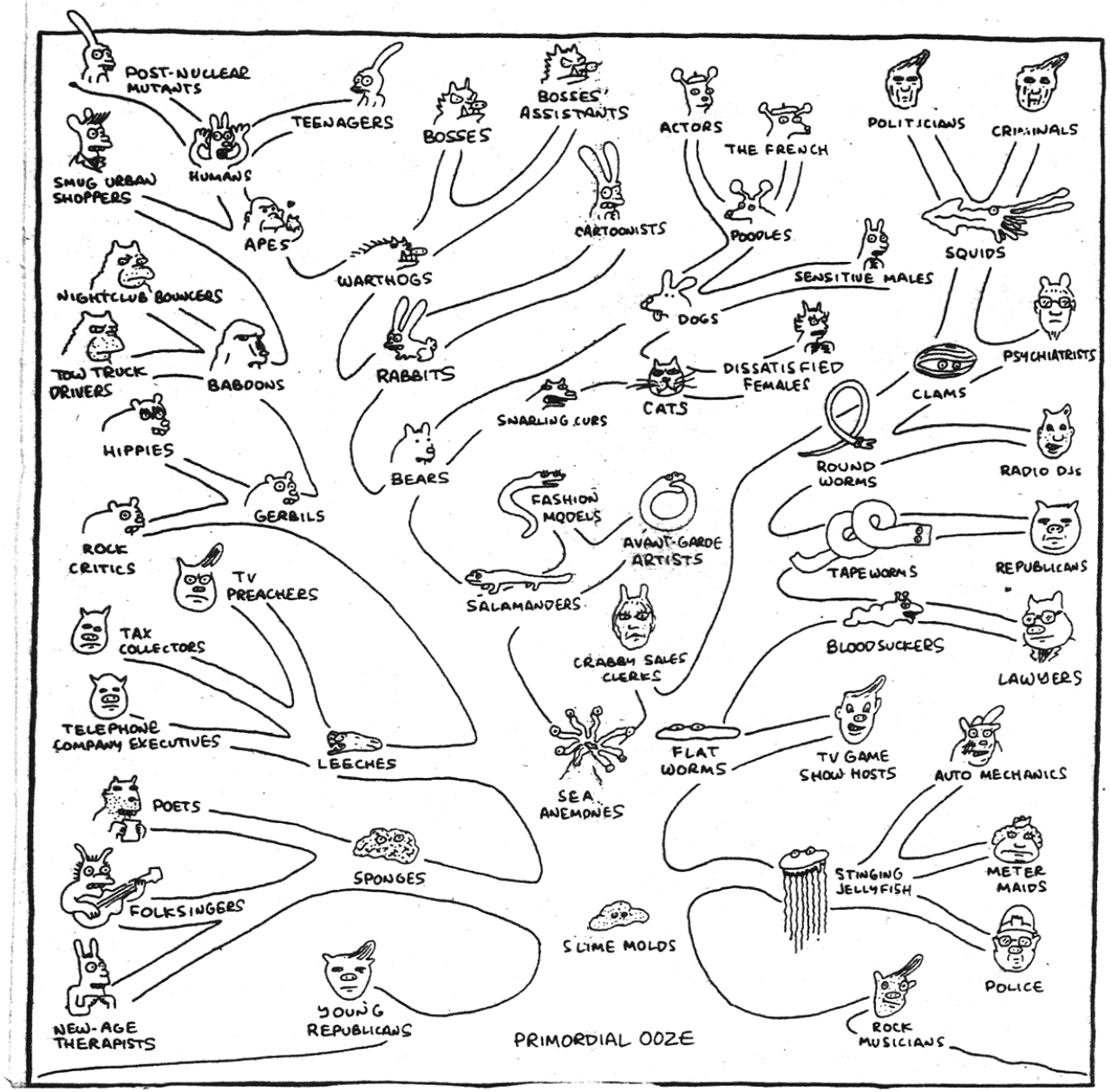
Trickovic	21-Apr	9:05
Milhaven	21-Apr	9:12
Versoza	21-Apr	9:19
Coffman	21-Apr	9:26
Cooley	21-Apr	9:33
Garber	21-Apr	9:40
Spencer	21-Apr	9:47
Deptula	21-Apr	9:54
Gonzalez Cruz	26-Apr	9:05
Harvey	26-Apr	9:12
Hoskinson	26-Apr	9:19
Urquidez Negrete	26-Apr	9:26
Lin	26-Apr	9:33
Sandler	26-Apr	9:40
Yanagisawa	26-Apr	9:47
Baca	26-Apr	9:54
Bilolikar	28-Apr	9:05
Faye	28-Apr	9:12
Garris	28-Apr	9:19
Mallett	28-Apr	9:26
Serrano Vicente	28-Apr	9:33
Shapiro	28-Apr	9:40
Trias	28-Apr	9:47

LIFE IN HELL

By Matt Groening © 1984



Origins of Organismal Complexity

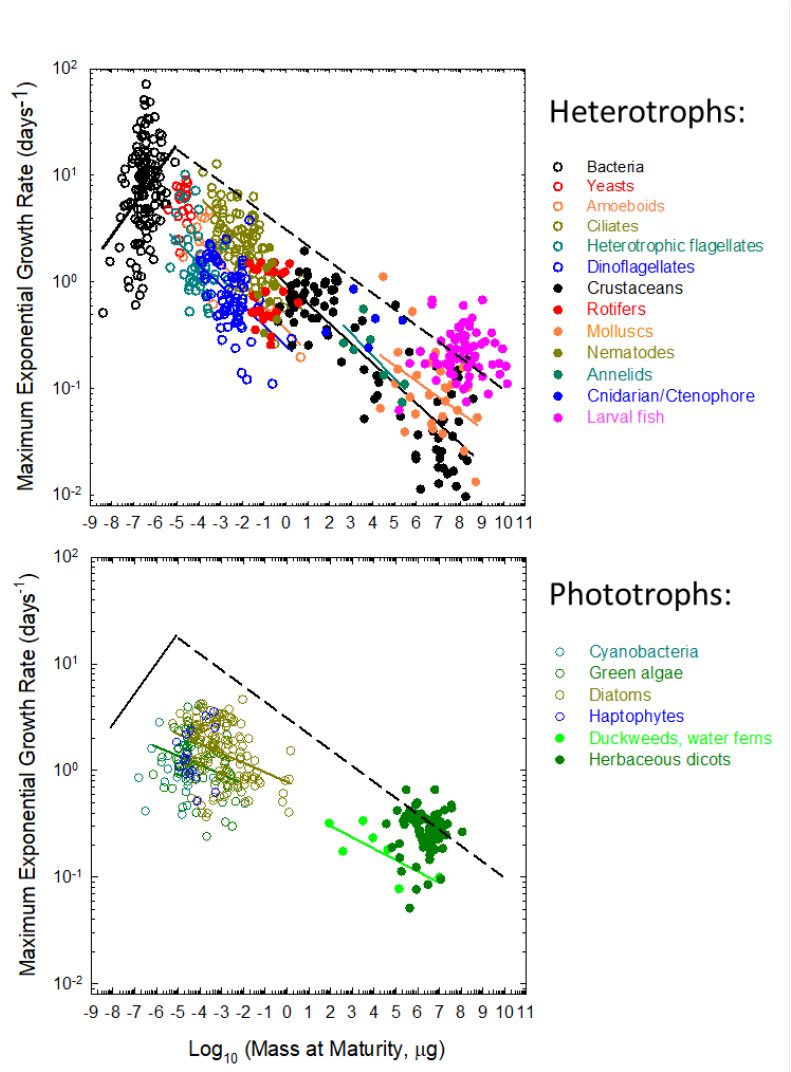
- Deconstructing the great chain of being.
  - Genome complexity and organismal complexity.
  - A shake-up of genomic organization in the ancestral eukaryote.

- The origins of multicellularity.
  - Multiple origins in eukaryotes, but few to a high level of refinement.
  - Multicellularity and cooperativity in bacteria.
  - The costs of multicellularity.
  - The emergence of cell-type specialization.

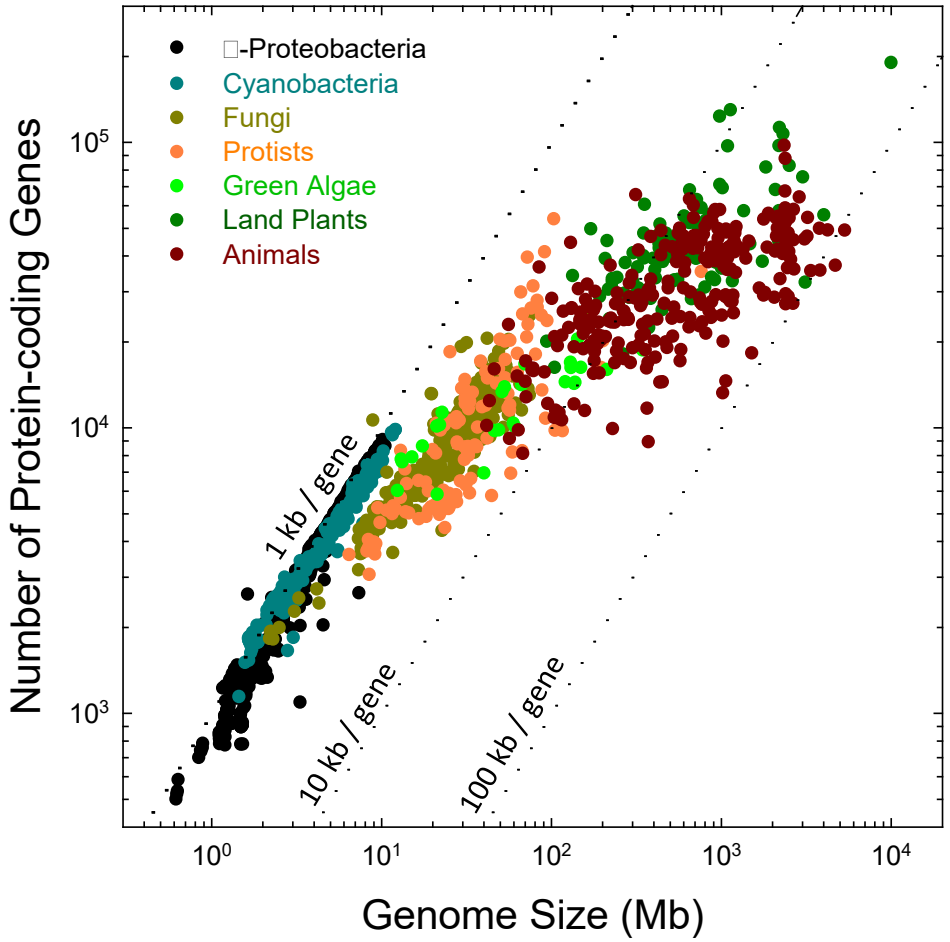
Didacus Valades
(Rhetorica Christiana, 1579)

Dispelling the Myth That Complexity is the Goal of Evolution

- The universal outcome of natural selection is the promotion of genetic changes that enhance the rate of allelic transmission into the gene pool.
- No evidence that complexity is a direct target of natural selection.
- Intrinsic costs to complexity at the energetic and mutational levels.
- Decline in rates of biomass productivity with increasing organism size.



Genome Complexity and Organismal Complexity



- The increase in organismal complexity is accompanied by a modest increase in gene number, with substantial overlap in gene number between bacteria and unicellular eukaryotes.

- Passive origin of increased genome size is a consequence of an increase in the power of random genetic drift:
  - Mobile-genetic elements.
  - Introns.

Shake-Up in Genomic Organization in the Stem Eukaryote?

- Increased complexity of multimeric proteins in eukaryotes. Many features of eukaryotic cell biology rely on heteromeric protein complexes (with component parts encoded by different genes) whose orthologs in prokaryotes are homomeric.
  - Meiosis and mitosis.
  - RNA processing, e.g., SM proteins.
  - Chaperones, proteasomes, exosomes.
  - Nuclear pore complex.
  - Alpha and beta tubulins.

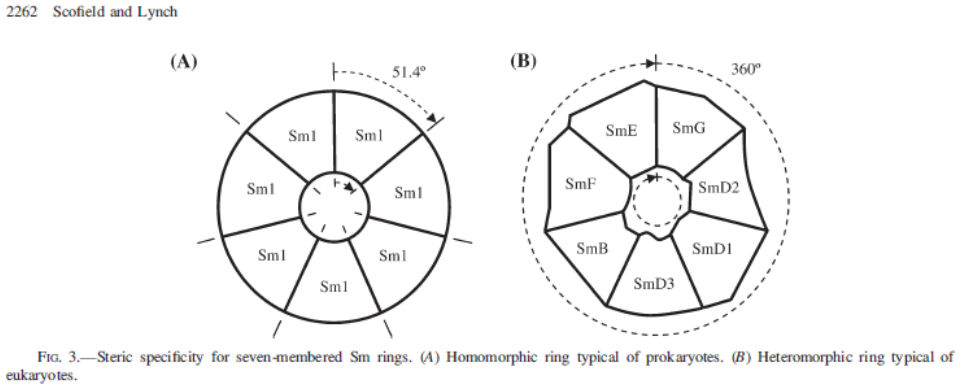


FIG. 3.—Steric specificity for seven-membered Sm rings. (*A*) Homomorphic ring typical of prokaryotes. (*B*) Heteromorphic ring typical of eukaryotes.

- Two major episodes of global glaciation: ~2.4 and ~0.7 BYA, near the times of origin of eukaryotes and animals, respectively.

- Preservation of duplicate genes by subfunctionalization, divergent resolution, and the passive emergence of reproductively isolated lineages.

Evolution of Multicellularity

- Has occurred numerous times in eukaryotes and bacteria.
- A key to understanding is the cost of cooperative, altruistic behavior relative to the overall gains of the system.
- What is the unit of evolution?
- What is an individual?
- What prevents the invasion of cheaters?

Multicellularity and Cellular Differentiation Has Evolved Multiple Times in Eukaryotes

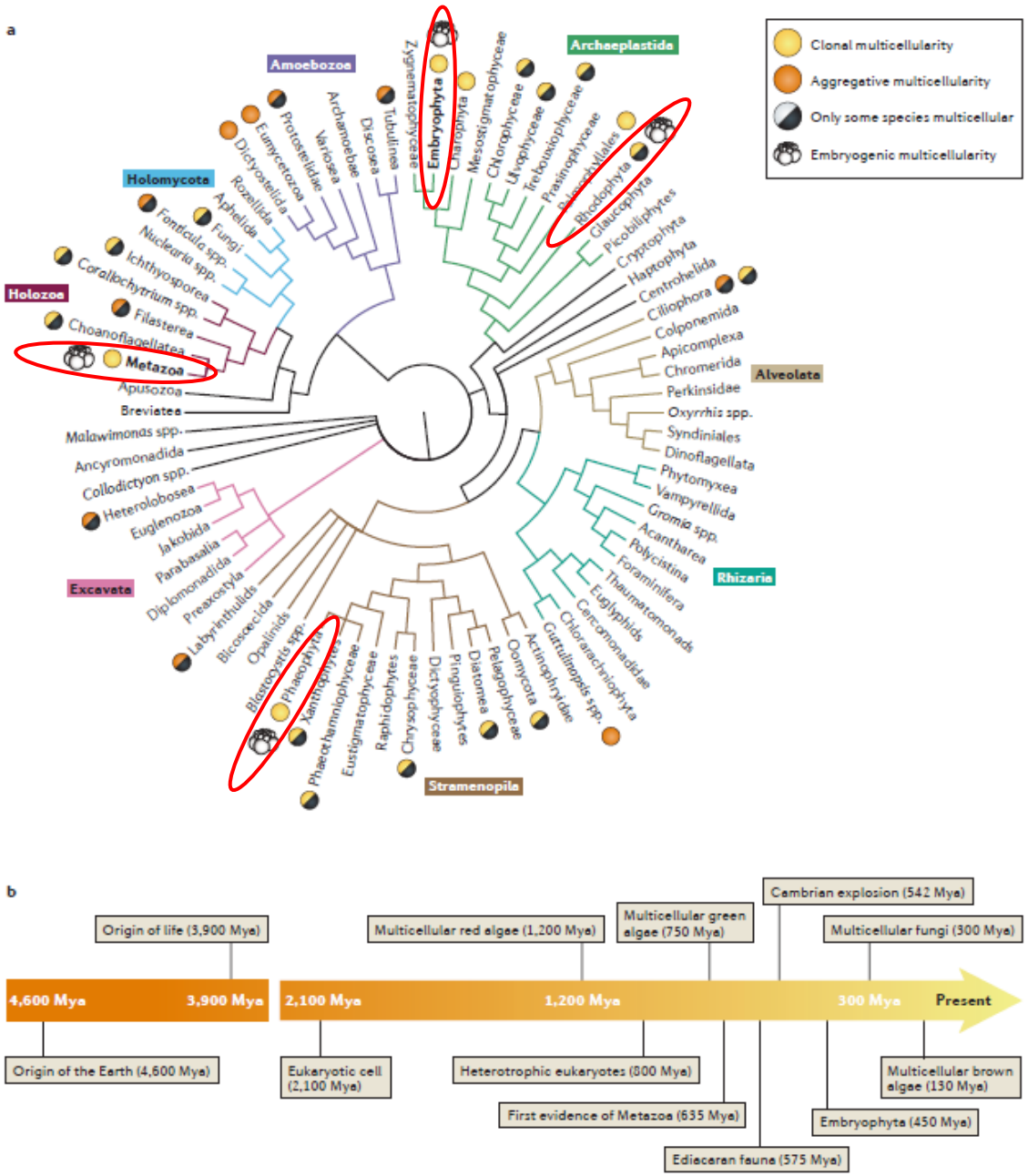


Figure 1 | **The multiple origins of multicellularity. a** | The phylogenetic distribution of multicellularity among eukaryotes. Multicellular forms (clonal or aggregative; see BOX 1) are present in several eukaryotic lineages. Some lineages, such as animals (Metazoa; highlighted in bold) and plants (Embryophyta; highlighted in bold), are entirely multicellular (that is, all species are multicellular), whereas other lineages have only a few multicellular species, with the majority being unicellular. From this widespread distribution, it can be inferred that multicellularity has evolved independently multiple times, although only in four lineages is this multicellularity linked to embryonic development and complex body plans. The tree is a consensus composite based on several recent phylogenomic studies[19,130–138]. **b** | A timeline of the origins of the major multicellular eukaryotic clades showing that transitions to multicellularity have occurred at very different times in the history of life. The estimations are based on fossil record and molecular clock estimates[4,119–123,125–127,139]. Time units are millions of years ago (Mya).

(Sebe-Pedros et al. 2017)

Gravity Quickly Selects for “Snowflake” Colonial Phenotypes in *S. cerevisiae*

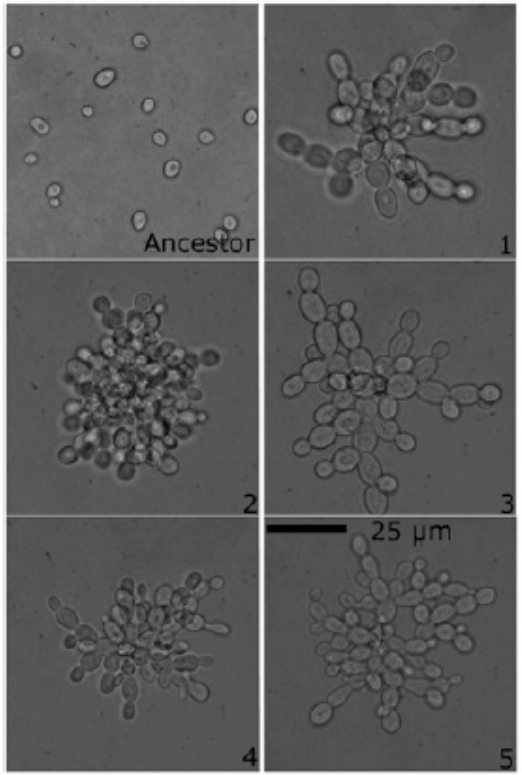


Fig. 1. Rapid and convergent evolution of the multicellular “snowflake” phenotype. All 10 replicate populations (replicate population number in lower right corner) evolved similar multicellular phenotypes after 60 rounds of selection for rapid settling (shown are replicate populations 1–5; see Fig. S2 for replicate populations 6–10). These genotypes display a similar growth form: the cluster is composed of related cells that do not disassociate after budding, resulting in branched multicellularity.

- Not difficult to rapidly evolve multicellularity in experimental laboratory populations.

Ratcliff et al. (2012, PNAS)

Multicellularity and Cellular Differentiation is Common in Prokaryotes

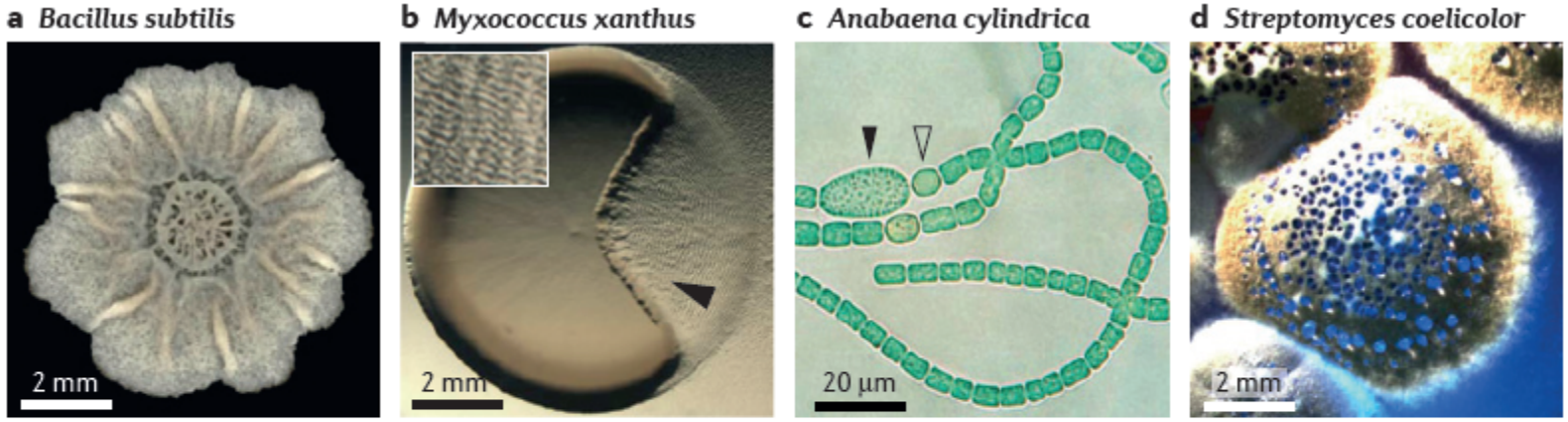


Figure 1 | **Bacterial manifestations of multicellularity. a** | A mature *Bacillus subtilis* biofilm. **b** | Predation of an *Escherichia coli* colony (left) by swarming *Myxococcus xanthus* cells (right), which is characterized by a rippling pattern (arrowhead and inset). **c** | Formation of heterocysts (open arrowhead) and akinetes (closed arrowhead) in chains of the filamentous cyanobacterium *Anabaena cylindrica*. **d** | A mature colony of *Streptomyces coelicolor*, which is indicated by the fluffy, grey layer of sporulating aerial mycelium on the colony surface. The colony produces the blue-pigmented polyketide antibiotic actinorhodin. Image in part **a** is reproduced, with permission, from REF. 28 © (2013) Macmillan Publishers Ltd. All rights reserved. Image in part **b** courtesy of S. Müller and J. Kirby, University of Iowa, USA. Image in part **c** courtesy of J. E. Frías and E. Flores, Centro de Investigaciones Científicas, Universidad de Sevilla, Spain.

- Coming together vs. staying together.
- Division of labor.

Claessen et al. (2014, Nature Rev. Microbiol.)

Prokaryotes Exhibit Many "Behaviors" That Parallel Features in Metazoans

Table 1. Social traits exhibited by bacteria compared with examples from vertebrates and invertebrates.

cooperative behaviour	group-derived benefits	microbe examples	higher organism comparisons
chemical communication (quorum sensing)	coordinated population behaviour	*Vibrio fischeri*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, etc.	pheromone production in many social animals
biofilm formation	protection from adverse environmental conditions	many species of bacteria	Burrows, nests, hives, cities
nitrogen fixation: mutualistic behaviour	nutrients and niche protection in nodules	*Rhizobium* spp. with legume plants	yucca plant and yucca moth
foraging/hunting: nutrient acquisition	enhanced growth and colonization sometimes in specialized niches	siderophore production for iron acquisition in many bacteria	wolves, lions, humans
autolysis (suicide)	provides nutrients and DNA for biofilm development	*P. aeruginosa*	apoptosis in eukaryotic cells
motility (swarming)	coordinated motility to a nutrient source	*Yersinia* spp., *Myxococcus xanthus*, *P. aeruginosa*	ants, termites
antibiotic resistance	production of extracellular enzymes (e.g. β-lactamase) to break down antimicrobials	*Escherichia coli*, *Klebsiella* spp.	group defence, antipredator vigilance
immune modulation	modulation of immune response to facilitate survival within the host	*P. aeruginosa*, *Porphyromonas gingivalis*, *Helicobacter pylori*	helminth parasites

Quorum Sensing: cell-cell communication involving the production and detection of extracellular secretions.

- Deployed in many group contexts, eliciting features that are of little utility when exhibited by single cells – biofilm formation, bioluminescence, food-degrading enzymes, antibiotic production.

  Low cell density (asocial behavior) ←→ High cell density (social production of “public goods”)

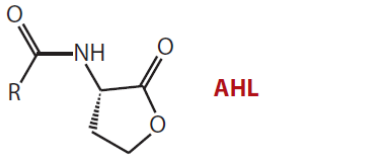
- Low molecular weight autoinducers are synthesized and released.

- When the autoinducer concentration exceeds a threshold level, cognate receptors bind them, triggering a signal-transduction cascade that coordinately turns on a group of response genes within the local population of cells.

- Some species harbor multiple quorum-sensing systems.

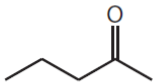
Gram-Negative Species Generally Deploy Lactones as Autoinducers: light organ in squid; *Pseudomonas* biofilm formation.

Autoinducers:



AHL

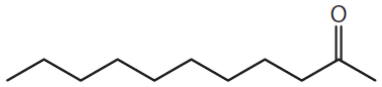
R group



V. fischeri (LuxI)

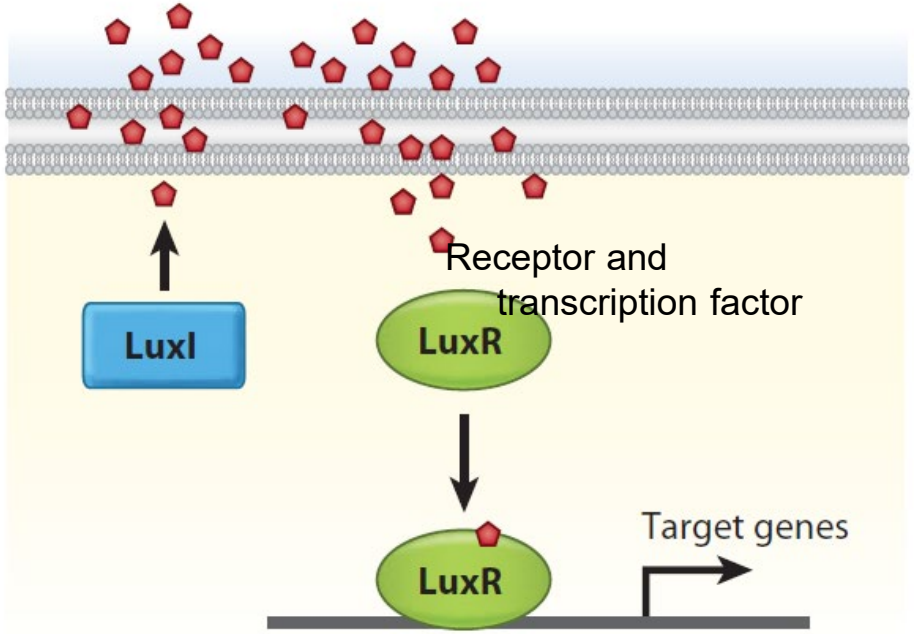
V. harveyi (LuxM)

P. aeruginosa (RhlI)



P. aeruginosa (LasI)

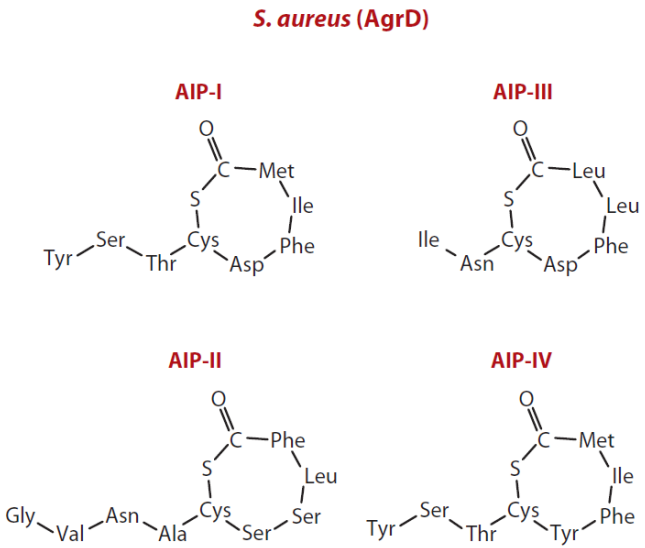
- Autoinducers move by simple diffusion.
- Sensors are cytoplasmic, and operate as transcription factors, as a one-component signal-transduction system.
- Cost of operating and maintaining the system?



Ng and Bassler (2009)

Gram-Positive Species Generally Deploy Small Modified Peptides as Autoinducers

- Because of their larger size, secretion requires specialized transporters.
- Sensors are also membrane-bound, and comprise the first part of a two-component system.
- Different species have distinct autoinducer sequences.



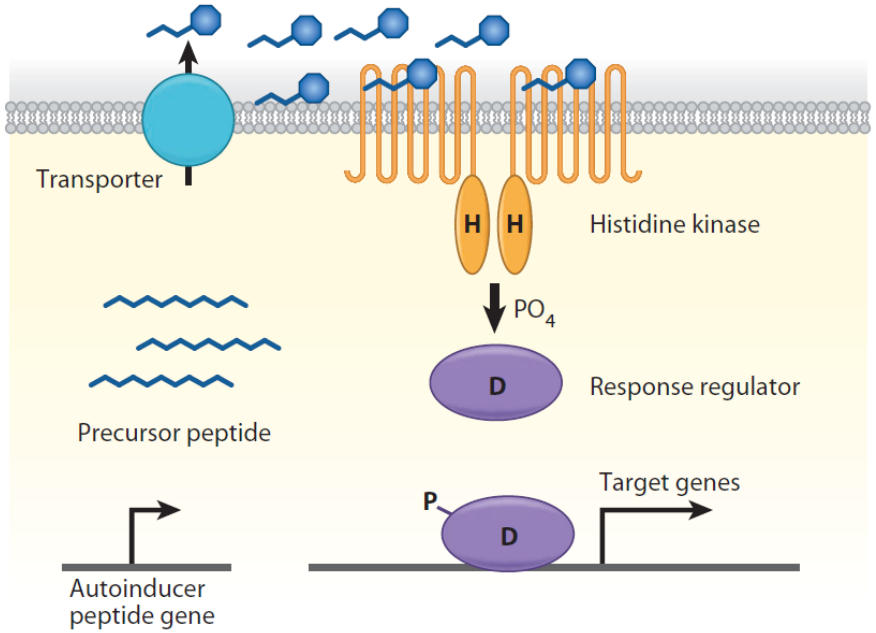
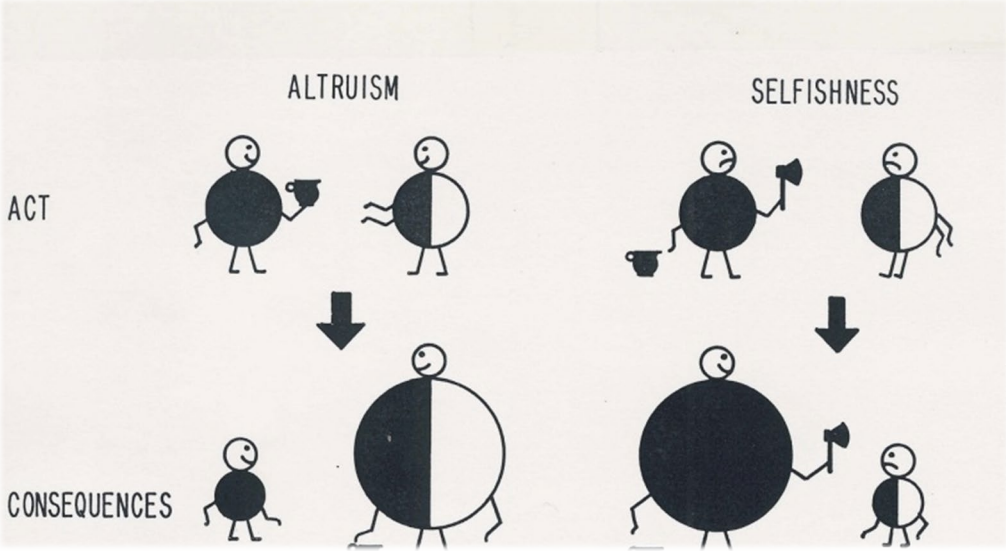


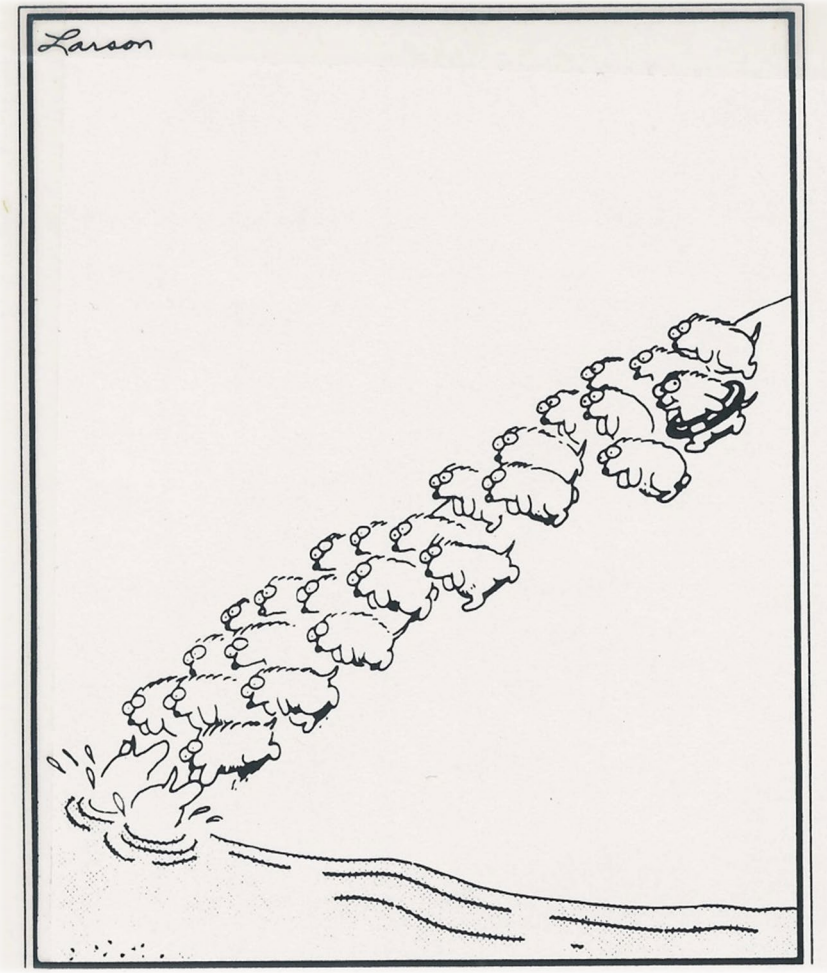
Figure 3

A canonical Gram-positive two-component-type quorum-sensing system. Blue octagons denote processed/modified peptide autoinducers.

How Do Social Systems Remain Evolutionarily Stable?

- Cheaters that forego the cost of producing a population-wide benefit while continuing to profit from the public goods provided by others.





Slime-Mold Social Systems: maintenance of multiple kin-recognition groups by frequency-dependent selection.

- Single cells aggregate to form a fruiting body.
- Cells that form the stem leave no progeny.
- Cheaters avoid the costs of producing the stem.

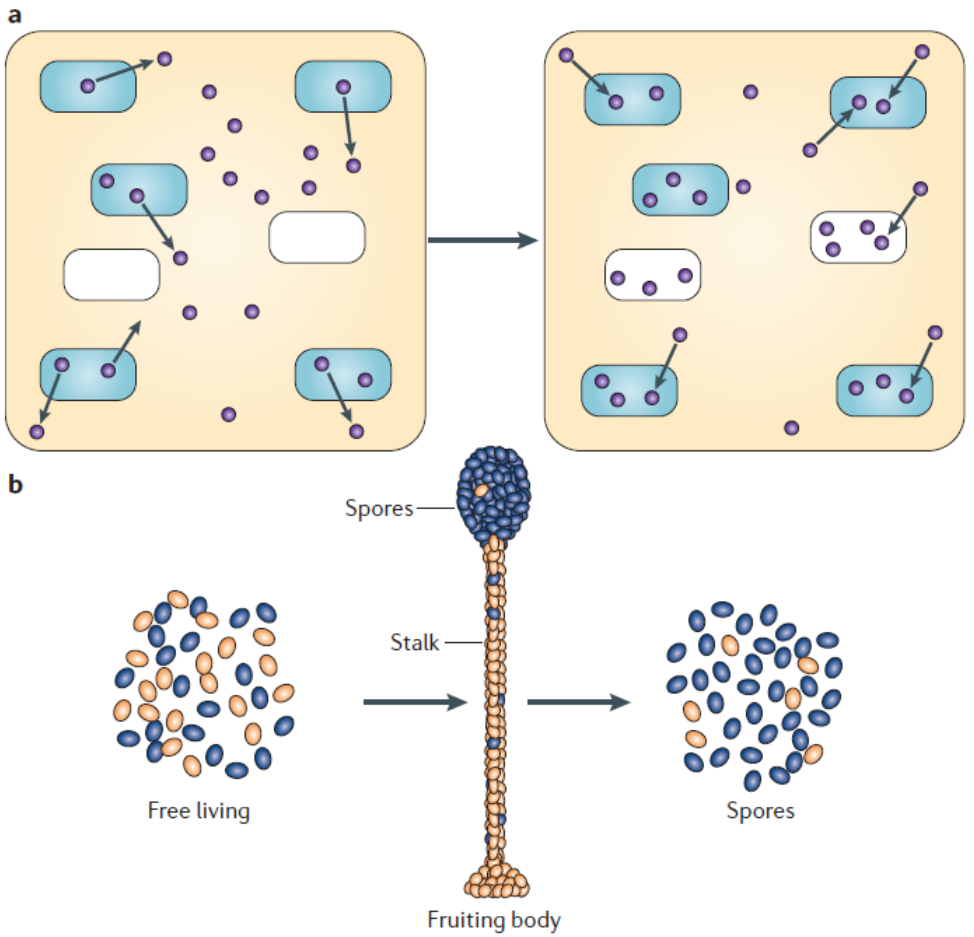


Figure 1 | **The problem of cooperation. a** | The tragedy of the commons with public goods. Cheats (white oblongs) who do not pay the cost of producing public goods (purple circles) can still exploit the benefits of public goods produced by other cells (green oblongs). **b** | Altruistic sacrifice. When two lineages come together to form a fruiting body, a cheat (blue lineage) would increase its reproductive success by contributing less towards stalk formation, and more towards spore production, compared with the other (orange) lineage.

How Can the Evolution of Altruistic Traits Be Explained?

"With sterile neuter insects, we have reason to believe that modifications in their structure and fertility have been slowly accumulated by natural selection, from an advantage having been thus indirectly given to the community to which they belonged over other communities of the same species.

This difficulty [of sterile insects]… disappears … when it is remembered that selection may be applied to the family, as well as to the individual."

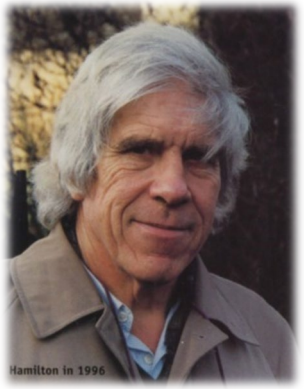
Darwin, *The Origin of Species*

Units of Selection: Hamilton's Theory of Kin Selection

- An allele that reduces an individual's immediate fitness can nevertheless increase in frequency if it sufficiently increases the fitness of close relatives.

  - Inclusive fitness = individual fitness + fitness through relatives.

    Fitness through relatives = Σ relatedness x fitness of relative.



W. D. Hamilton
(1936-2000)

Hamilton's Rule: Inclusive fitness consequences = - cost + (benefit * relatedness)

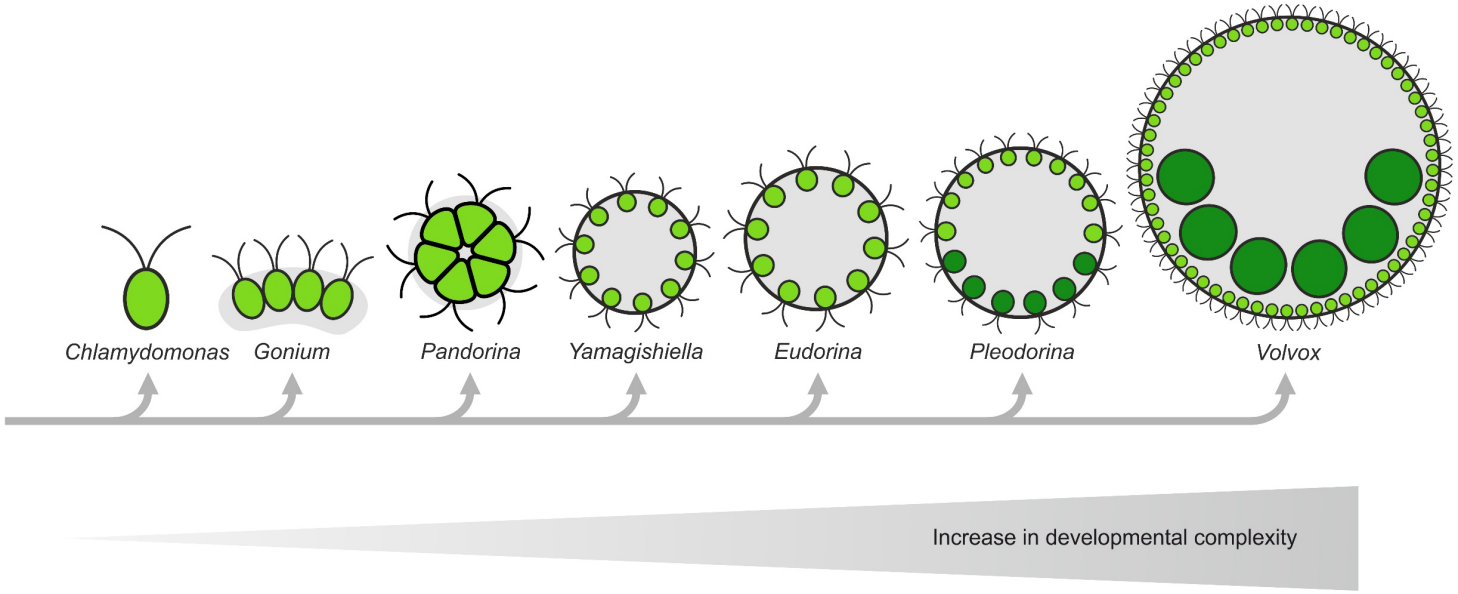
- A behavior that is disadvantageous to individual fitness will evolve if the cost (c) in individual fitness is less than the gain in fitness of relatives (b) discounted by the degree of relationship (r),

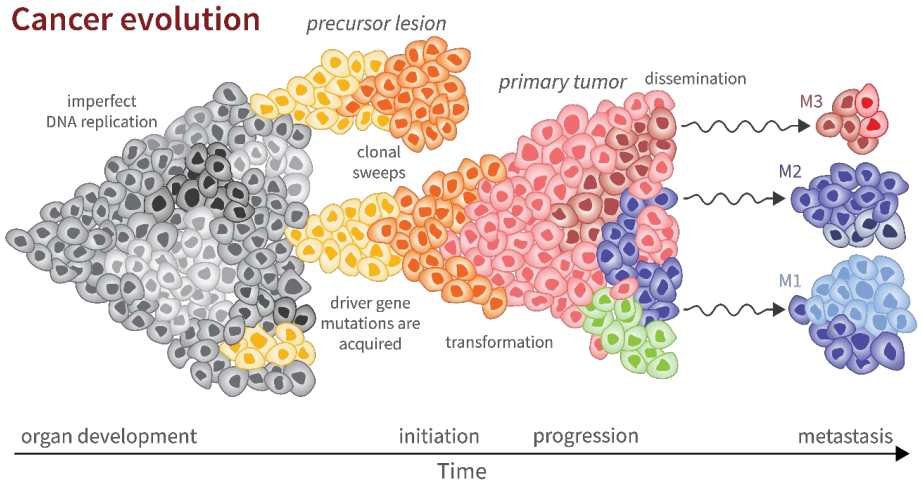
$$c < br$$

Example. An act that leads to an individual's death (c = 1), but saves the life of more than two brothers (b > 2, r = 1/2) or more than eight first cousins (b > 8, r = 1/8) will evolve by kin selection if it has a genetic basis.

Costs of Multicellularity

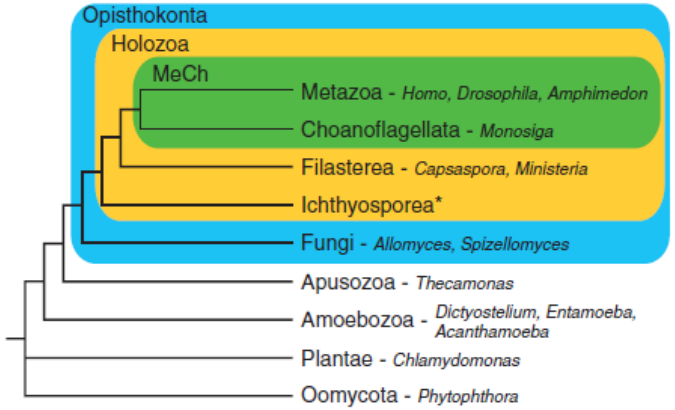
- Energetic burden.
- Cost of complexity.
- Paradox of robustness.
- Vulnerability to renegade cells.

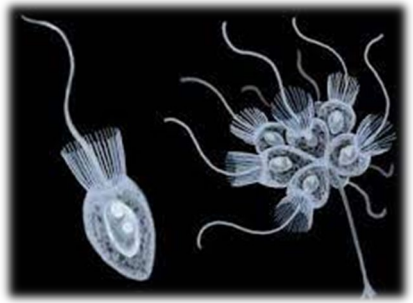




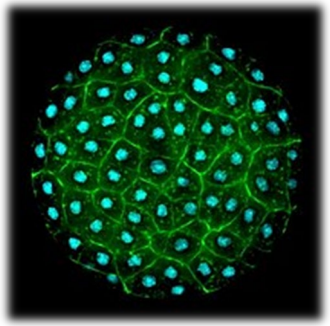
The Evolution of Complex Multicellularity in Animals Did Not Involve a Major Influx of New Genes

- Many of the genes originally thought to have been unique to animals have since been found in basal unicellular lineages.





Choanoflagellate



Ichthyosporean

- Integrin proteins used for cell-cell adhesion in animals are present in the apusozoan lineage but absent from fungi and choanoflagellates (Sebe-Pedros et al. 2010).

- Many proteins involved in cell signaling, immune response, and animal development are found in choanoflagellates (King et al. 2008; Richter et al. 2018).

- While there are many gene gains on the branch subtending the metazoan lineage, the number of gene losses (including genes for biosynthesis of 9 amino acids) appears to be just as great (Richter et al. 2018).

Apusozoan

Emergence of Cell-Type Specialization: Division of Labor vs. Multi-Tasking

- Subfunctionalization at the level of cell-type specialization: rather than evolving entirely new sets of tasks, most cell types in multicellular species have simply lost a range of features found in ancestral unicellular species (Arendt 2016).

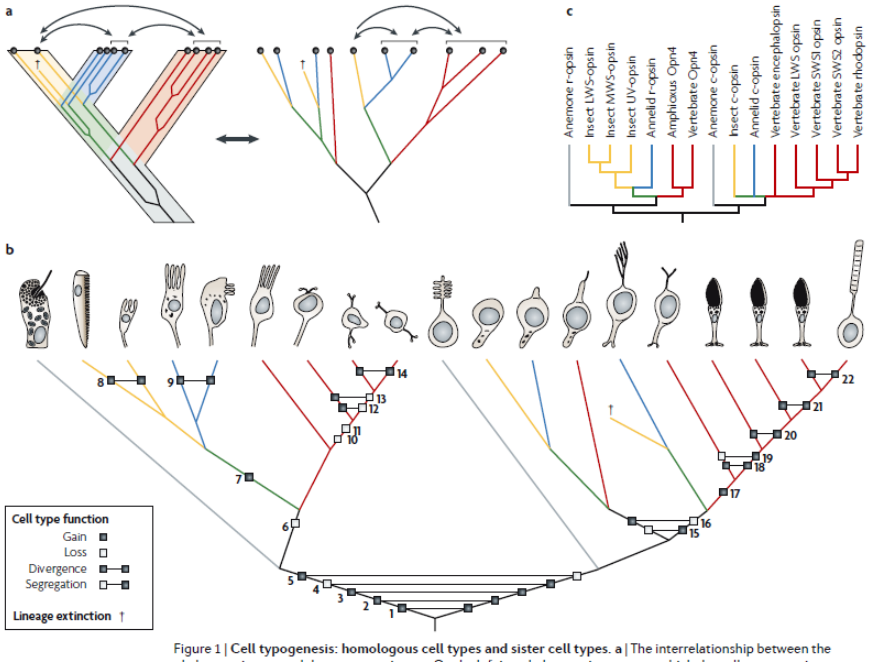
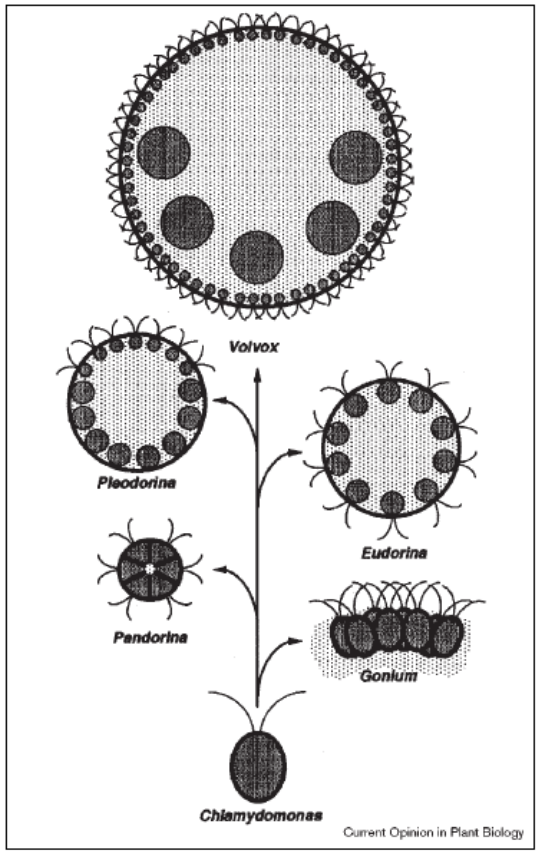


Figure 1 | **Cell typogenesis: homologous cell types and sister cell types.** a | The interrelationship between the

- Once established, division of labor among cell types plays a key role in ensuring the stability of complex body plans.
  - A complexity ratchet: as cell types become more specialized, the likelihood of reversion to a single-cell form with all features necessary for independent living becomes less and less likely (Libby and Ratcliff 2014; Cooper and West 2018).

Volvocales: evolution of multicellularity with progressive germ-soma division of labor, embryonic morphogenesis, and oogamy.



A conventional representation of 'the volvocine lineage', with organisms drawn at progressively decreasing magnification from bottom to top. The diameters of the biflagellate cells would be in the range of 5–10 μm in each organism. Dark gray shading represents the cell bodies, light gray shading represents the ECM and thick black lines represent the tripartite layer that is discussed below.

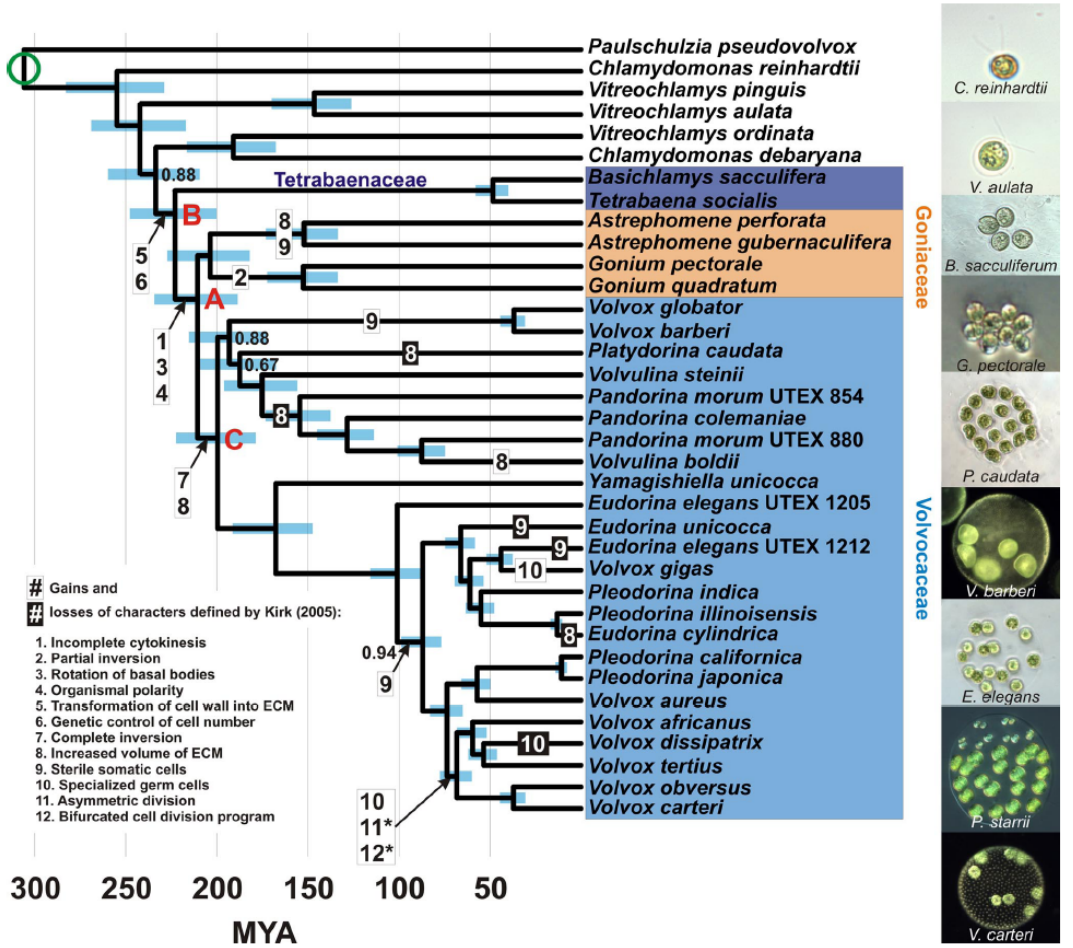


Fig. 2. Chronogram showing estimated divergence times among volvocine algae. Colored boxes identify the 3 multicellular families; ingroup species not highlighted in this manner are unicellular (*Paulschulzia pseudovolvox*, the outgroup, represents a separate origin of multicellularity). Blue bars are the central 95% of estimates from 300 Bayesian posterior trees. Bayesian posterior probabilities <0.95 are shown. The green circle indicates the calibration estimated in the broad-scale analyses. Red letters indicate nodes referred to in the text. Character state changes are those supported by hypothesis tests in ref. 5. We have retained Kirk's (4) original numbering for these steps. *, steps 11 and 12 may have had 2 separate origins in the clade including *V. africanus* and *V. carteri*.

Kirk (1999, Curr. Opin. Plant Biol.); Herron et al. (2009, PNAS)

Descendant Cell Types Acquire New Regulatory Domains Enabling Tissue-Specific Expression

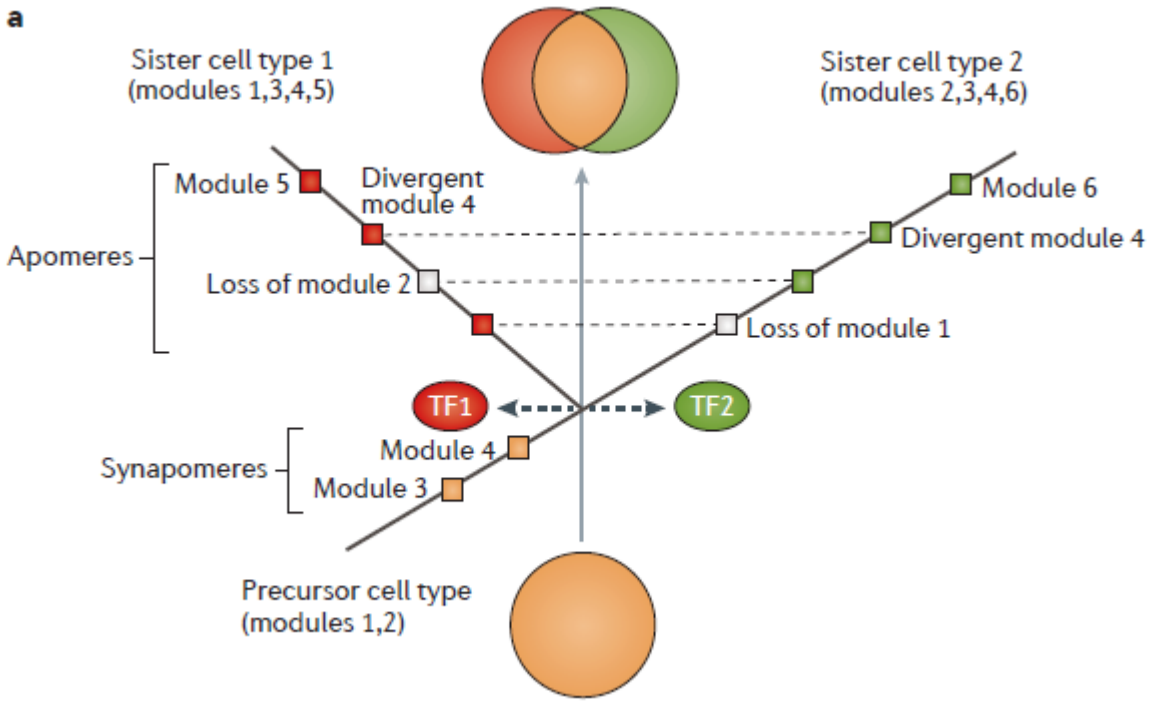


Figure 3 | **Sister cell types evolve by individuation.** **a** | A model of sister cell type diversification. The starting point was a precursor cell type with two modules (1, 2). Before diversification, two new modules had arisen (3, 4) that became synapomeres after the split. A key step in the formation of sister cell types was the evolution of two distinct core regulatory complexes (CoRCs) employing transcription factors TF1 and TF2. Phenotypically, cell type diversification involved division of labour events (modules 1, 2), module divergence (module 4) and the acquisition of new modules (5, 6). Corresponding modules in the sister cells are connected by dashed lines. **b** | Venn

Arendt et al. (2016, Nature Rev. Genetics)