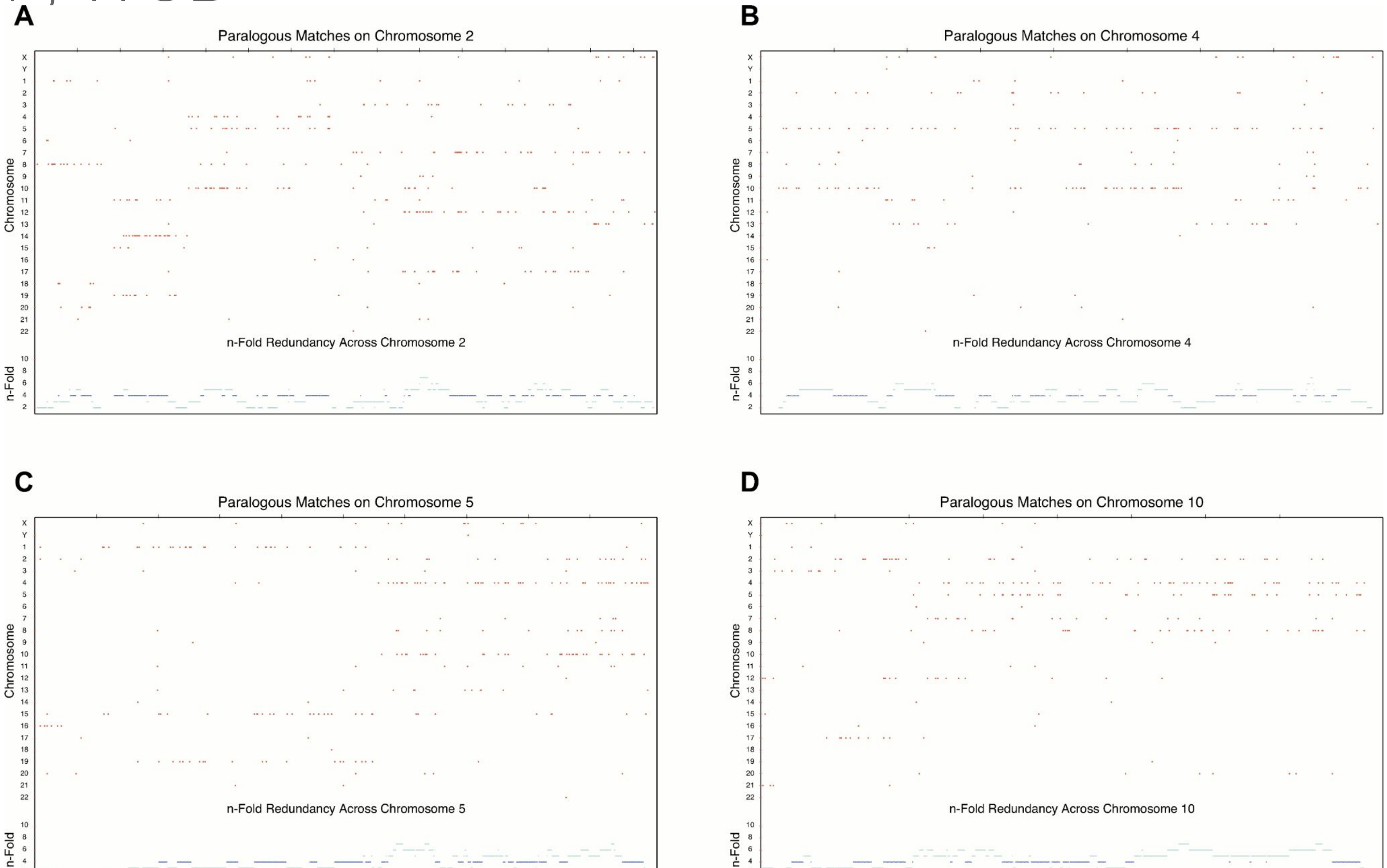
# Phylogeny of a gene family



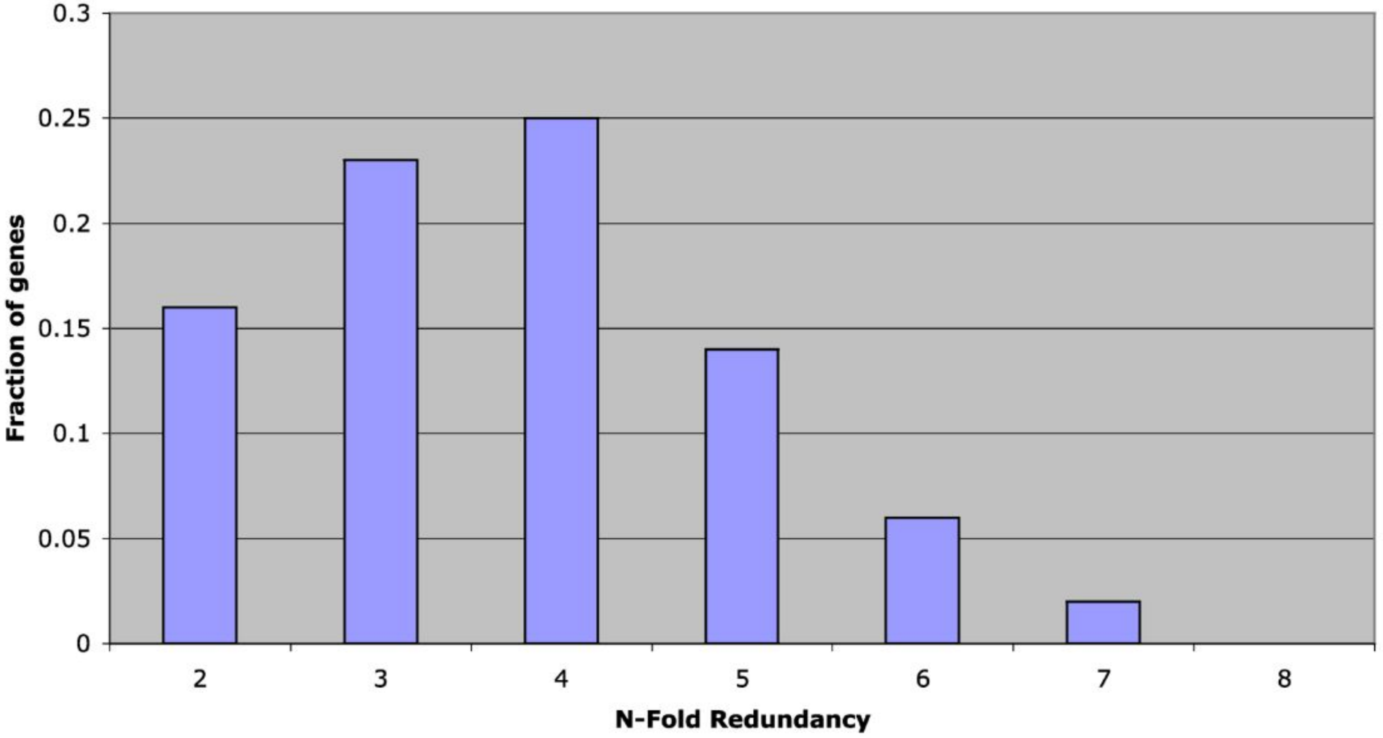
# Detecting WGD



# Detecting WGD



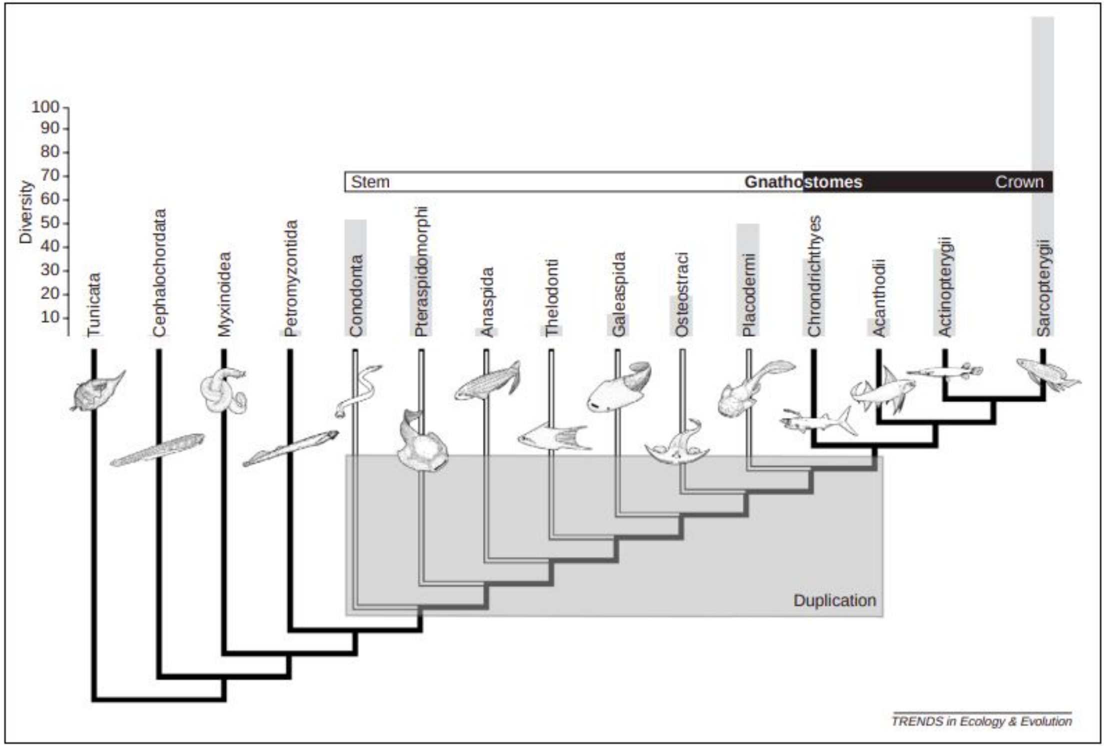
# Detecting WGD



# WGDs in evolutionary context

# Reducing the risk of extinction

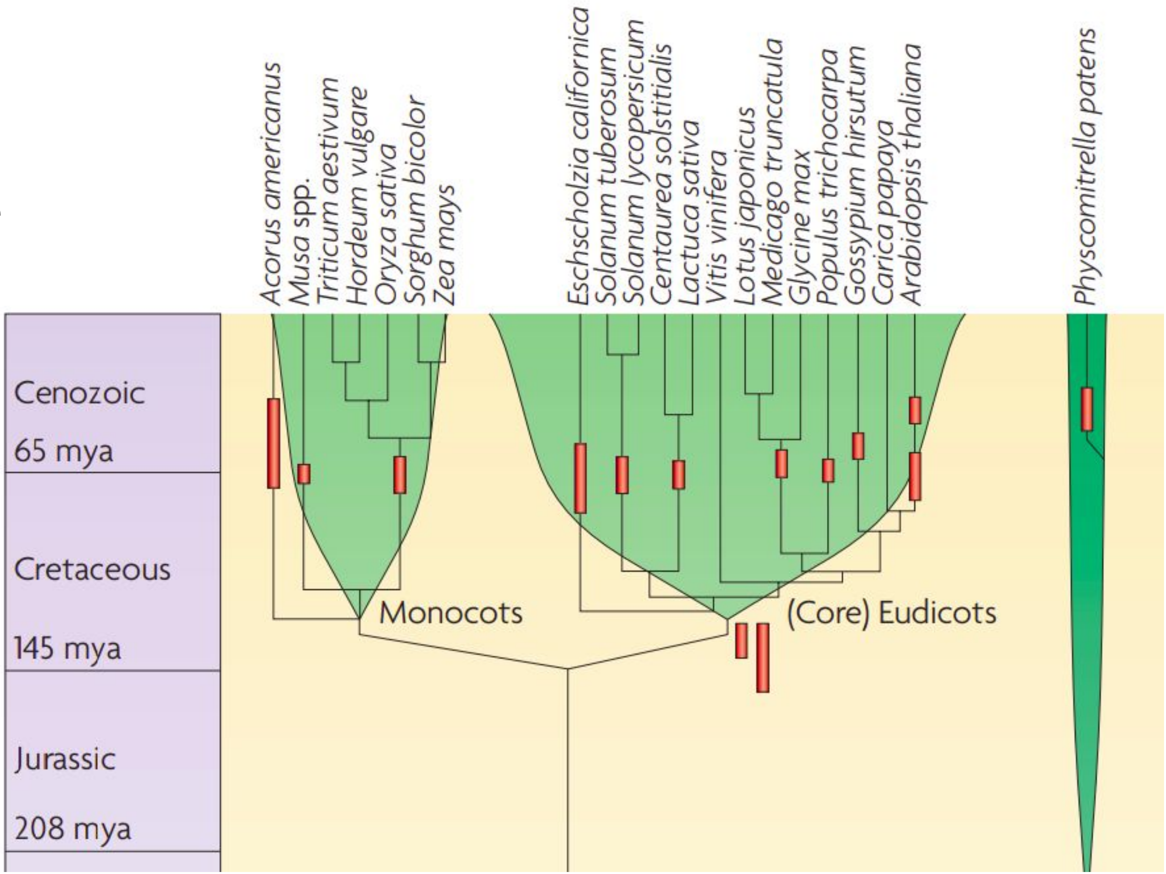
· Gnatosthome origins , extinction risk and increase on diversity



# Reducing the risk of extinction

· Several independent duplications around the K-T boundary

(~65Myears)



# increased species diversity

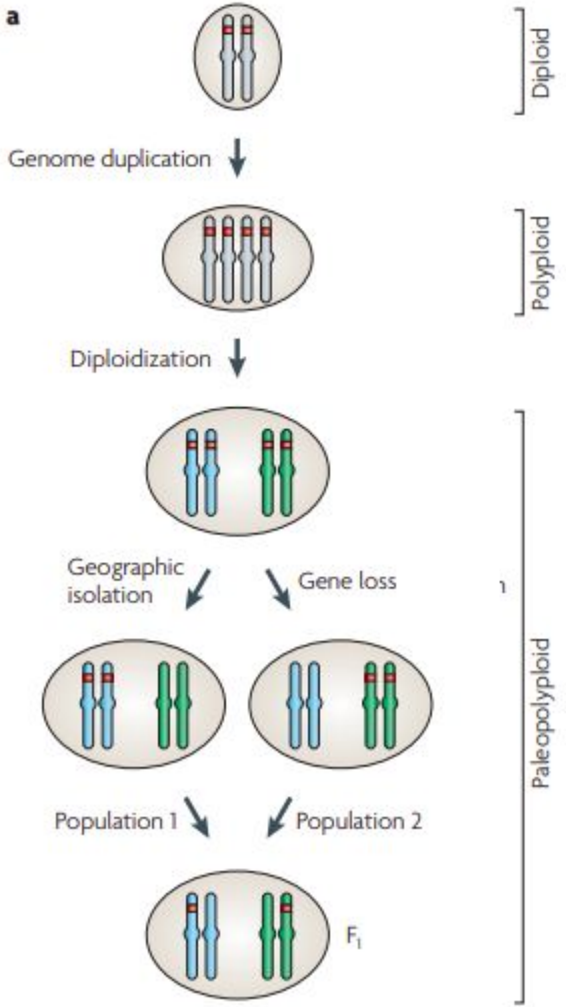
· Correlational no causation.

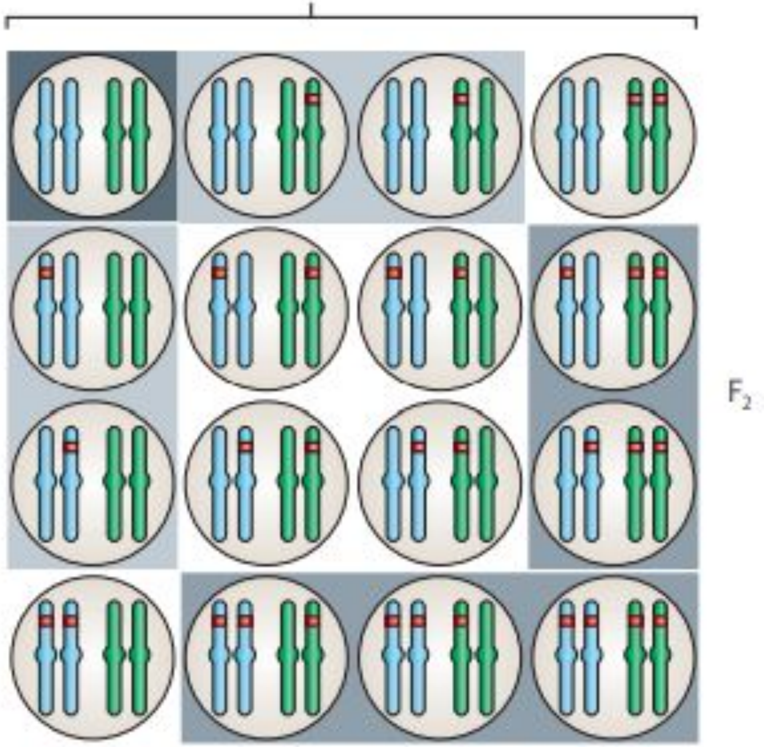
· Reciprocal gene loss. Has been observed in studies in Zebrafish and *Fugu rubripes*.

· Yeast species.

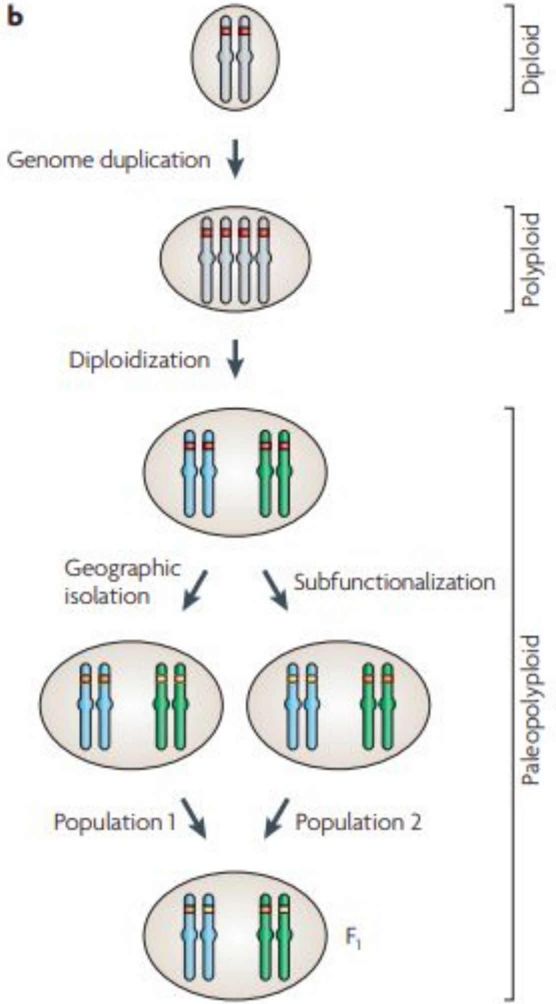
· Neutral and selective mechanisms may operate

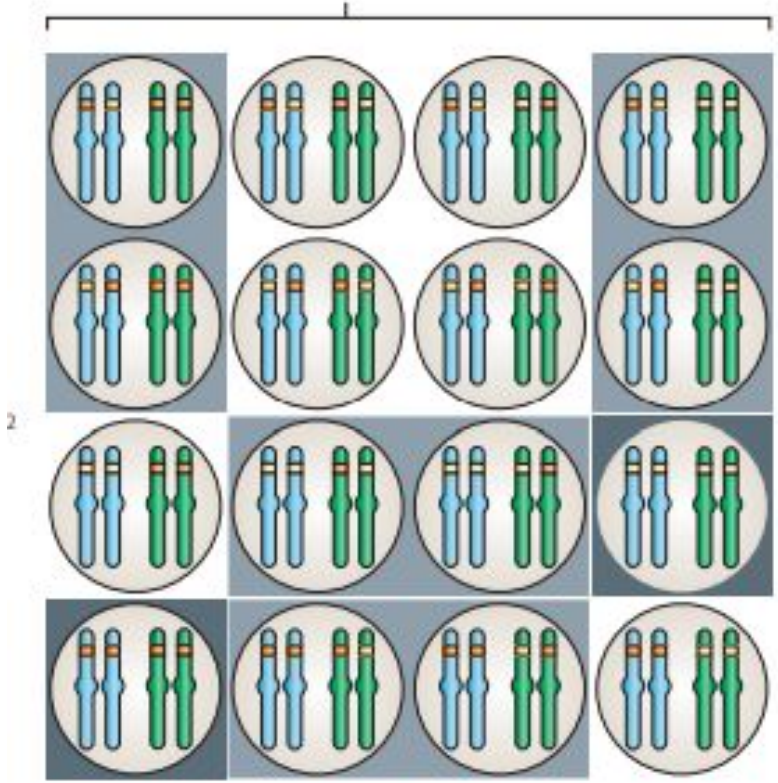
# Reciprocal Gene Loss



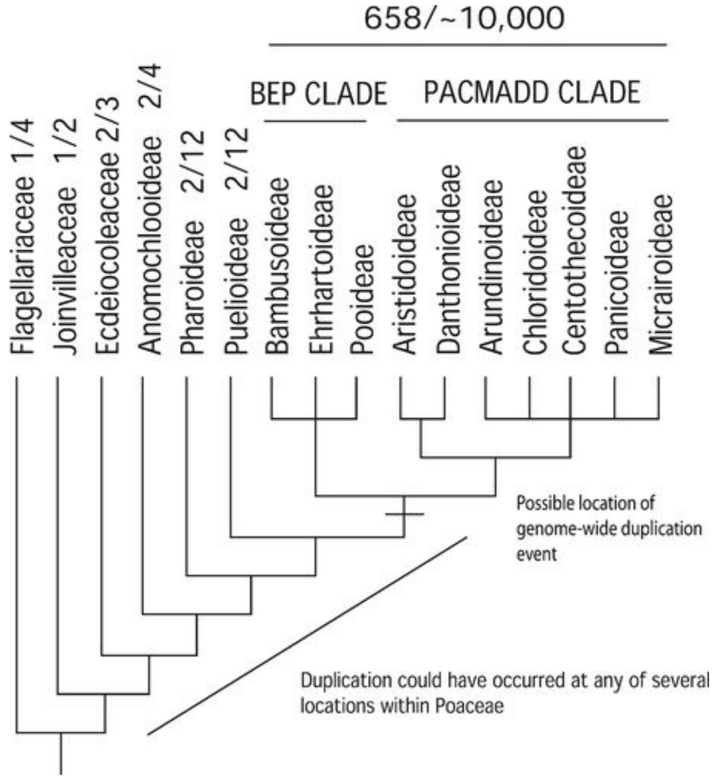



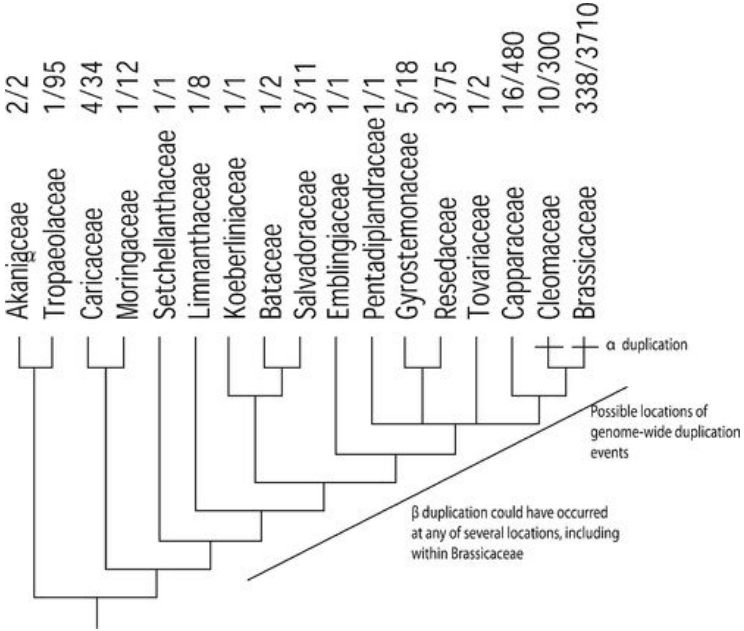
# Subfunctionlaization



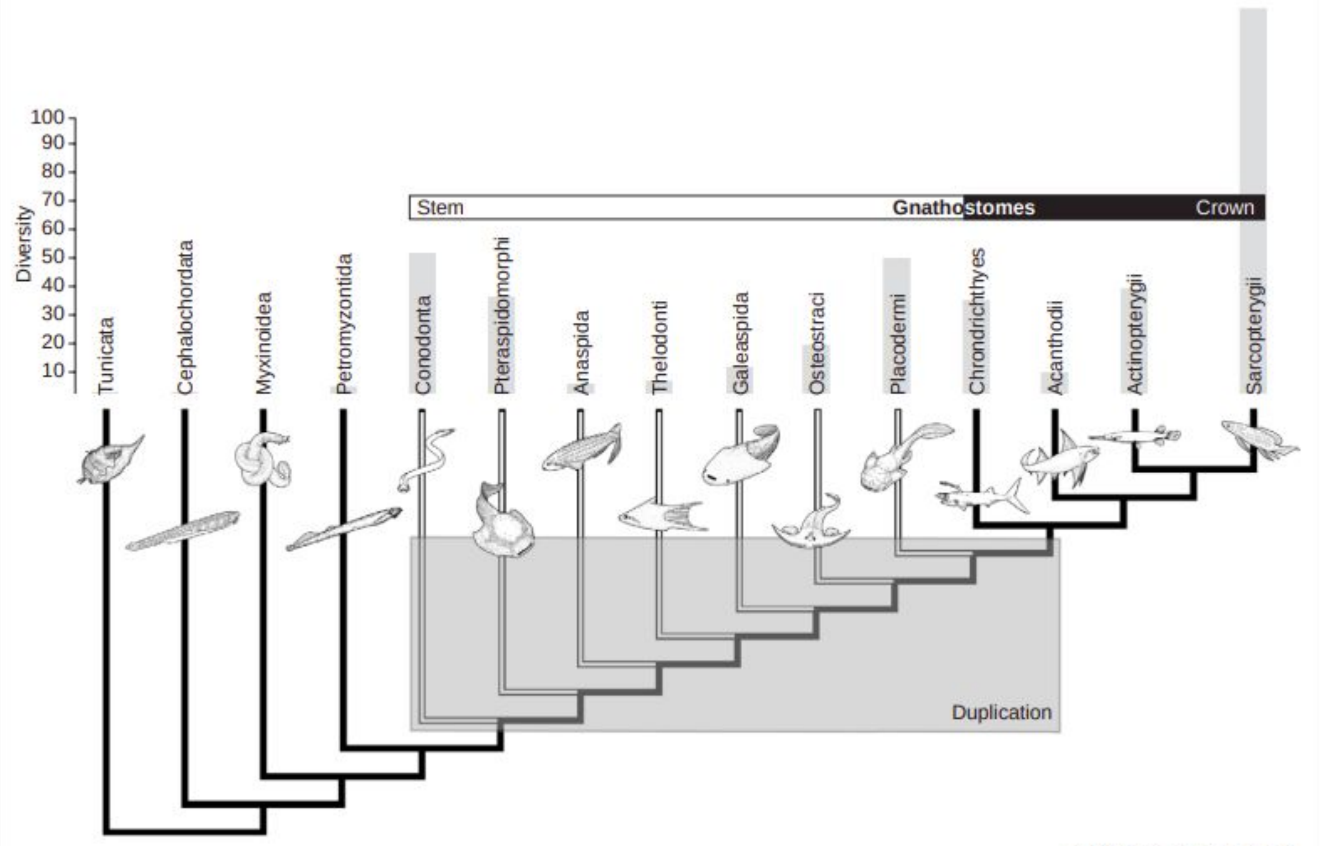



# Speciation events



# Speciation events



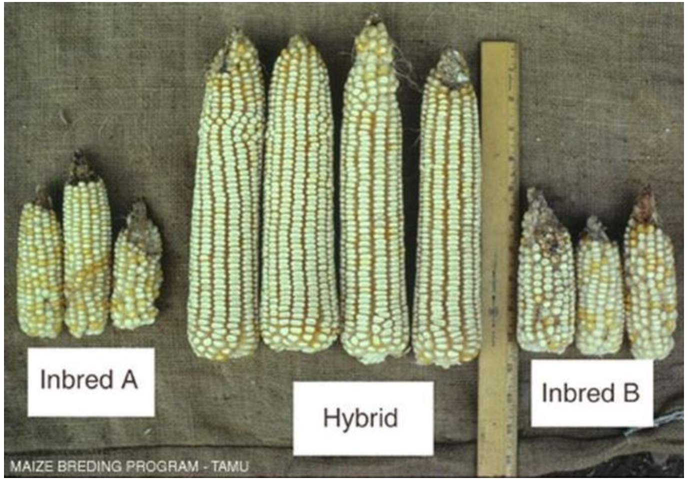

TRENDS in Ecology & Evolution

# Evolutionary innovations

Evolutionary innovations In the longer run, polyploidy may pave the way for evolutionary innovations or elaborations of existing morphological structures that allow exploration of fundamentally different regions of phenotype space.

# Increased vigour

· Heterotic effects and rapid genomic and epigenetic changes underlie the ability of polyploids to quickly adapt to more extreme environment



# Increased vigour

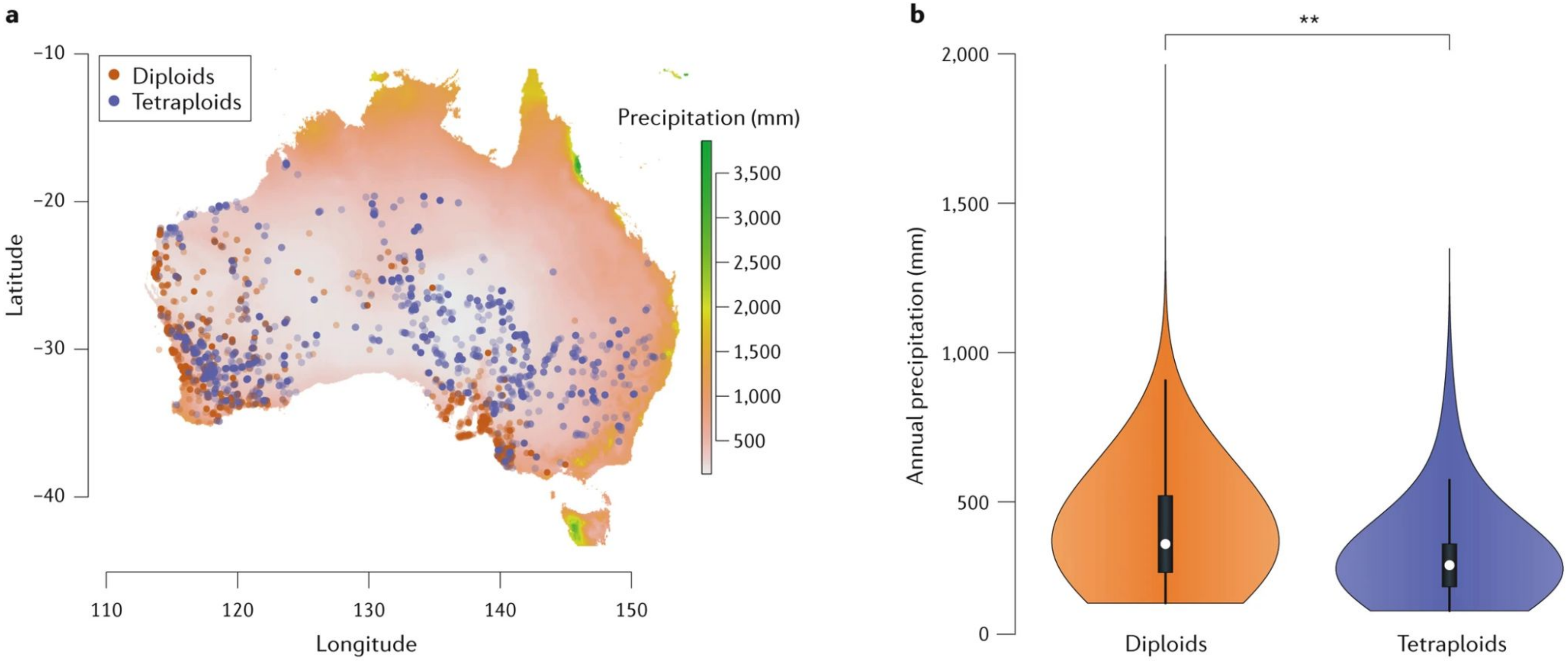
· polyploid plants are more tolerant to a wider range of environmental conditions compared with their diploid relatives

· Many polyploids are invasive and can exploit habitats that their diploid progenitors cannot

· Polyploid insects also have a wider geographical distribution than their diploid progenitors, often colonizing northern and mountain regions.

· *Xenopus laevis* (tetraploid) a highly invasive species, It is also extremely tolerant to salt, drought, cold and starvation, and is more disease resistant than its diploid relative *Silurana tropicalis*

# Increased vigour




Nature Reviews | Genetics

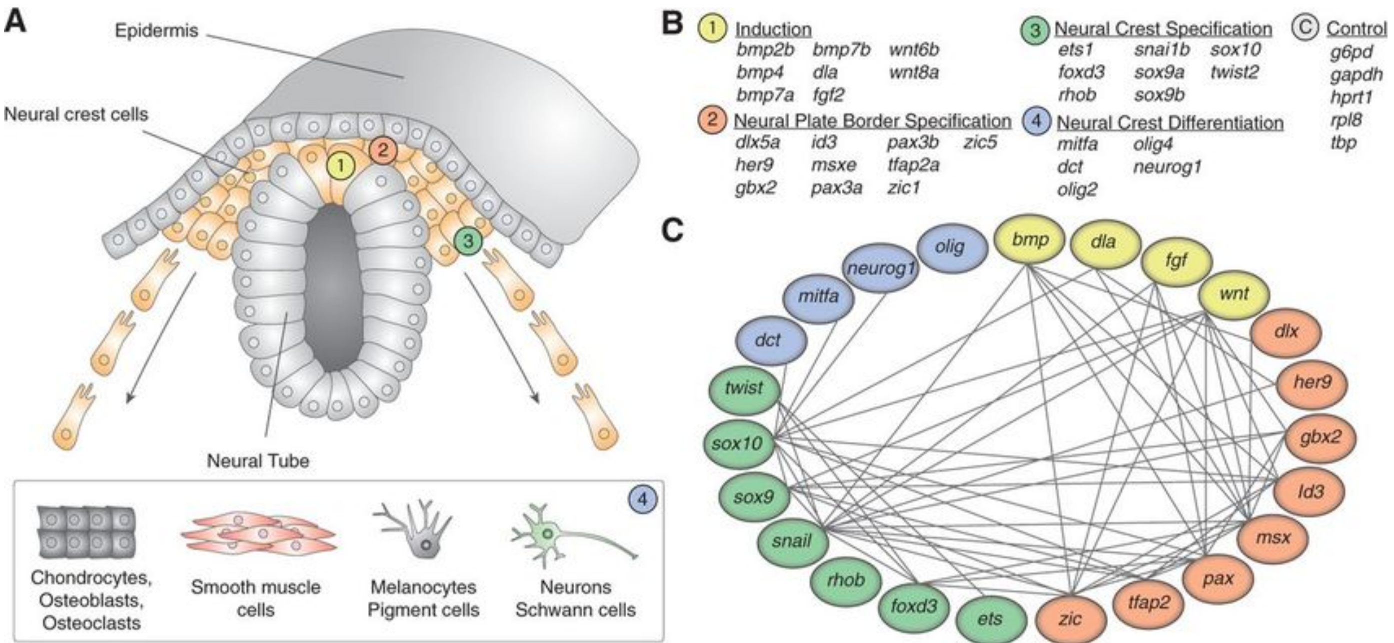
# Evolutionary innovations

Transcriptional and developmental regulators and signal transducers have been preferentially retained in duplicate after all genome duplications in Arabidopsis thaliana, after the 1r and 2r WGDs in vertebrates, after 3r in fish, and after the WGD in yeast

· more than 90% of the increase inn regulatory genes in the Arabidopsis lineage in the last ~150 million years is caused by genome duplications

# Evolutionary innovations

. In vertebrates, 1r and 2r are thought to be responsible for the expansion of the number of homeobox (Hox) clusters and other Hox genes, transforming growth factor-β pathway genes, insulin receptors, nuclear receptors and genes that specify the neural crest.



# Changing environments