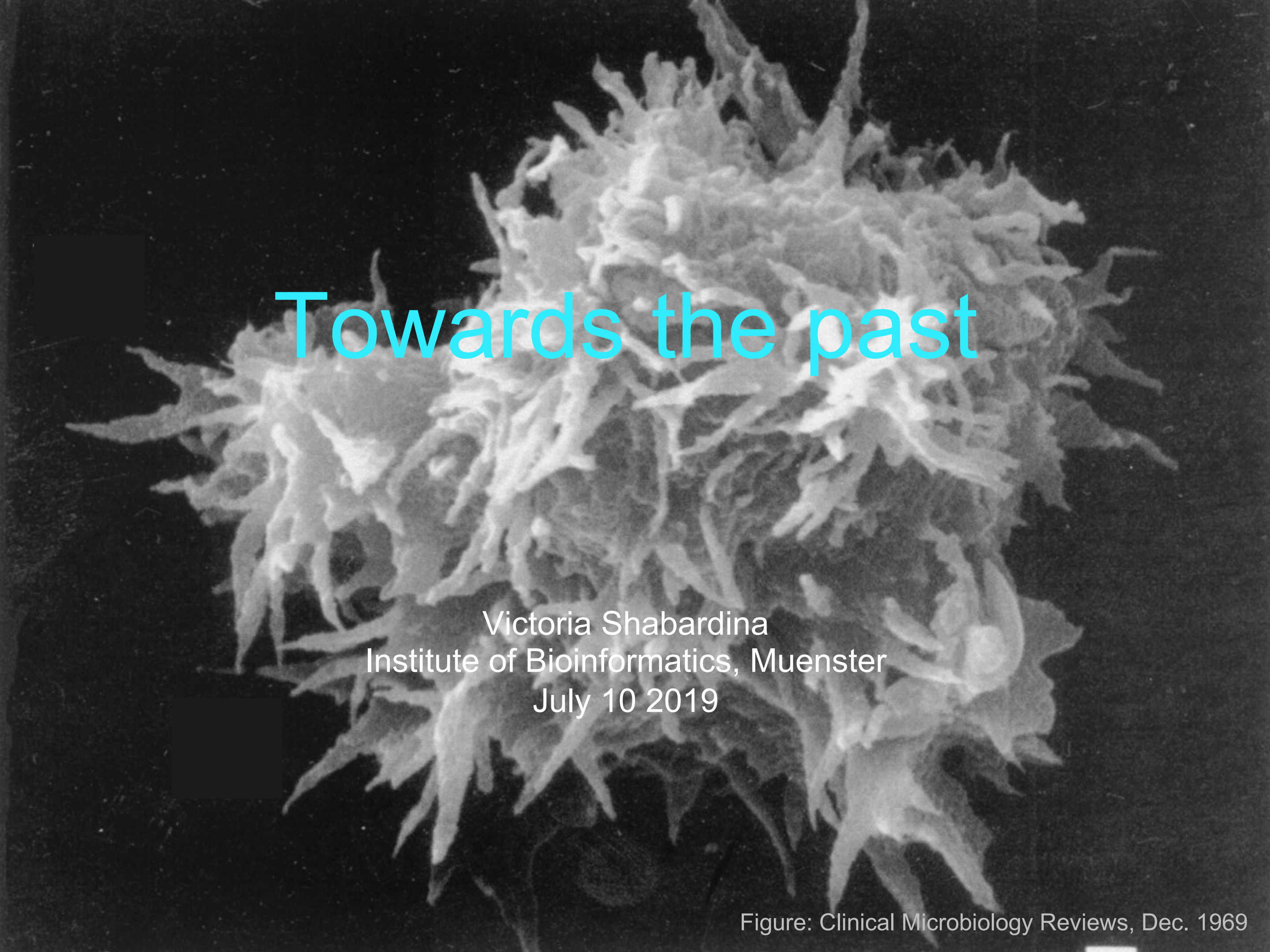


# Towards the past

Victoria Shabardina
Institute of Bioinformatics, Muenster
July 10 2019

Figure: Clinical Microbiology Reviews, Dec. 1969

# Architectural and functional rearrangement of genomes and the life style

| Features | Physiological adaptation | Mechanism |
|---|---|---|
| Free living<br>*Acanthamoeba castellanii* | Plasticity of gene expression (high activity) | Transcription regulation |
| | Big variety of serine/threonine kinases (environment) | Gene diversification and organism adaptation |
| | Acquirement of new genes (from surrounding bacteria) | Horizontal Gene Transfer |
| Parasitic<br>*Entamoeba histolytica* | Minimizing biosynthesis (amino acids, pyrimidines) | Gene lost |
| | Increase of some genes copy number or number of orthologs (host lysis, phagocytosis) | Gene duplication |
| | Specific physiology (oxygen level, host immunity) | Diversification, adaptation, **transcription machinery** |

***Entamoeba histolytica*** ***Acanthamoeba castellanii***

Genome

**8163 protein coding genes**
**20 Mbases**
vs
**14974 protein coding genes**
**42 Mbases**

Number of ribosomal proteins with multiple (3-5) gene copy number

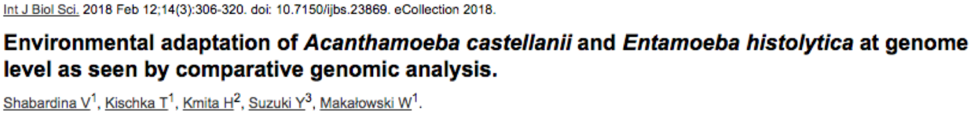
**44** vs **4**

Gene copy number for each aminoacyl-tRNA ligase

**1** vs **2-4**

# Architectural and functional rearrangement of genomes and the life style

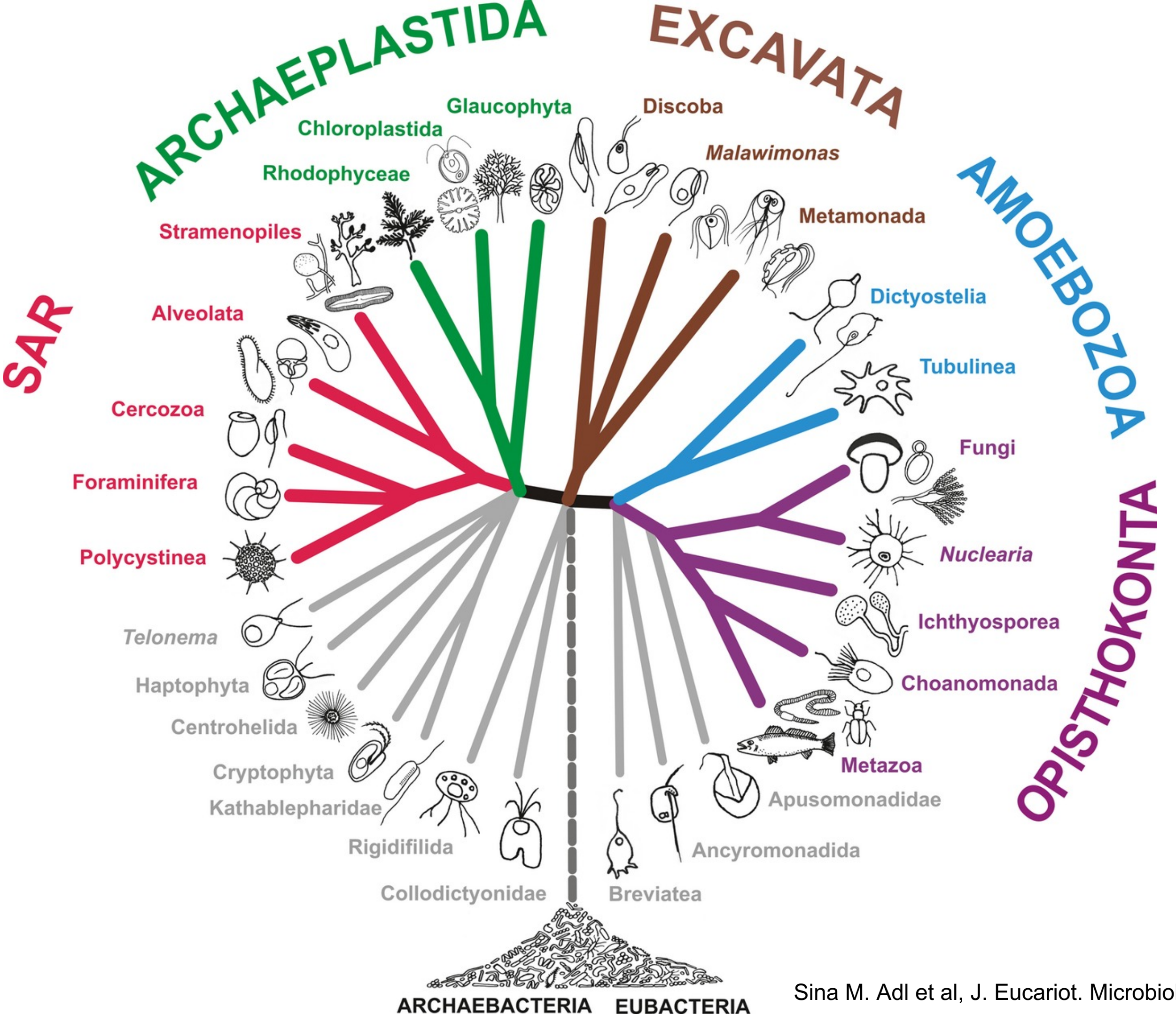
- *Eh* and *Ac* underwent expansion of **different genes families**
- **High efficiency** in genome usage of *Entamoeba*: stable translation levels, intensified transcription machinery, high gene copy number
- New step towards learning about **“ribosomal code”**
- Saving on energy metabolism: **minimized** activity in pathways related to **pyrimidines** in *Eh*
- Unique cytoskeletal proteins in *Eh* (possibly compensation for the lost of ER)
- **Highly** expressed proteins/whole orthology clusters in both amoebas with yet unknown functions



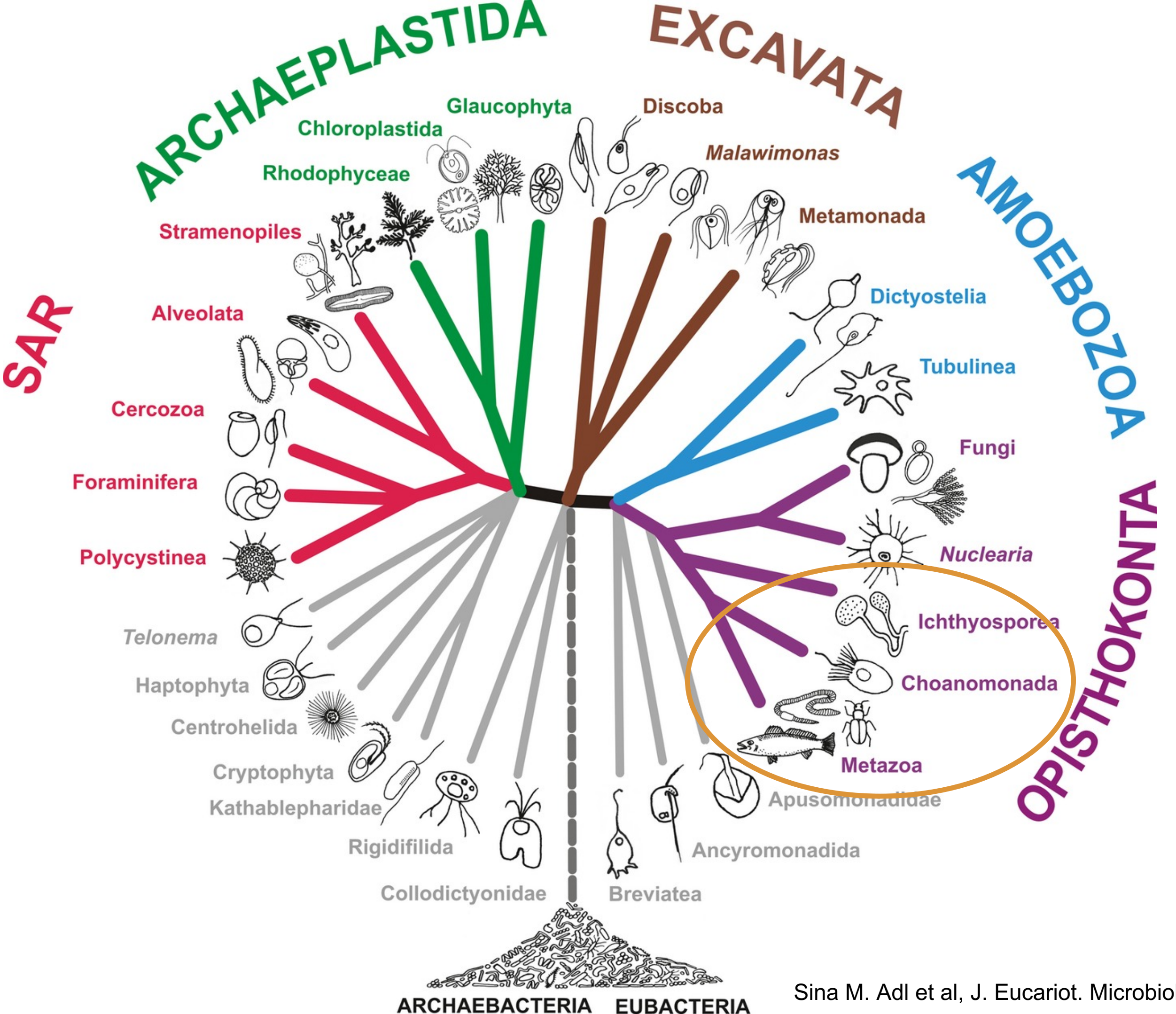
Int J Biol Sci. 2018 Feb 12;14(3):306-320. doi: 10.7150/ijbs.23869. eCollection 2018.

**Environmental adaptation of *Acanthamoeba castellanii* and *Entamoeba histolytica* at genome level as seen by comparative genomic analysis.**

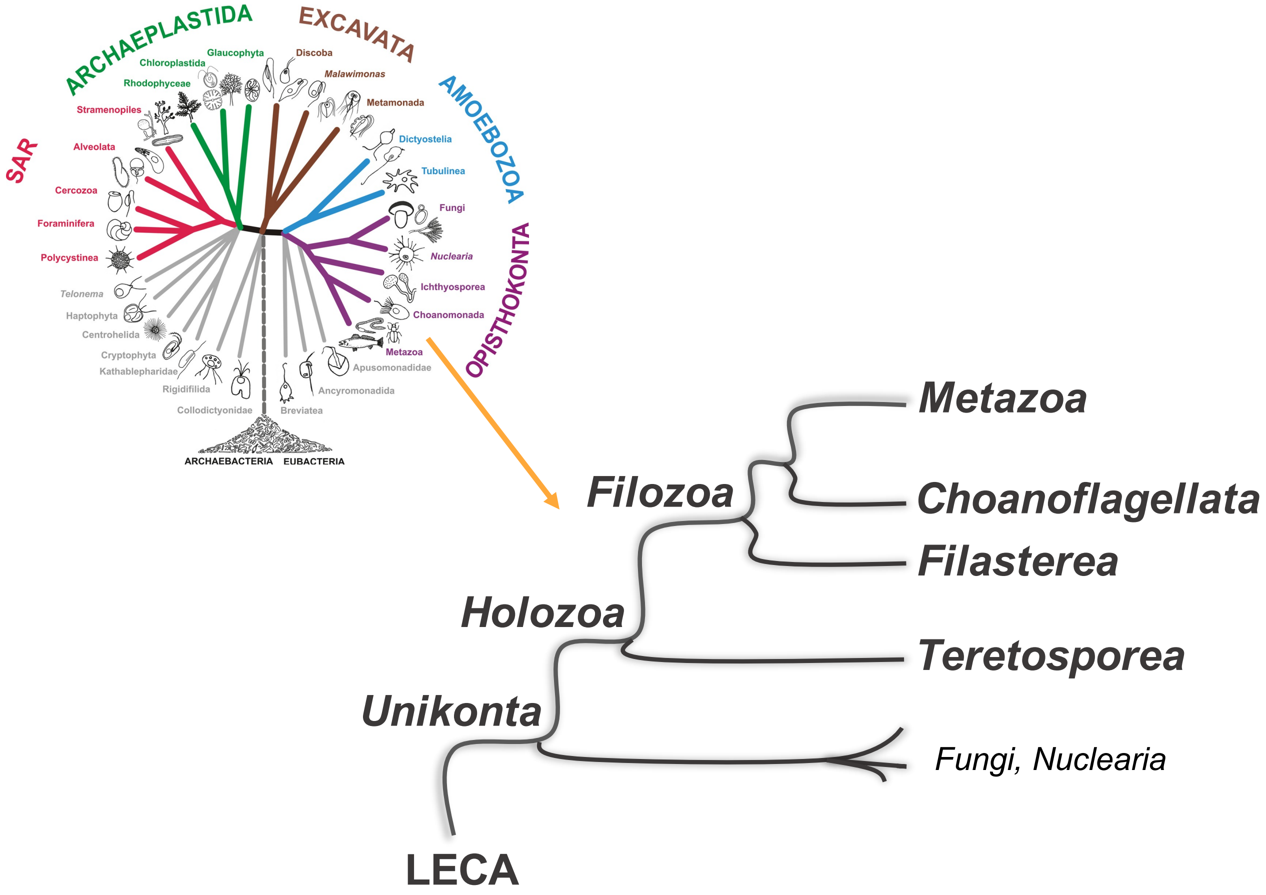
Shabardina V[1], Kischka T[1], Kmita H[2], Suzuki Y[3], Makałowski W[1].

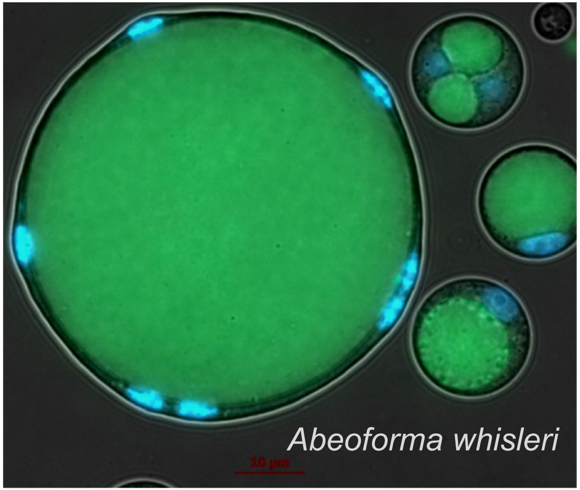


Sina M. Adl et al, J. Eucariot. Microbiol., 2012

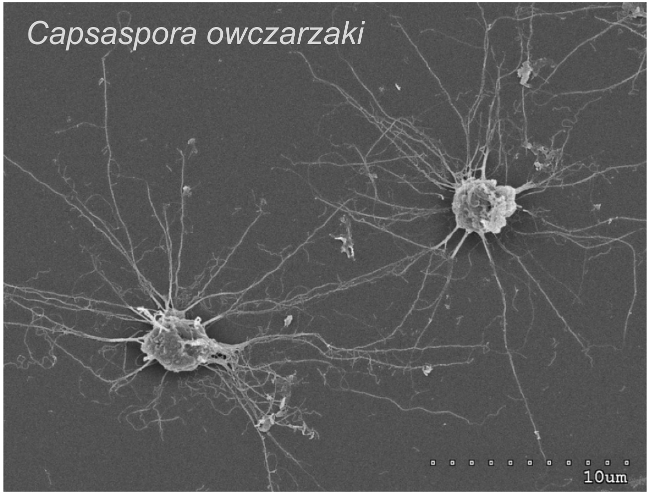


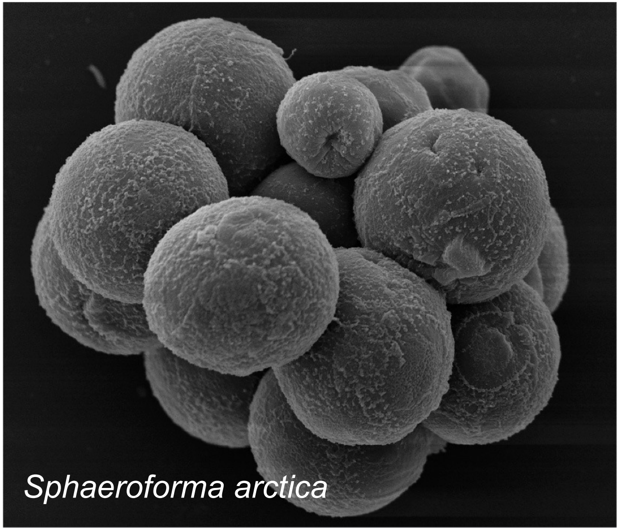
Sina M. Adl et al, J. Eucariot. Microbiol., 2012


ARCHAEPLASTIDA
EXCAVATA
AMOEBOZOA
OPISTHOKONTA
SAR
Glaucophyta
Chloroplastida
Rhodophyceae
Discoba
Malawimonas
Metamonada
Dictyostelia
Tubulinea
Fungi
Nuclearia
Ichthyosporea
Choanomonada
Metazoa
Apusomonadidae
Ancyromonadida
Breviatea
Stramenopiles
Alveolata
Cercozoa
Foraminifera
Polycystinea
Telonema
Haptophyta
Centrohelida
Cryptophyta
Kathablepharidae
Rigidifilida
Collodictyonidae
ARCHAEBACTERIA
EUBACTERIA
Metazoa
Choanoflagellata
Filozoa
Filasterea
Holozoa
Teretosporea
Unikonta
Fungi, Nuclearia
LECA

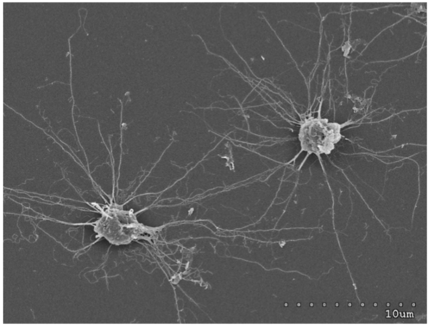

Abeoforma whisleri


Ichthyophonus hoferi


Capsaspora owczarzaki


Sphaeroforma arctica

MulticellgenomeLab: www.flickr.com/photos/146564503@N06/albums



*Capsaspora owczarzaki*

Complex genome structure

Transcription regulation

Cell type specific phosphosignalling

Cell type specific long ncRNAs

Alternative splicing

Cell type specific histone marks

Animal specific proteins:

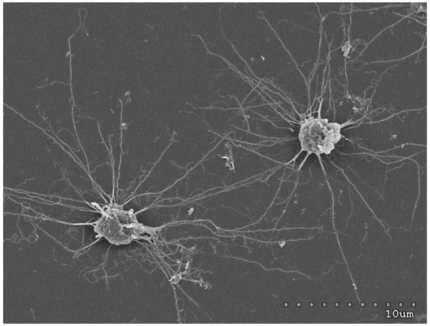
c-type lectins, cadherins, integrins (cell adhesion)

Some tyrosine kinases responsible for cells communication

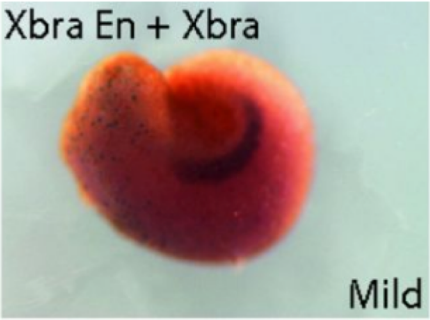
Myc, Runx and T-box TF (developmental regulation in animals)

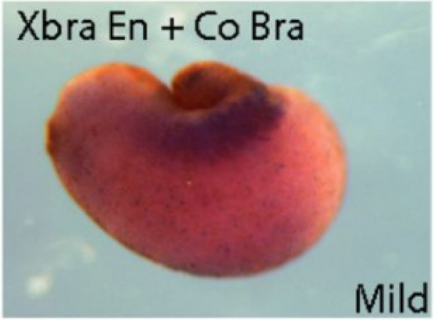
P53 (tumor antigen)

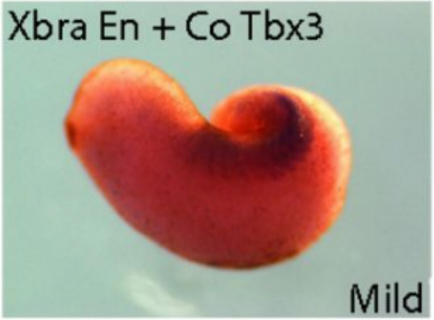
*Capsaspora owczarzaki*



Sebe-Pedros et al, PNAS, 2013







Xbra En – defected Brachyury
Xbra – xenopus mRNA rescue
Co Bra – capsaspora mRNA rescue
Co Tbx3 – T-box3 mRNA rescue

# Ways of evolution:

Re-use of molecular mechanisms and pathways

Domain shuffling and alternative splicing – new genes

Exploratory behavior, physiological adaptation

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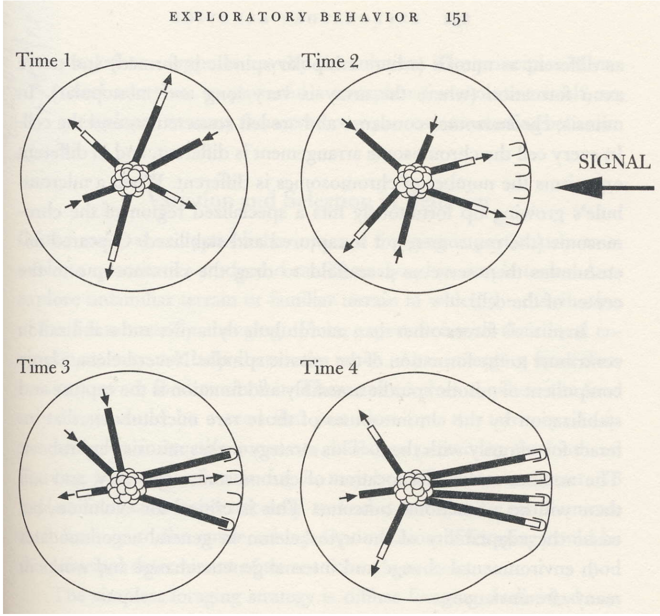
Re-use of molecular mechanisms and pathways

Domain shuffling and alternative splicing – new genes

Exploratory behavior, physiological adaptation



EXPLORATORY BEHAVIOR 151

“The plausibility of life”
M. W. Kirschner & J. C. Gerhart
Yale University Press, 2005

# Long read sequencing

| species | Scaffold count | Scaffold N50, bases | technology | Coverage | year |
|---|---|---|---|---|---|
| *Limulus Polyphemus* (horseshoe crab) | 286 792 | 254 089 | Roche 454 | 18x | 2014 |
| *Octopus bimaculoides* | 151 674 | 475 182 | Illumina HiSeq 2000 | 92x | 2015 |
| *Amphimedon queenslandica* (sponge) | 13 397 | 120 365 | Sanger | 8x | 2010 |
| *Phascolarctos cinereus* (koala) | 1 906 | 11 587 828 | PacBio | 57.3x | 2017 |
| *Ornithorhynchus anatinus* (platypus) | 304 | 83 338 043 | PacBio RSII, 10X Genomics, Bionano Genomics DLS, Dovetail Genomics HiC, Arima Genomics | 58.5x | 2019 |