

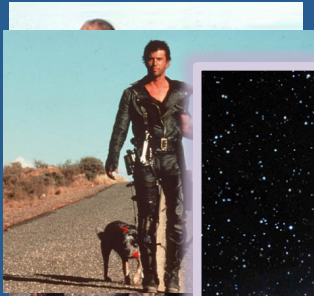
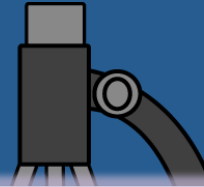
Owen Gilbert, Independent and KITP

A critical look at the field of microbial social evolution

22 January 2013

A caricature of the field

After N generations



Grand Theory of Life

Cooperator prevails

Cheater persists



structured

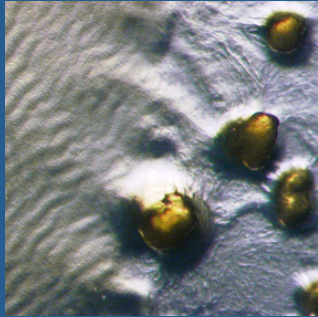
unstructured

Kill non-humans



Experimental manipulations of population structure

Myxobacteria

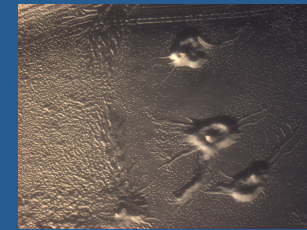


Pseudomonas



Figure 1. *Pseudomonas aeruginosa* Provided by Julia Plotnikov

Dictyostelium



Developmental cheating in the social bacterium *Myxococcus xanthus*

Gregory J. Velicer^{*†}, Lee Kroos^{*} & Richard E. Lenski[†]

^{*} Department of Biochemistry, Michigan State University, East Lansing, Michigan 48824, USA

[†] Center for Microbial Ecology, Michigan State University, East Lansing, Michigan 48824, USA

Competitive fates of bacterial social parasites: persistence and self-induced extinction of *Myxococcus xanthus* cheaters

Francesca Flegna and Gregory J. Velicer^{*}

^{*} Department of Evolutionary Biology, Max-Planck Institute for Developmental Biology, Spemannstrasse 37, 72076 Tübingen, Germany

Endemic social diversity within natural kin groups of a cooperative bacterium

Susanne A. Kraemer[†] and Gregory J. Velicer

Department of Biology, Indiana University, Bloomington, IN 47405

Edited by John C. Avise, University of California, Irvine, CA, and approved May 18, 2011 (received for review February 22, 2011)

The spatial structure of genetic diversity underlying social variation (22). The precise advantages of sporulation within fruiting bodies

Cooperation and competition in pathogenic bacteria

Ashleigh S. Griffin¹, Stuart A. West¹ & Angus Buckling²

¹Institute of Cell, Animal & Population Biology, University of Edinburgh, King's Buildings, West Mains Road, Edinburgh EH9 3JT, UK

²Department of Biology and Biochemistry, University of Bath, Bath BA2 7AY, UK

Explaining altruistic cooperation is one of the greatest challenges

Viscous medium promotes cooperation in the pathogenic bacterium *Pseudomonas aeruginosa*

Rolf Kümmerli¹, Ashleigh S. Griffin^{1,2}, Stuart A. West^{1,2}, Angus Buckling² and Freya Harrison^{2,3,*}

¹Institute of Evolutionary Biology, University of Edinburgh, West Mains Road, Edinburgh EH9 3JT, UK

²Department of Zoology, Oxford University, South Parks Road, Oxford OX1 3PS, UK

³Biodiversity Lab, Department of Biology and Biochemistry, University of Bath, Bath BA2 7AY, UK

There has been extensive theoretical debate over whether population viscosity (limited dispersal) can favour cooperation. While limited dispersal increases the probability of interactions occurring between relatives, which can favour cooperation, it can also lead to an increase in competition between relatives and this can be detrimental to the evolution of cooperation. Despite much theoretical attention

Dictyostelium amoebae lacking an F-box protein form spores rather than stalk in chimeras with wild type

Herbert L. Ennis[†], Dee N. Dao^{†*}, Stefan U. Pukatzki, and Richard H. Kessin

Department of Anatomy and Cell Biology, Columbia University, 630 West 168th Street, New York, NY 10032

Communicated by J. T. Bonner, Princeton University, Princeton, NJ, January 6, 2009 (received for review November 16, 2009)

Using a selection for *Dictyostelium* mutants that preferentially form spores, we have recovered a mutant called Cheater₂. *Dictyostelium* offers powerful molecular genetic tools for the study of social evolution.

High relatedness maintains multicellular cooperation in a social amoeba by controlling cheater mutants

Owen M. Gilbert^{*}, Kevin R. Foster^{*}, Natasha J. Mehdiabadi, Joan E. Strassmann, and David C. Queller

Department of Ecology and Evolutionary Biology, Rice University, MS 170, 6100 Main Street, Houston, TX 77005

Edited by Gene E. Robinson, University of Illinois at Urbana-Champaign, Urbana, IL, and approved April 10, 2007 (received for review March 23, 2007)

The control of cheating is important for understanding major transitions in evolution, from the simplest genes to the most complex societies. Cooperative systems can be ruined if cheaters that lower group productivity are able to spread. Kin-selection theory predicts that high genetic relatedness can limit cheating, because separation of cheaters and cooperators limits opportunities for them to spread. The best known social amoeba, *Dictyostelium discoideum*, is a model organism that, unusually, allows both estimation of relatedness in the field and the study of cheater mutants. Relatedness of vegetative *D. discoideum* cells naturally occurring in very small soil samples (0.2 g) has been estimated as 0.52 (26), but relatedness in actual fruiting bodies has not been estimated.

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High Relatedness Is Necessary and Sufficient to Maintain Multicellularity in *Dictyostelium*

Jennie J. Kuzdzal-Fick^{1,2}, Sara A. Fox¹, Joan E. Strassmann^{1,3}, David C. Queller^{1,3,*}

¹Department of Biology, University of Texas at Dallas, Richardson, TX 75080

²Department of Zoology, University of Oxford, South Parks Road, Oxford OX1 3PS, UK

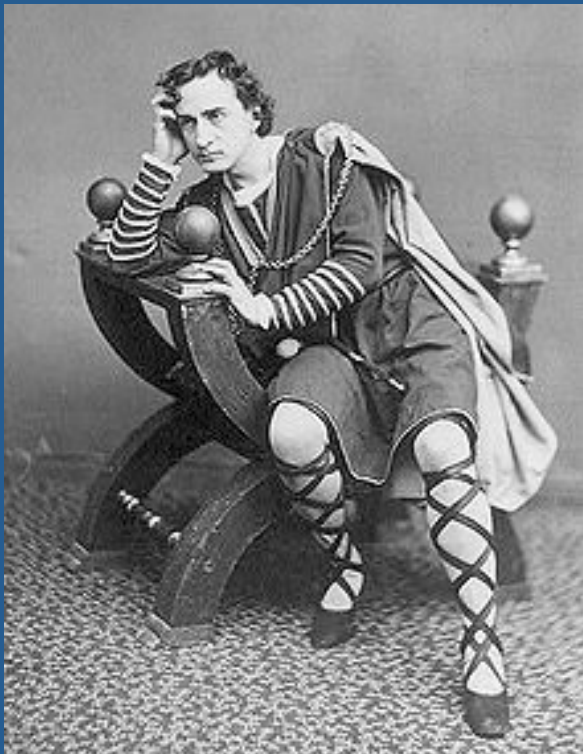
³Biodiversity Lab, Department of Biology and Biochemistry, University of Bath, Bath BA2 7AY, UK

Most complex multicellular organisms develop clonally from a single cell. This should limit conflicts between cell lineages that could threaten the extensive cooperation of cells within multicellular

yield the both kin reproduction in the only fruiting body (n) = 1 typically direct evolution that reduced sufficient eukaryotes

A Shakespearean concern

Hamlet



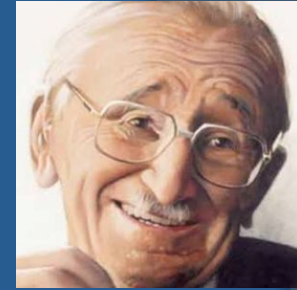
"There are more things
in heaven and earth,
Alien, than are dreamt
of in your petri dish."

☆⊙□□☆□!!!



Complex phenomena

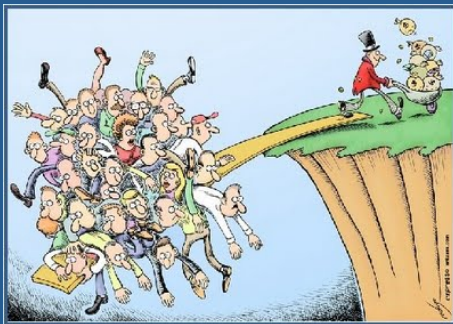
Hayek



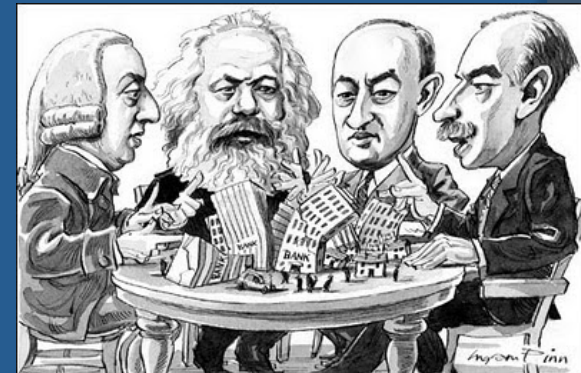
“...in the social sciences often **that is treated as important which happens to be accessible to measurement.**”

“...It sometimes almost seems as if the techniques of science were more easily learnt than **the thinking that shows us what the problems are and how to approach them.**”

2008



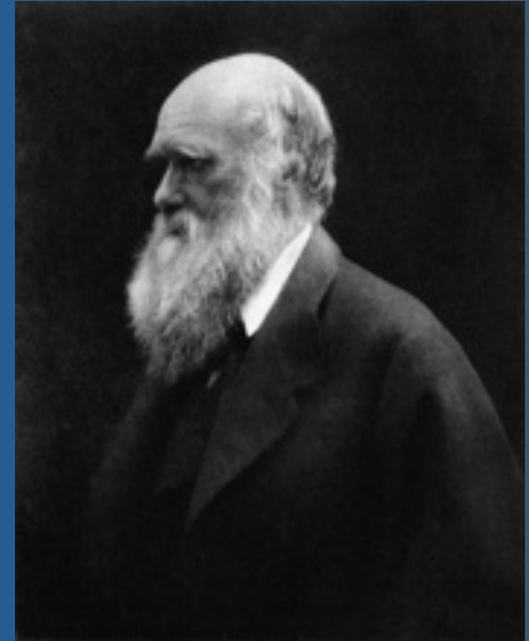
Stock Market



Hayek, 1974 *Nobel Lecture*

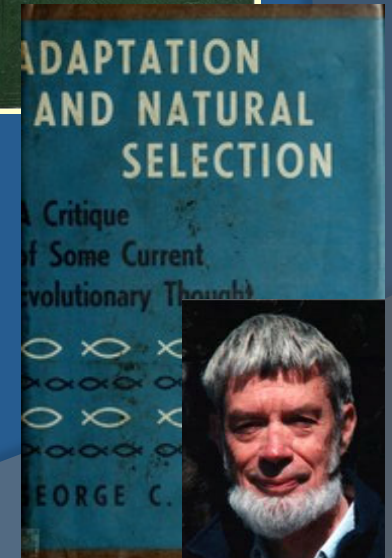
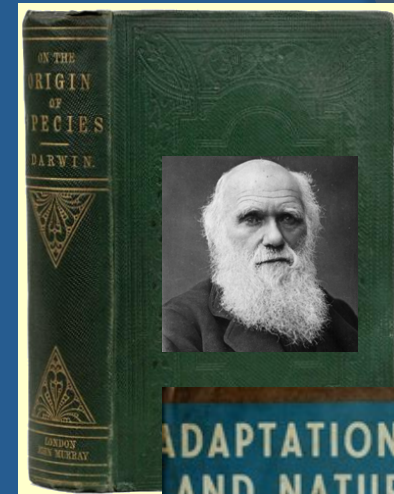
The Darwinian Approach to Biology

- ① Understand the organism in its natural environment.
- ② Use comparative evidence to formulate adaptive hypotheses.
- ③ Entertain alternative hypotheses if biologically plausible.



Withering scrutiny

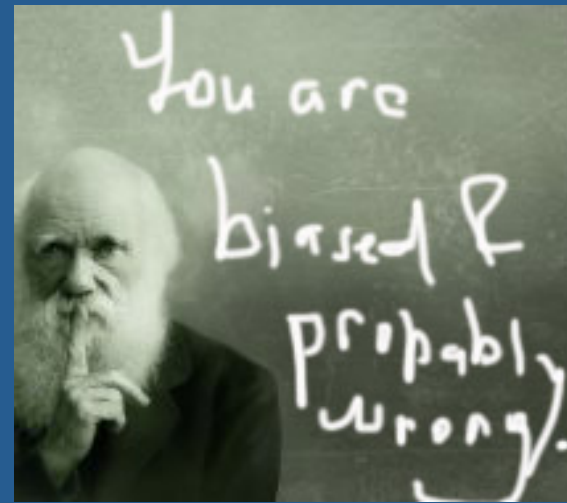
- Treat each adaptive hypothesis with contempt.
- Be willing to give up favored hypotheses.
- Be imaginative when thinking of alternatives.
- Use abductive reasoning.



Darwin (1859); Darwin (1887); G. C. Williams (1966); Harmon (1965)

Of course

- ◉ Most *darwinists* are biased in favor of pet theories.
- ◉ Their friends do not share the same commitments.
- ◉ Through discourse, *darwinists* formulate and test hypotheses.



Structure for talk

- ⦿ Introduction to the problem.
- ⦿ Review of means that it has been addressed.
- ⦿ Future work.

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Why study microbial social evolution?

- ① Understand human diseases
- ① Genetic basis of behavior
- ① The evolution of cooperation
- ① The evolution of multicellularity
- ① The origin of organisms

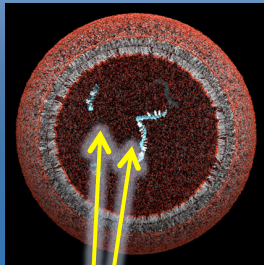
Why study microbial social evolution?

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- **The origin of organisms**

The Origin of Organisms

Cellular organisms

Protocell

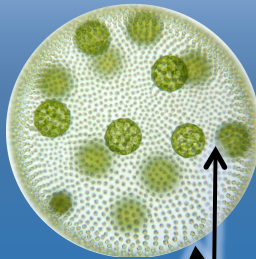


Credit: J. Iwasa

Cooperative replicators

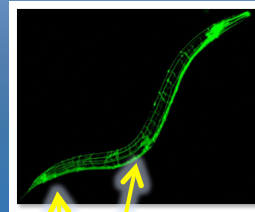
Multicellular organisms

V. carteri



Credit: A. Nedelcu

C. elegans



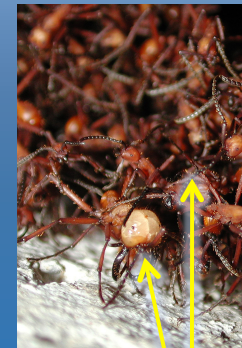
Credit: J. Bessereau

Cooperative cells

Colonial organisms

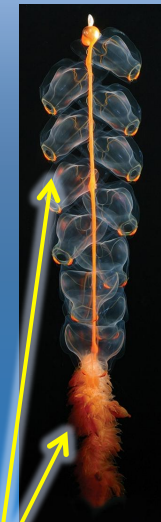
Siphonophore

E. hamatum



Credit: L. Gilbert

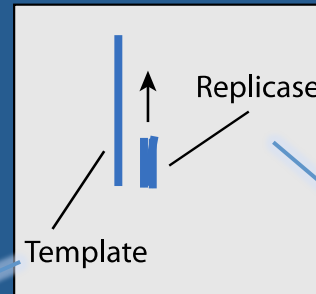
Credit: K. Raskoff



Cooperative Individuals

“Multiple levels of organization have emerged in the history of life, and each such emergence raises the same existence problem as does life itself.” –Fontana & Buss (1994)

Origin of life



+



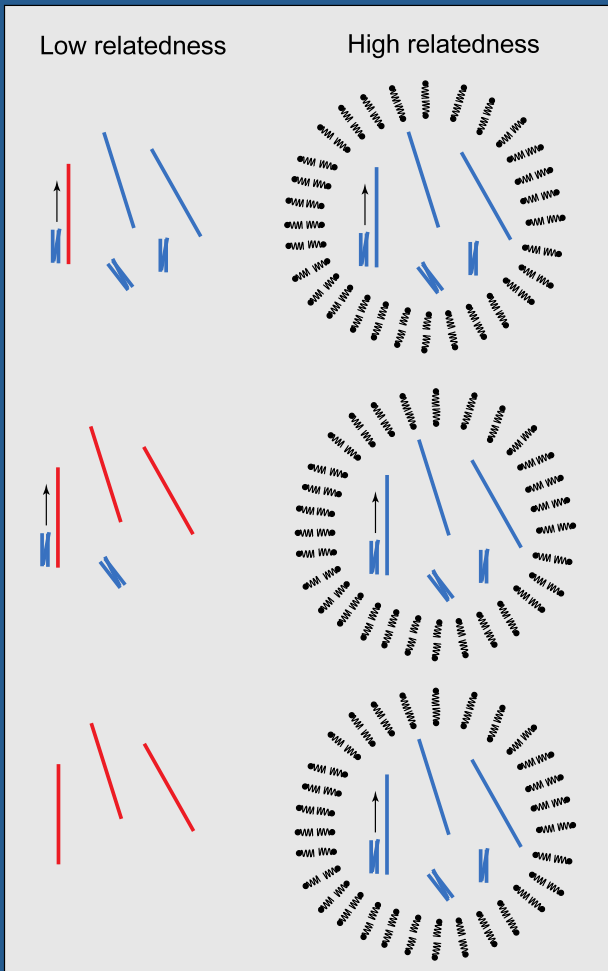
Template (what is copied)

Replicase (copier)

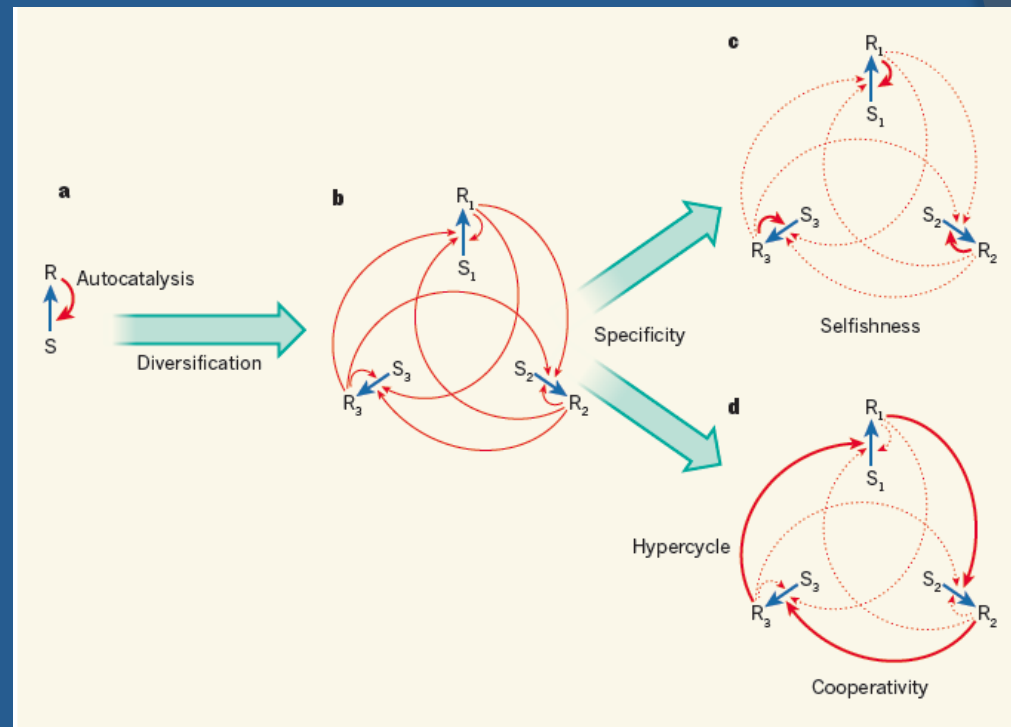
Szostak *et al.* (2001); Szathmari (2006); Chen (2006)

Population structure

Protocell



Hypercycles



Attwater & Holliger (2012); Vaidya *et al.* (2012)

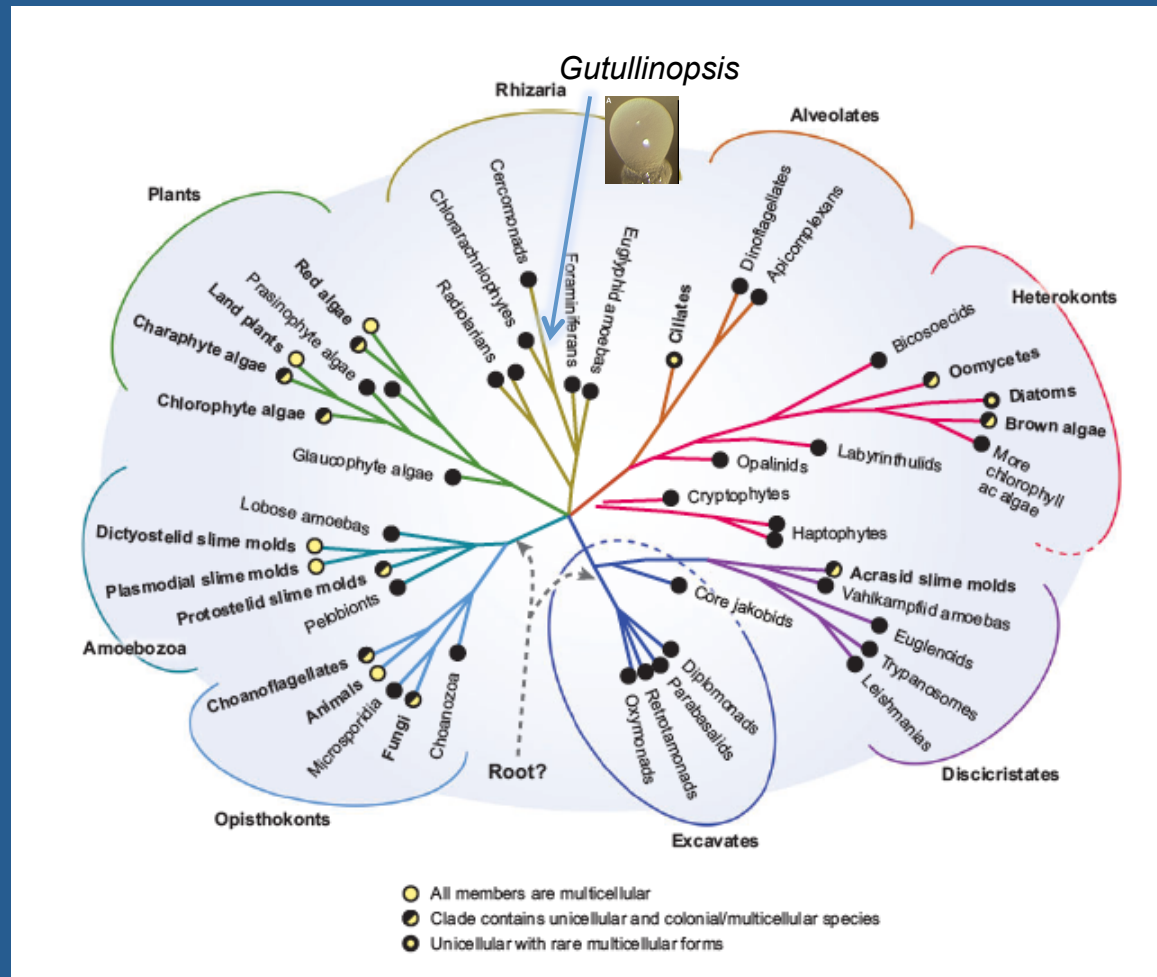
The problem of information loss



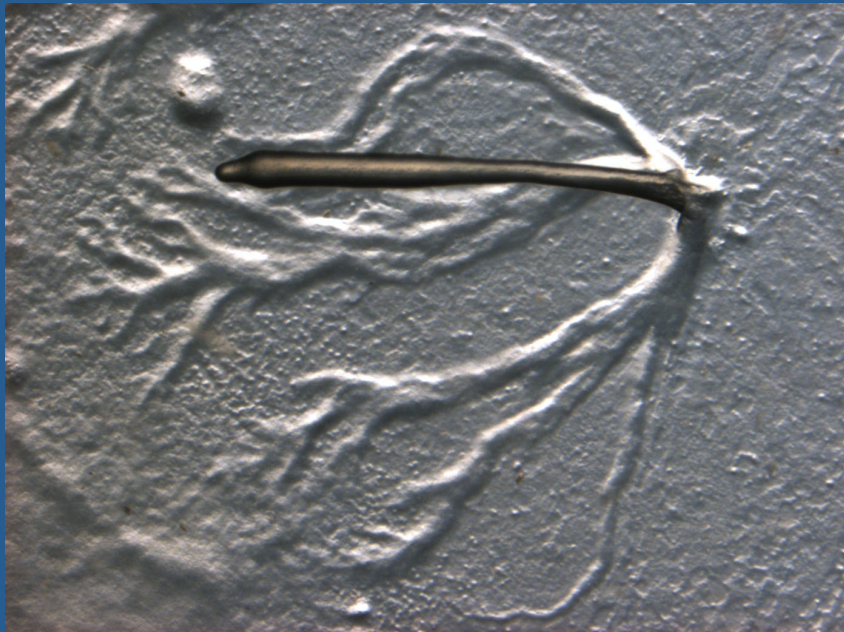
Tough to know what happened 3.8 bya



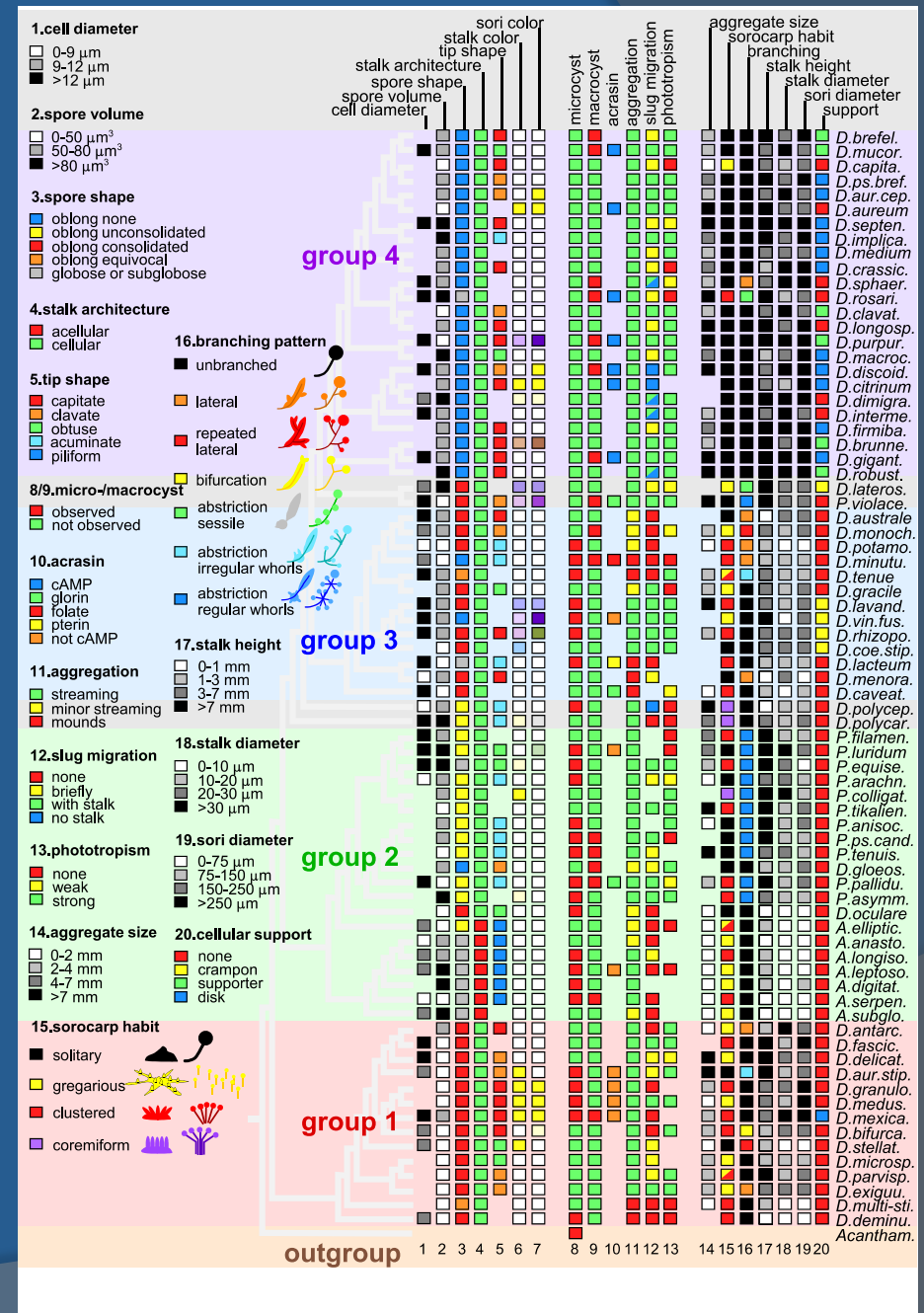
The relatively “recent” past



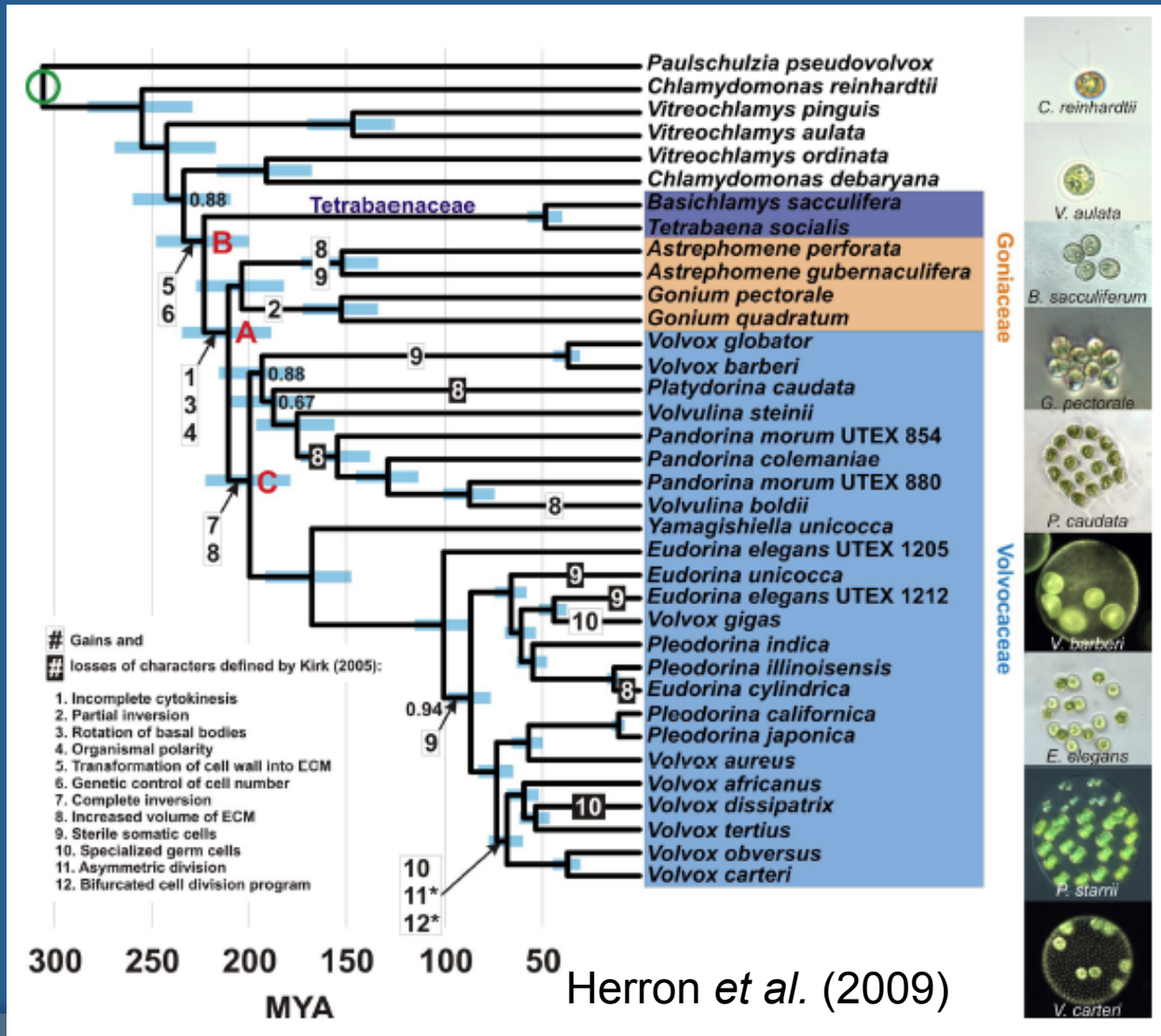
Social amoebae



Schaap et al. (2009)

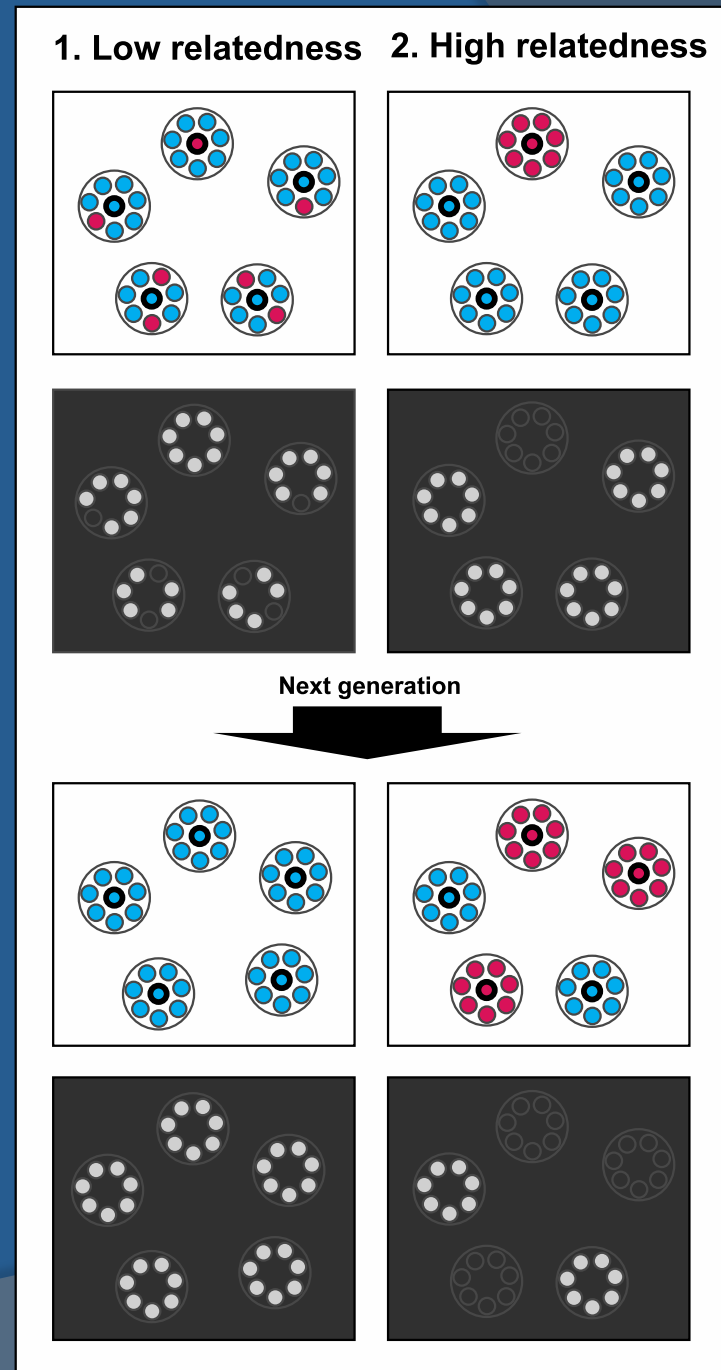


Volvocine green algae

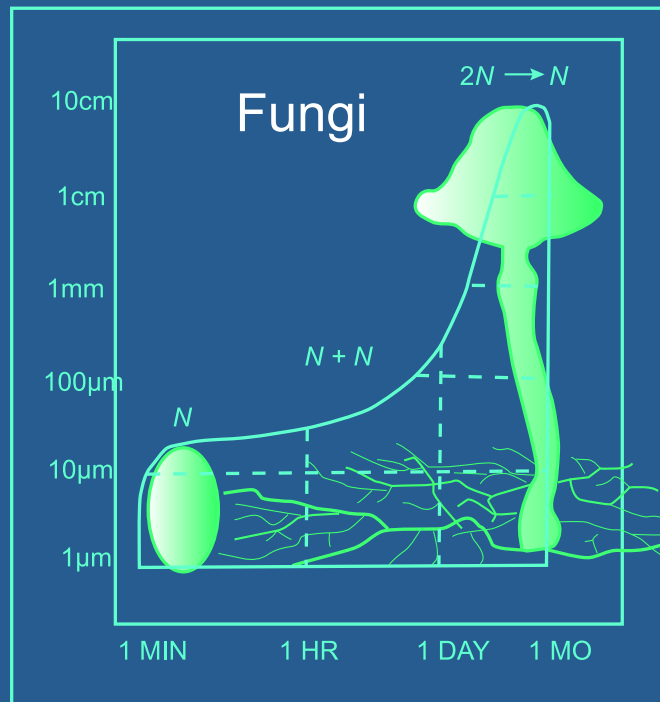
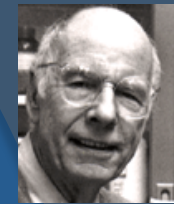


Evolvability

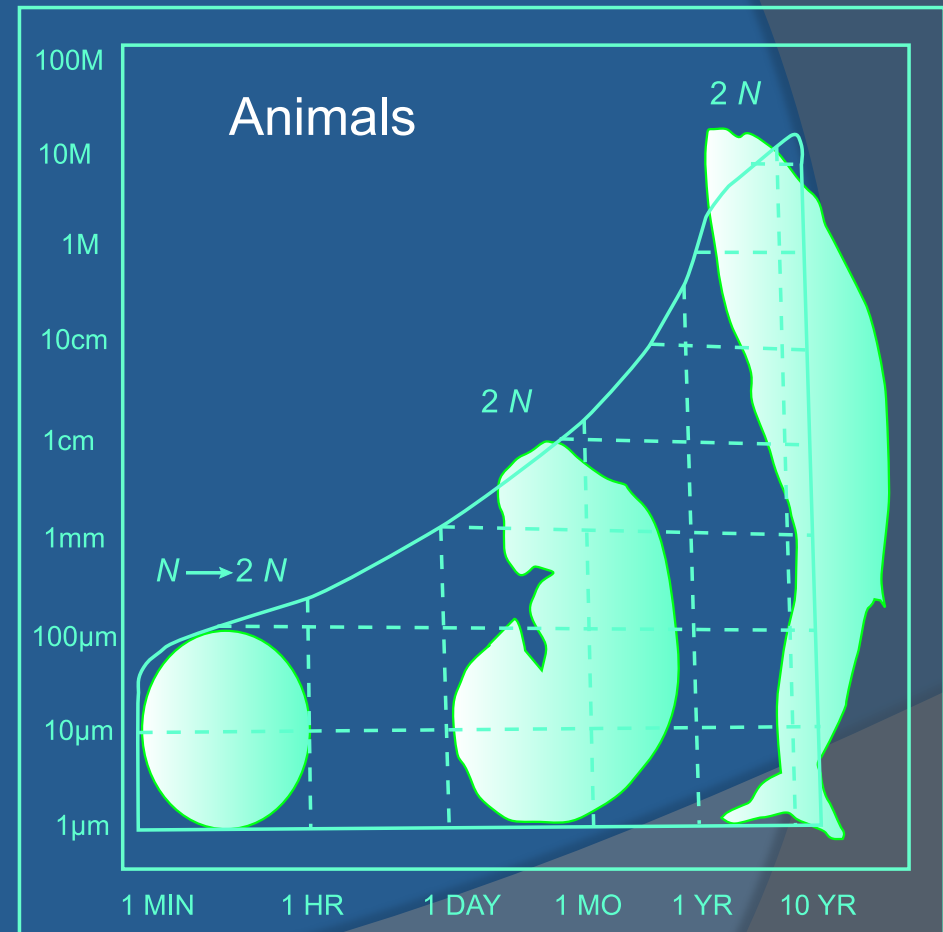
- Imaginary planktonic multicellular alga with sterile soma.
- Red mutation conveys camouflage in deep water.



Bottlenecked life cycles



Coprinus sterquilinus



Balaenoptera musculus

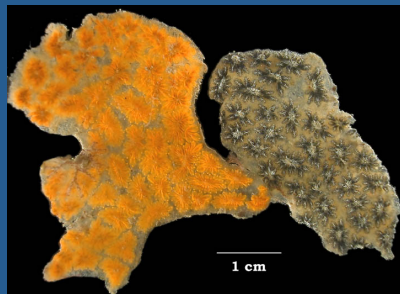
Bonner (1966) *Size and Cycle*

Fusion compatibility systems



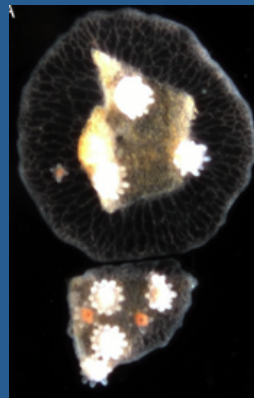
Multicellular organisms that fuse somatic tissue have somatic compatibility systems

Urochordates



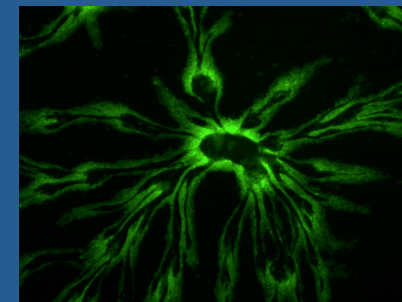
Credit: California Academy of Sciences

Cnidarians



Credit: A. Powell

Social amoebae

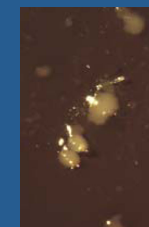


Tasmanian devil tumor



Credit: M. Jones

Dicty chta



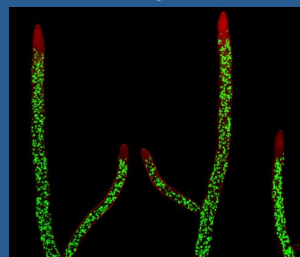
Credit: K. Foster

Myxomycetes



Credit: K. Simmons

Fungi



Credit: P. Hickey & N. Read

May help prevent spread of somatic parasites

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A tale of two unicellular organisms...

Myxococcus xanthus

Gram negative, gliding *Protobacteria*

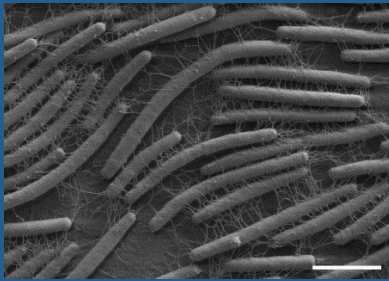


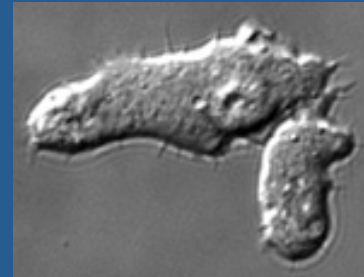
Image credit: Kearns & Shumkets (2001)

“Wolf pack” hunting behaviors

Secrete digestive enzymes

Dictyostelium discoideum

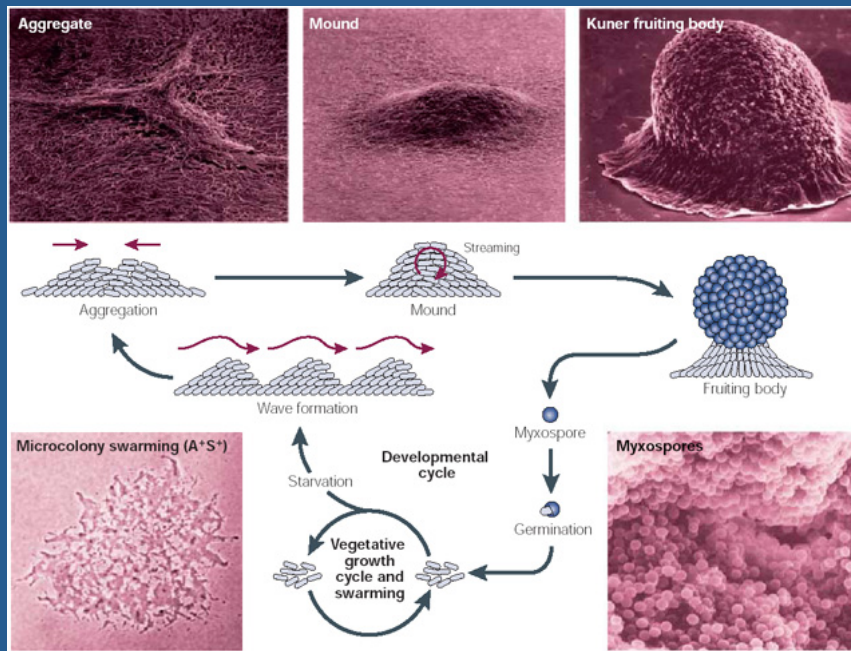
Cellular slime molds, “social amoebae”



Individual amoebae capable of feeding independently

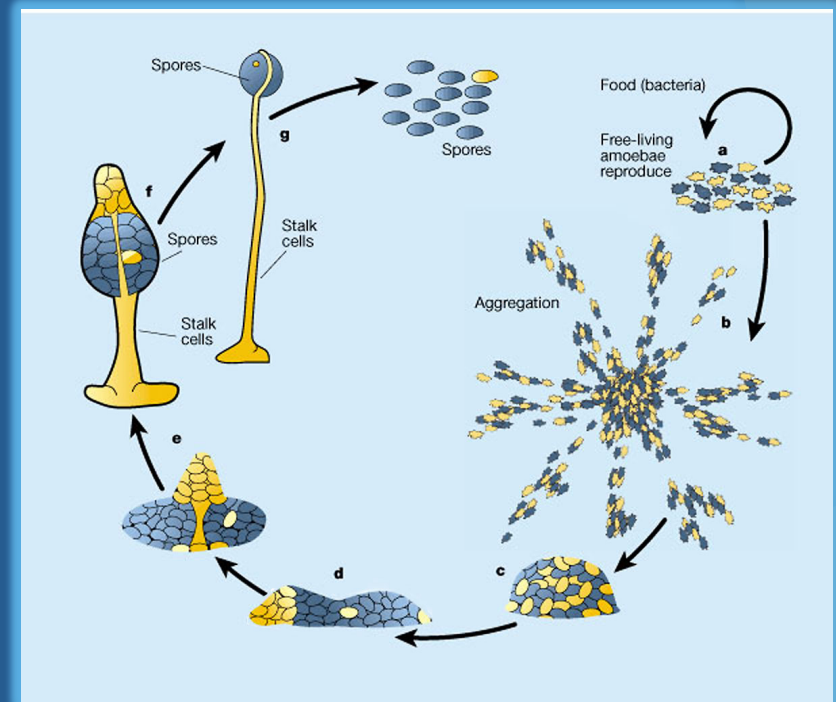
...also multicellular

Myxococcus xanthus



Credit: D. Kaiser

Dictyostelium discoideum



Credit: Kessin (2000) Nature

Myxo populations susceptible to cheating under well-mixed conditions

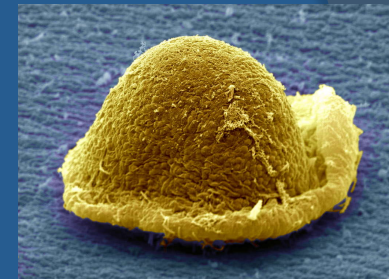
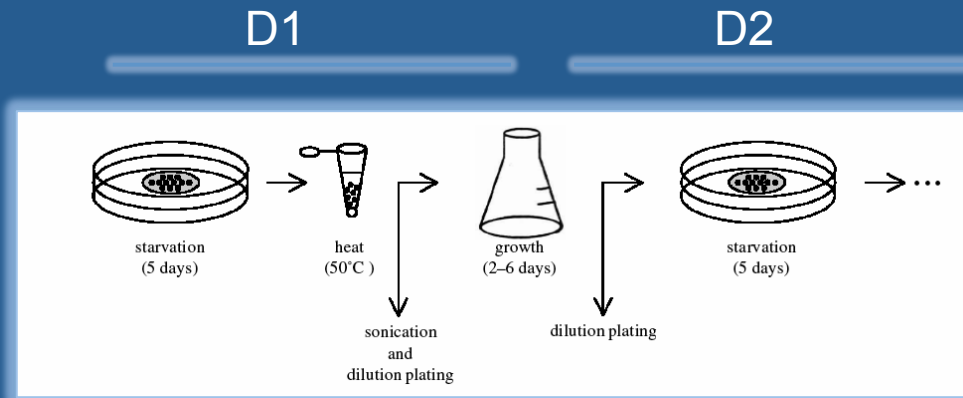
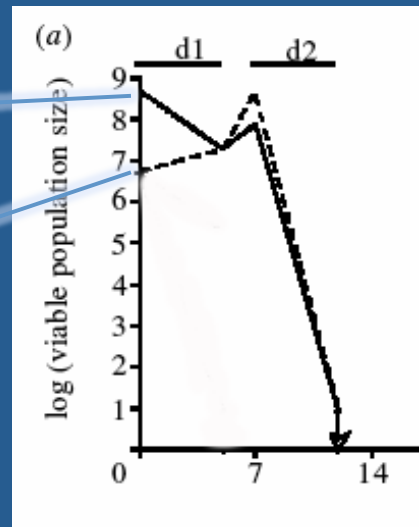
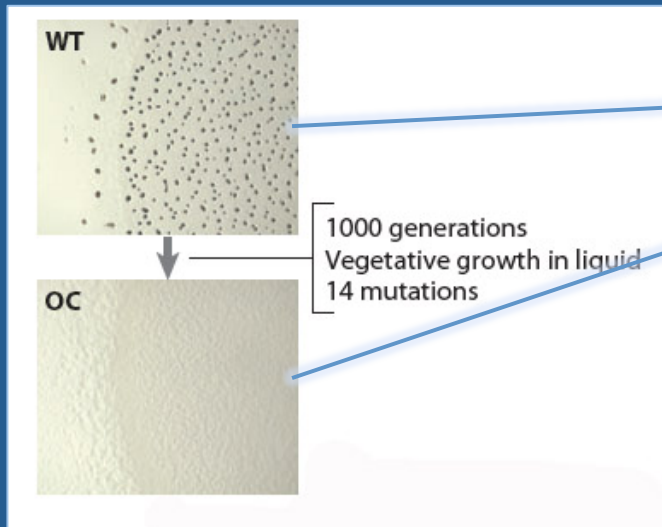


Image credit: G. Velicer



- 8 / 16 replicates of OC / WT incurred cheater-induced extinction

Preliminary data on natural structure

What is minimum average relatedness in sample?

Assume

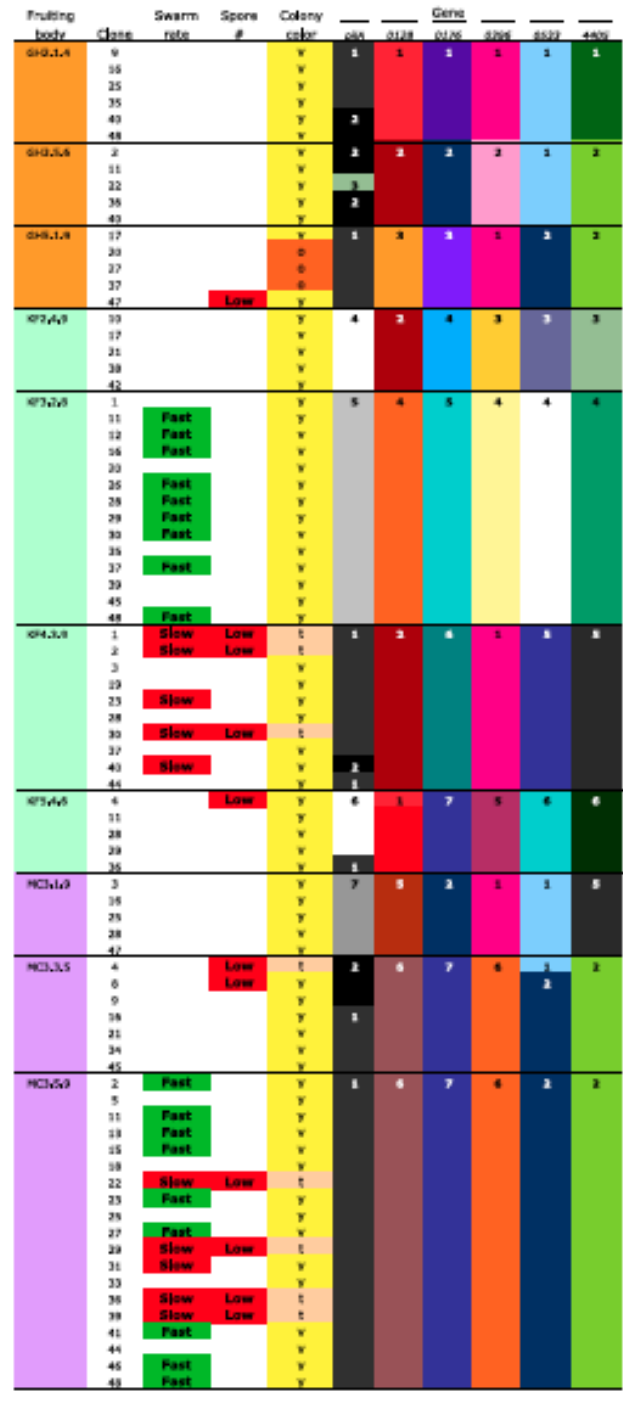
1. Any allelic difference = different clone
2. Different clones unrelated

$$R = \sum_i^n (p_i^2 + q_i^2 + (1 - p_i - q_i)^2) / n$$

N = 10

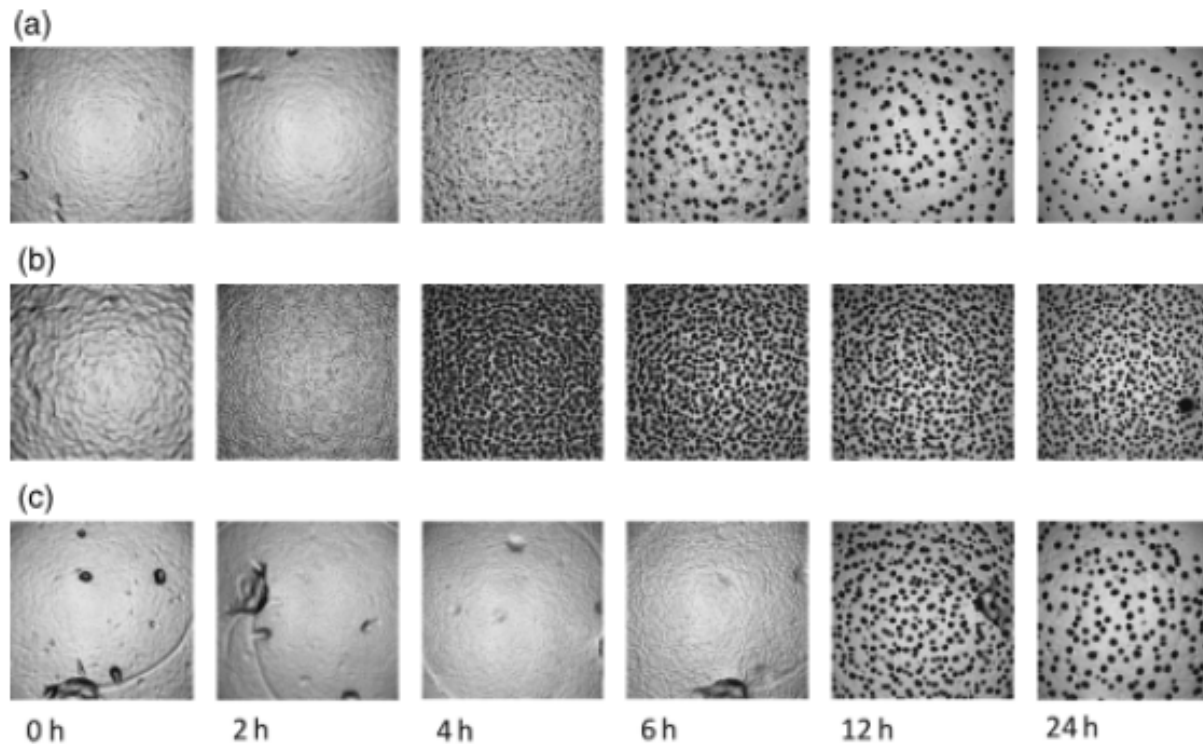
FB	# spores/clone			clone proportion			R_i
	Cl 1	Cl 2	Cl 3	p	q	$1 - p - q$	
GH2.1.4	4	2	0	0.67	0.33	0.00	0.56
GH3.5.6	5	1	0	0.83	0.17	0.00	0.72
GH5.1.9	6	0	0	1.00	0.00	0.00	1.00
KF2.4.9	6	0	0	1.00	0.00	0.00	1.00
KF3.2.8	14	0	0	1.00	0.00	0.00	1.00
KF4.3.9	9	1	0	0.90	0.10	0.00	0.82
KF5.4.6	5	1	0	0.83	0.17	0.00	0.72
MC3.1.9	6	0	0	1.00	0.00	0.00	1.00
MC3.3.5	4	2	1	0.67	0.33	0.14	0.58
MC3.5.9	19	0	0	1.00	0.00	0.00	1.00

$R = 0.84$



Are there obligate cheaters in nature?

Development time



(a) Moderate
(clone A30)

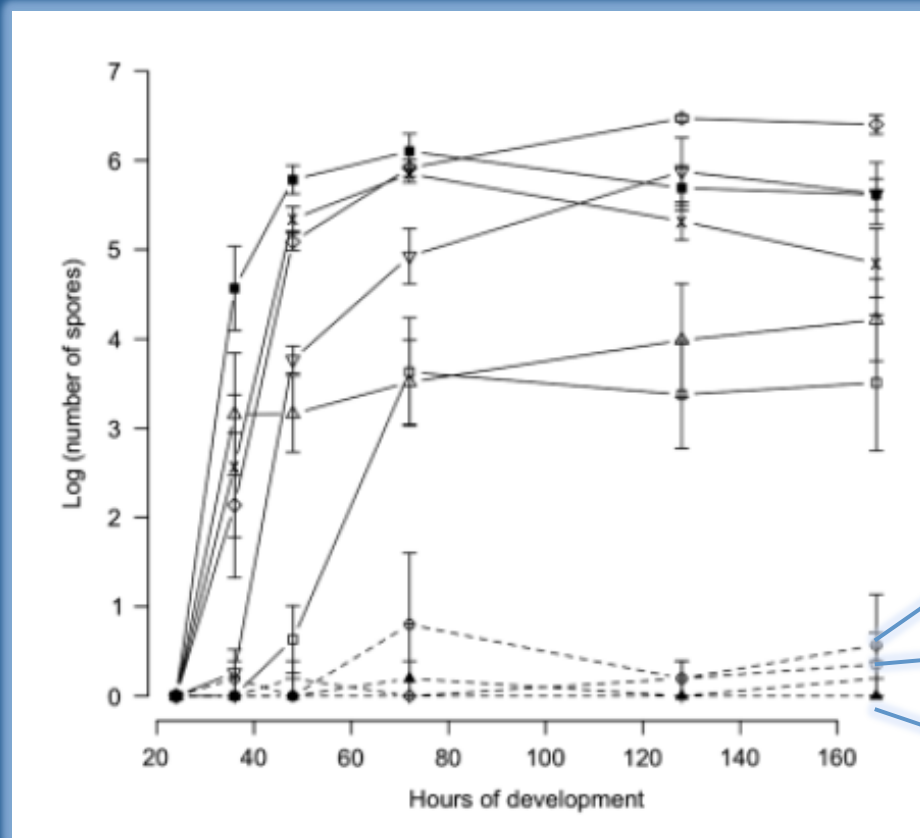
(b) Fast (clone A98)

(c) Slow (clone A94)

Are there obligate cheaters in nature?

Vos & Velicer (2009)

Clone	Competitiveness
A9	Victim
A41	Average
A66	Not tested



Clone A41

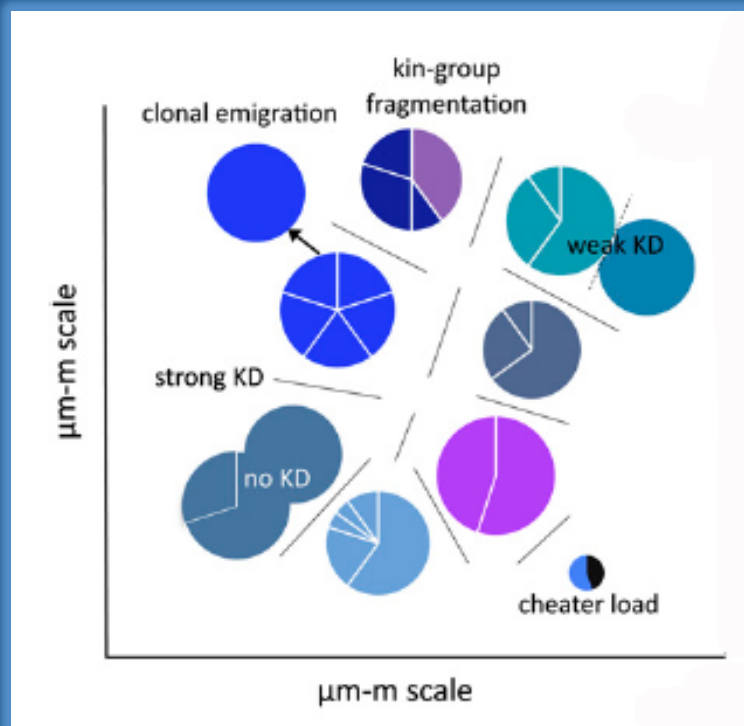
Clone A66

Clone A9

} Delayed development like OC

Kraemer *et al.* (2010)

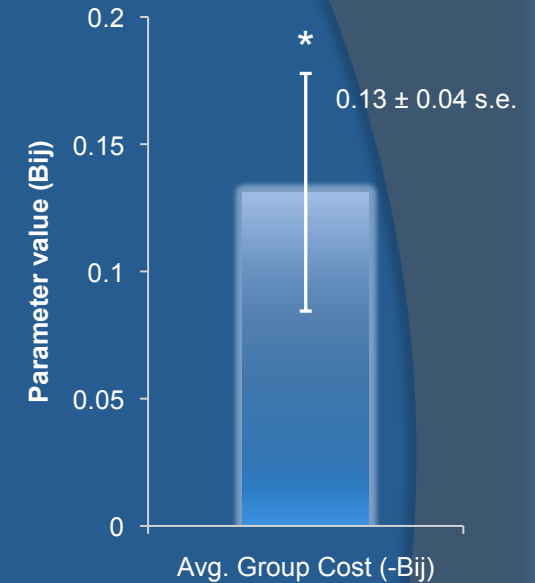
What are population dynamics?



- Do obligate cheaters build up?
- What is the role of kin discrimination?
- Do patches go extinct because of starvation / predation / environmental insult?

Kin discrimination

Avg. group cost in co-occurring clones

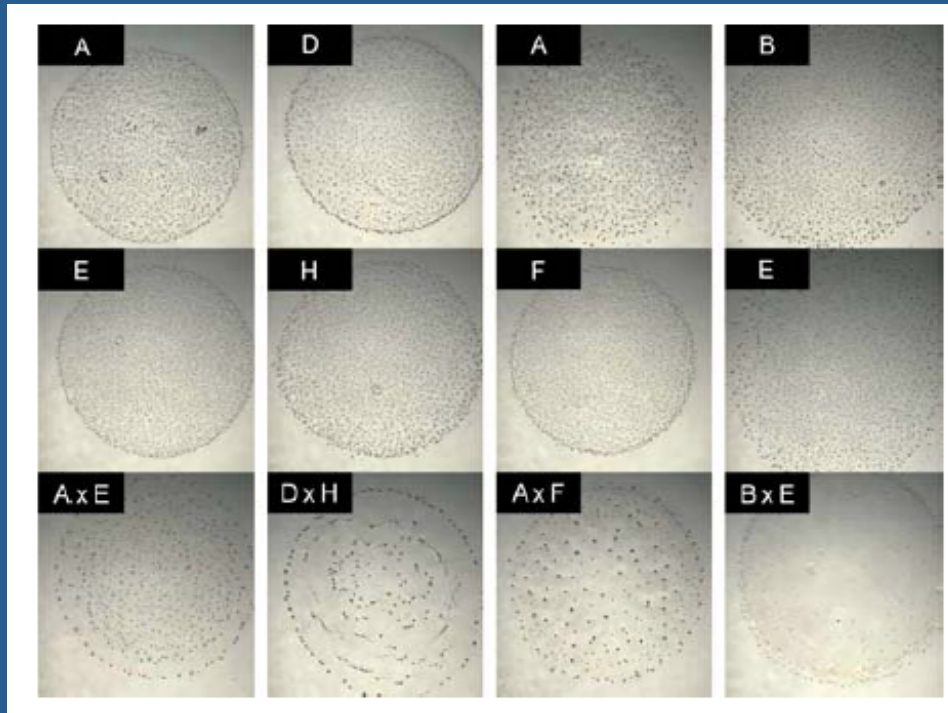


*Two-tailed t-test
 $P < 0.02$

Not diff. from Normal
 Shapiro-Wilks
 $p = 0.78$

} Pure Clones

} Mixes



45 allorecognition types in 78 local isolates

Origin of genetic polymorphism

R. Grosberg



J. Quinn



$$W_i = 1 + P_i (b_f - c_f)$$

Fitness of cue allele

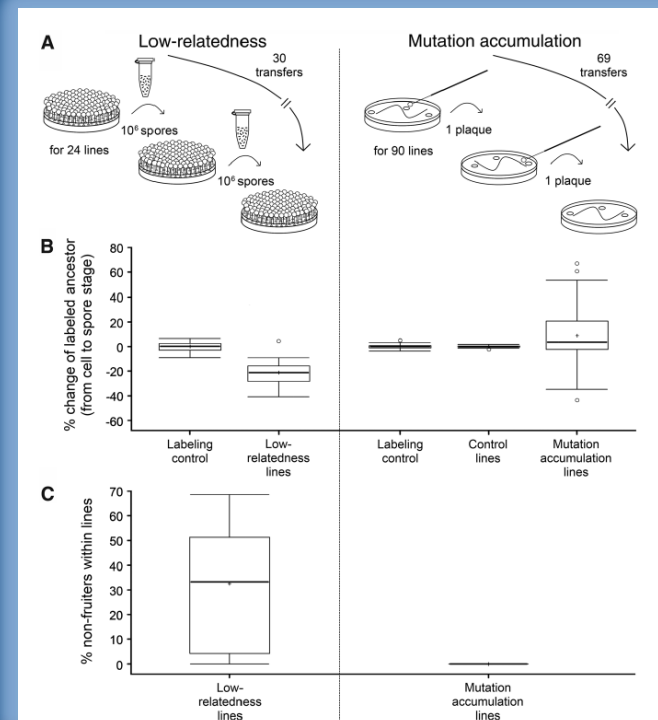
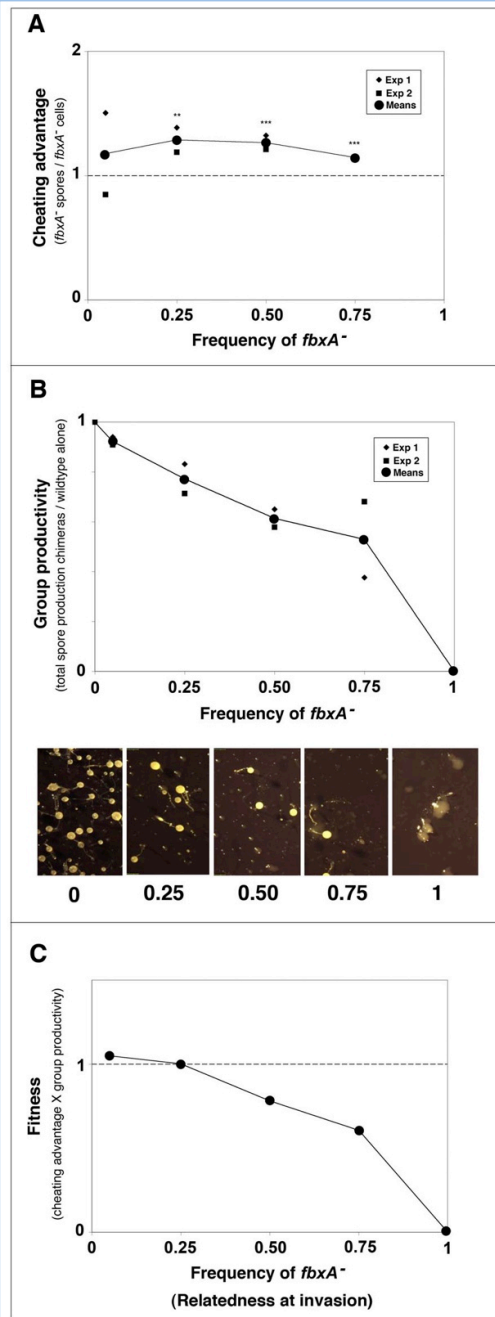
Benefit of fusion

Cost of fusion

Frequency cue allele

if $c_f > b_f$ then W_i increases with decreasing P_i

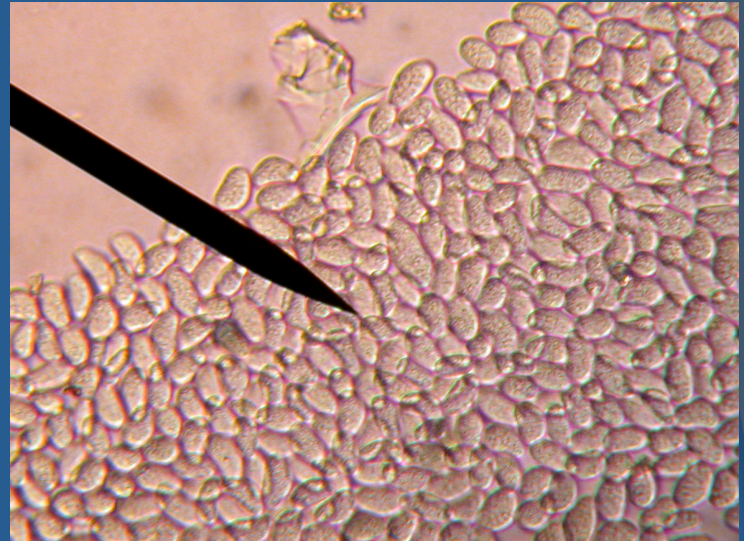
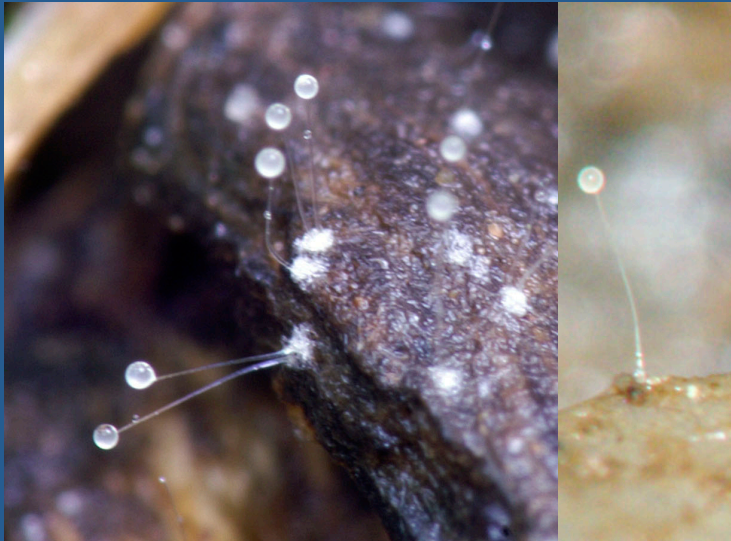
Dicty populations susceptible to obligate cheating under well-mixed conditions



Gilbert *et al.* (2007); Kuzdzal Fick *et al.* (2011)

What is relatedness in natural populations of *Dictyo*?

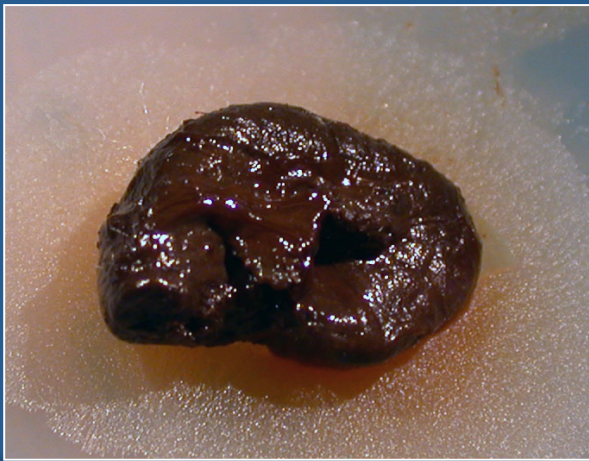
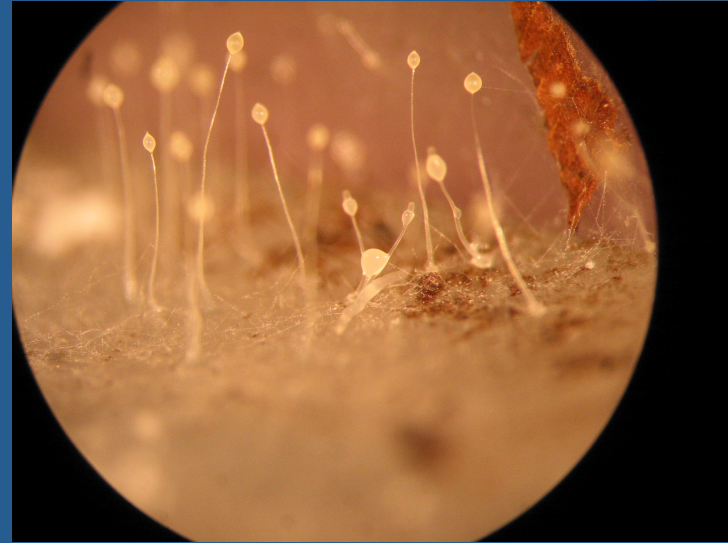
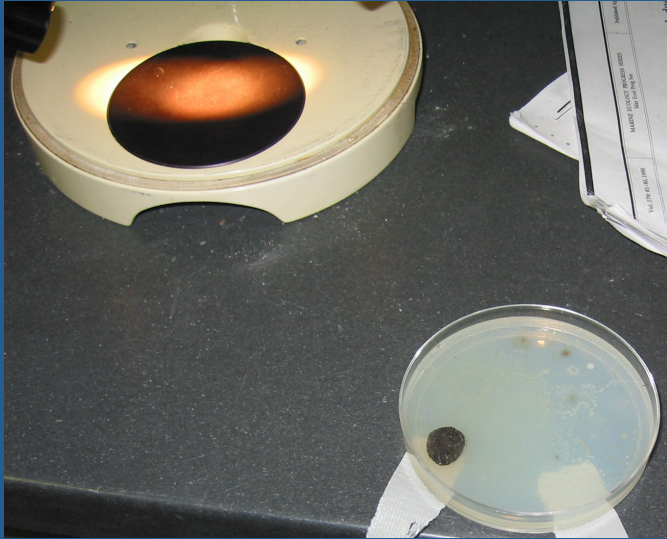


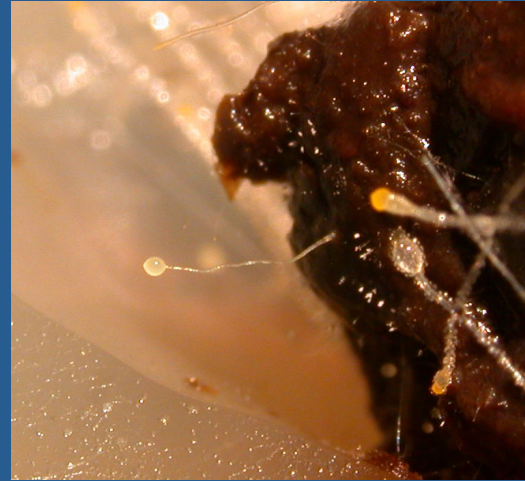
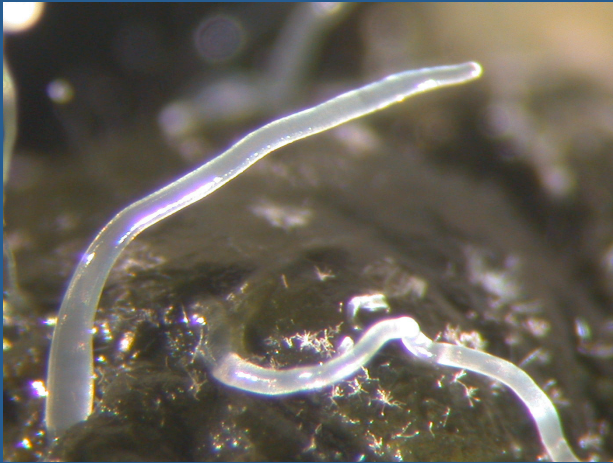








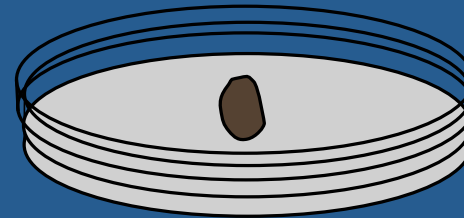
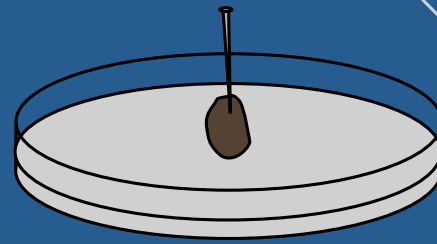
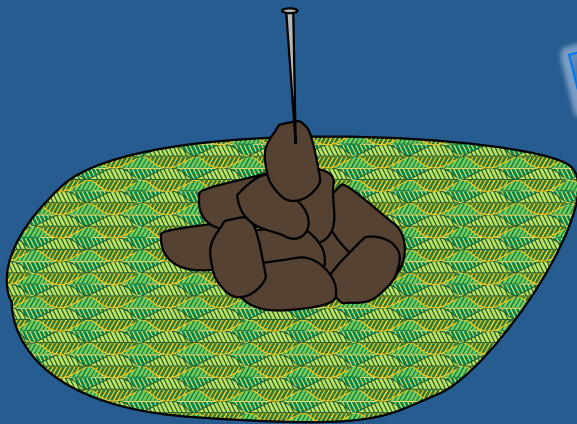




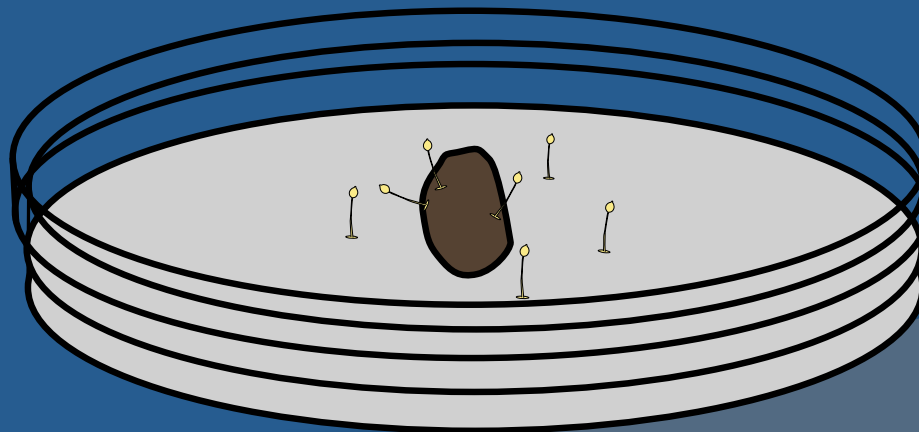


Methods

Non-nutrient
agar



Incubate
4-6 days



Fruiting bodies

Microsatellite genotyping

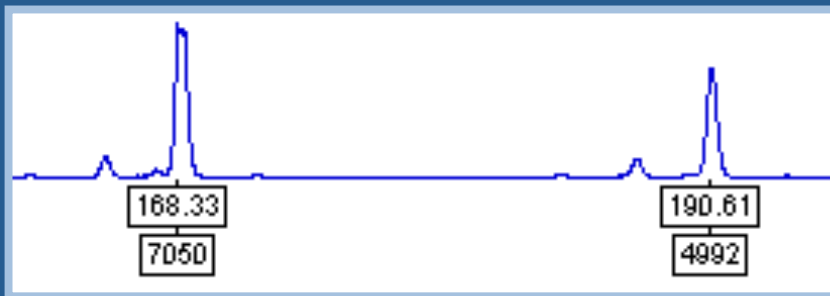
Microsatellites are DNA sequence repeats present in high copy number

High mutation rates – good for distinguishing closely related individuals

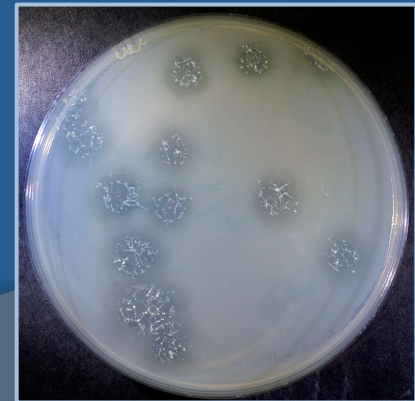
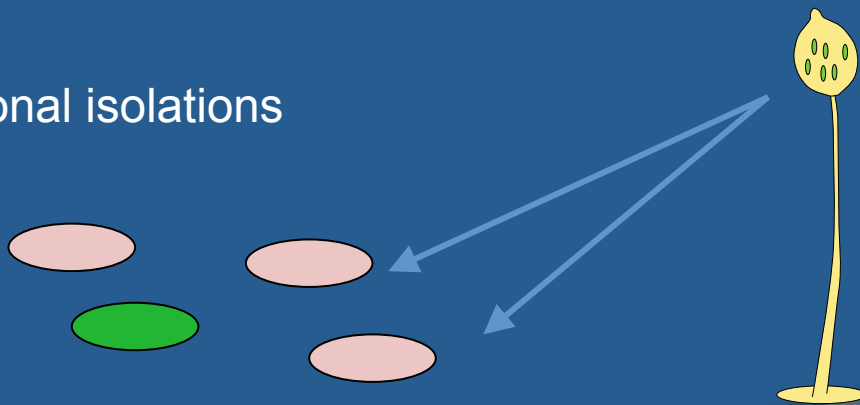


Two Methods of Genotyping

1. Whole fruiting bodies

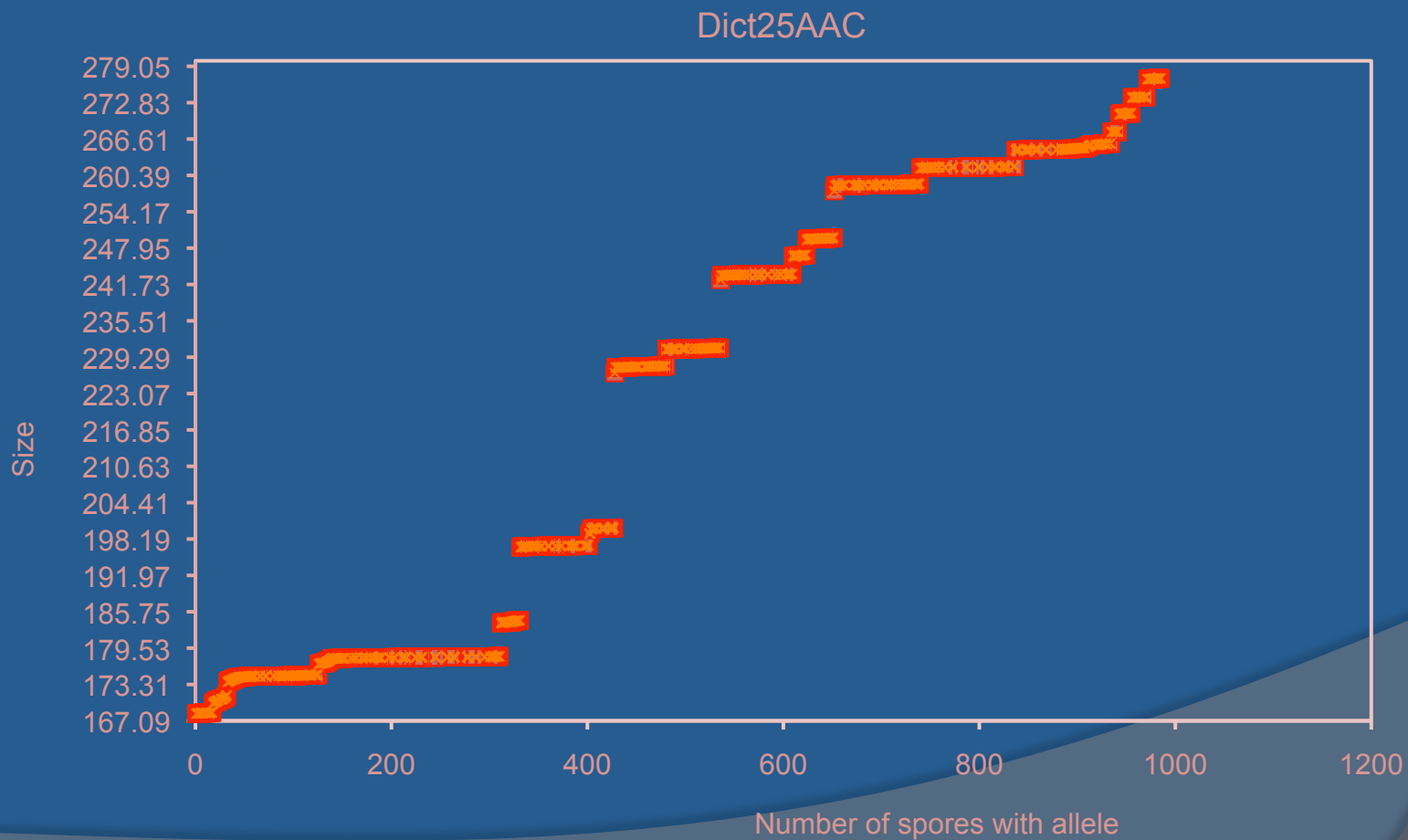


2. Clonal isolations

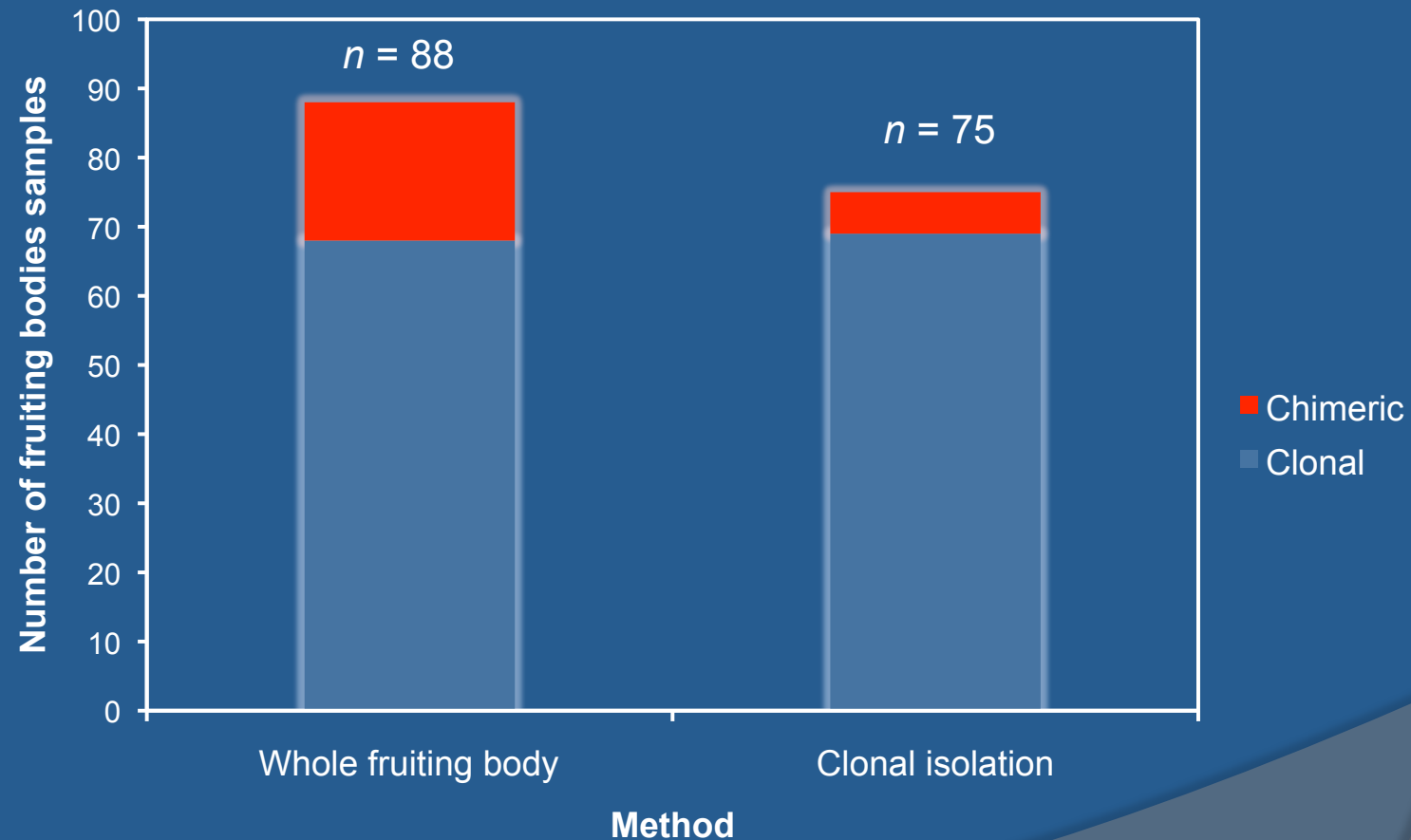


High variability of microsatellite loci

< 1 % probability of sharing 3 alleles by chance



Most fruiting bodies clonal



25 dung piles,
1 time of year

50 dung piles,
3 times of year

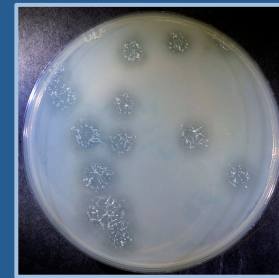
Relatedness very high in nature

Whole fruiting bodies



0.86 ± 0.03 SE

Clonal isolations

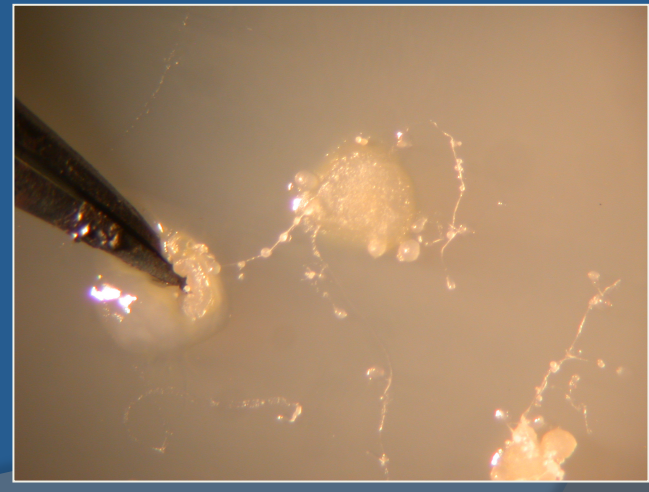
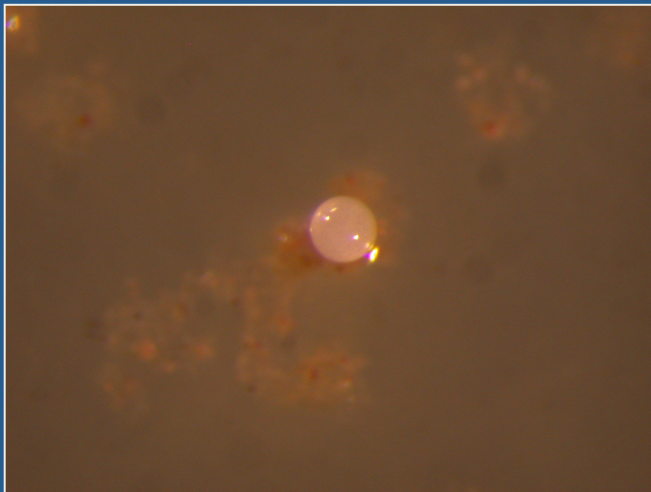
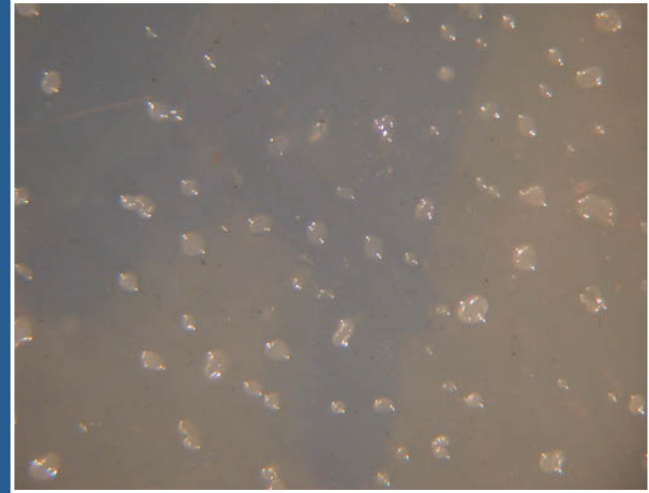
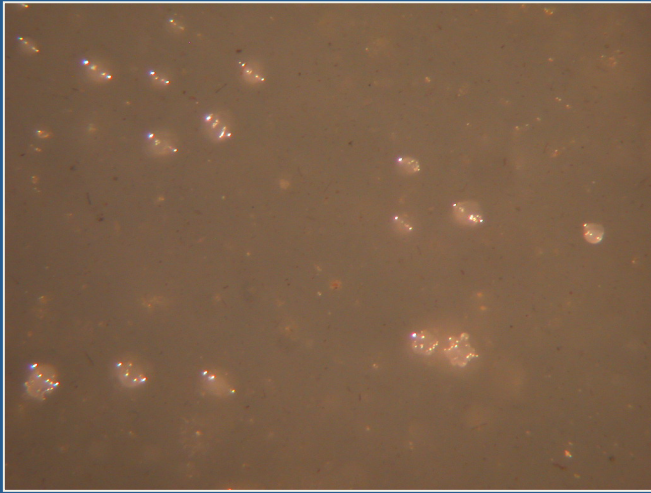


0.98 ± 0.01 SE*



*measured using Relatedness 5.0 (Goodnight Software)

How to isolate cheaters in nature?

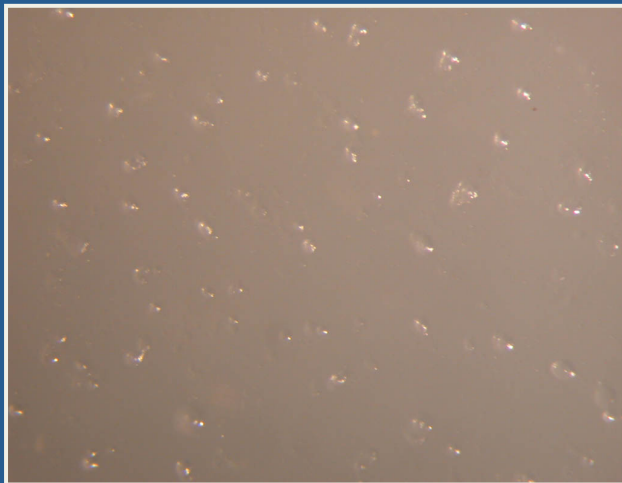


Normal methods do not see mutants

ChtA looks like primitive social amoeba



D. discoideum chtA

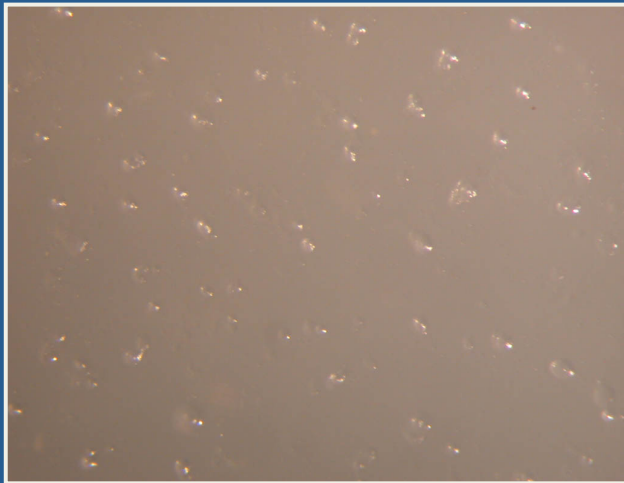


Guttulina sp.

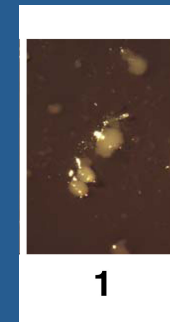


ChtA cannot be re-plated

D. discoideum chtA

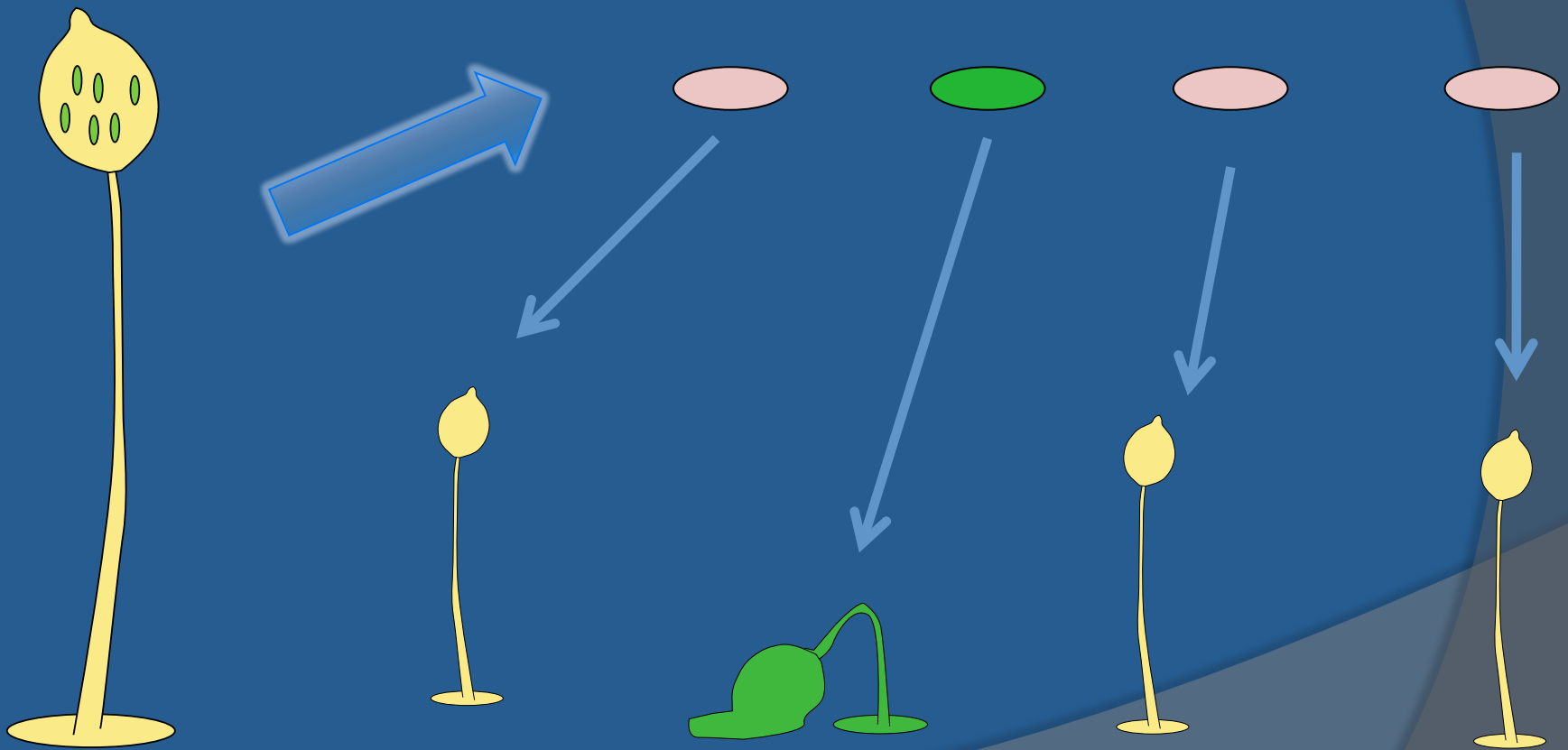


chtA



When clonal does not sporulate

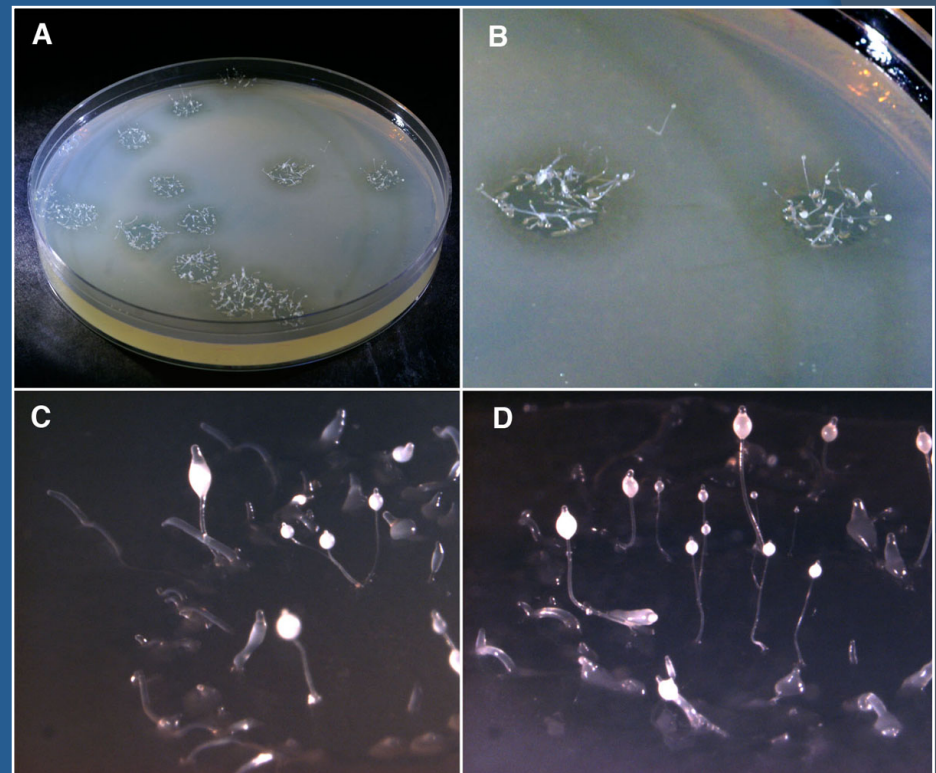
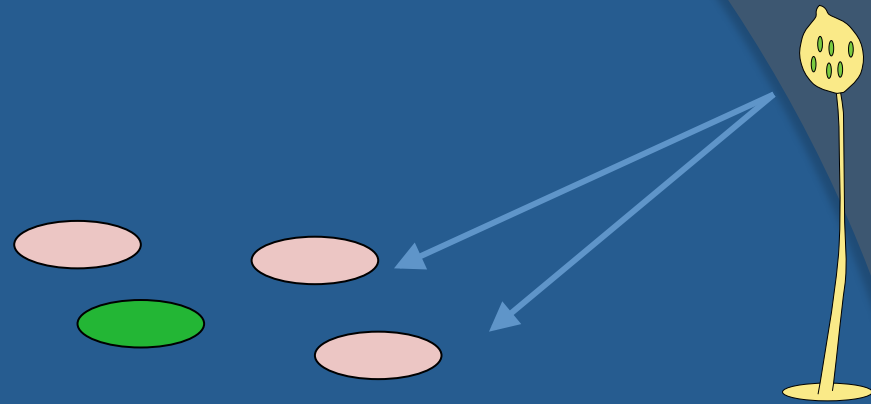
How to look for cheater mutants



Gilbert *et al.* PNAS (2007)

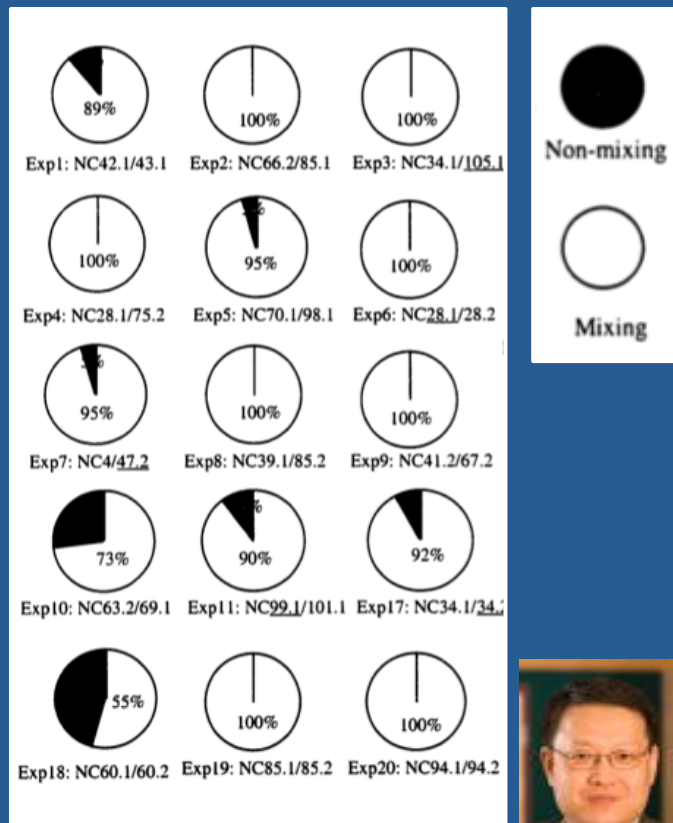
Results

- 95 wild fruiting bodies.
- 63 locations.
- 4 times of year.
- 3316 spores.

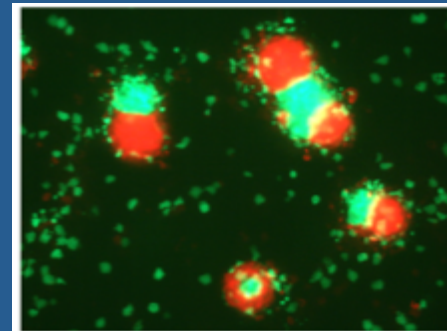


Does kin discrimination explain high relatedness in nature?

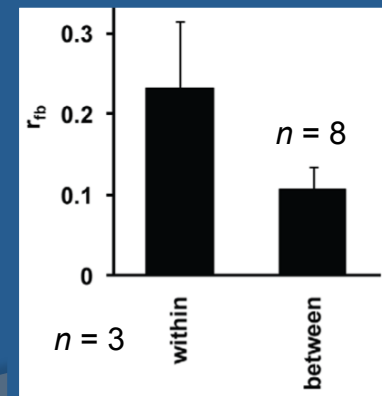
Unclear effect on relatedness



Clones from different geographic regions



Ostrowski *et al.* (2008)



Flowers *et al.* (2010)

Hypothesized role for kin discrimination

$R = 0.5$

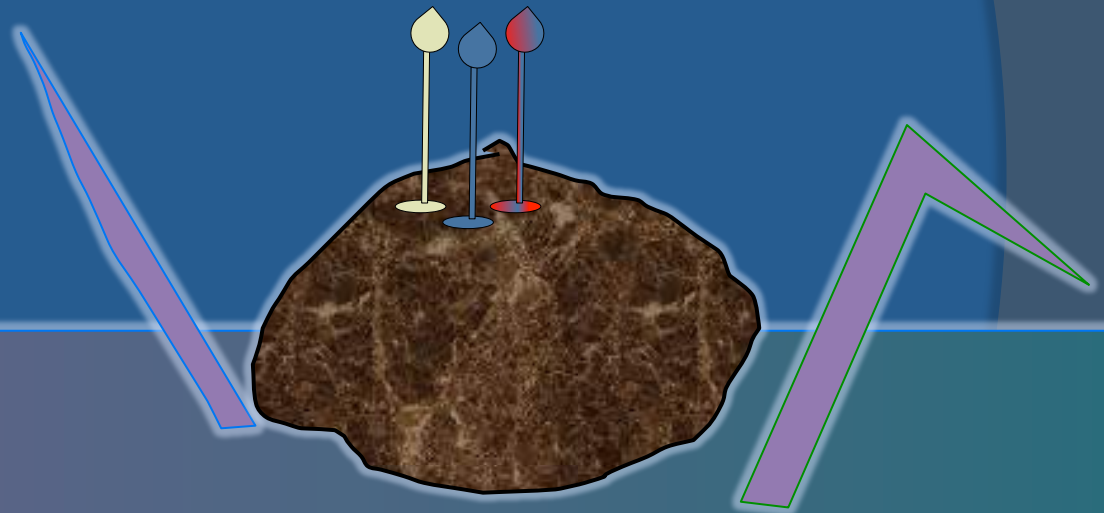


$R = 0.98$

6 mm



6-mm scale
population structure



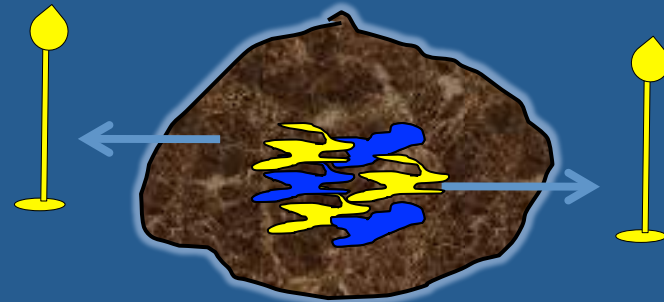
Actual fruiting bodies

Fortunato *et al.* (2003); Gilbert *et al.* (2007) *PNAS*

Possible factors



Within 6-mm pop. structure



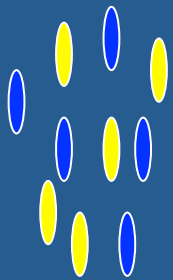
Competition / domination



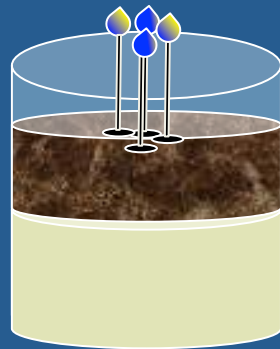
Kin discrimination / segregation

Protocol

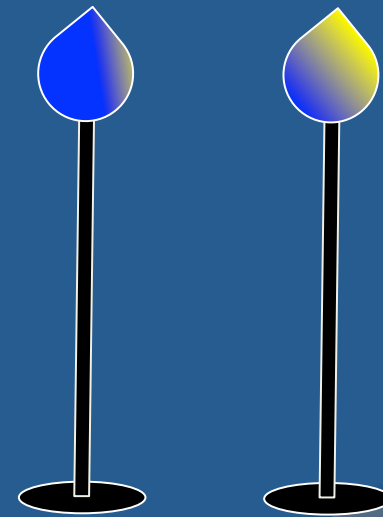
Mix Spores at High Density



50:50



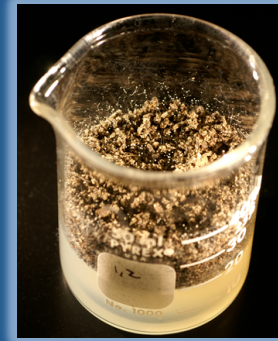
Genotype Individual Fruiting Bodies



Gilbert *et al.* (2012)

Methods

- 18 pairwise mixes
- 3 independent trials
- 16 fruiting bodies per mix per trial
- 1 control experiment
- 1047 fbs genotyped (14.8 ± 0.02 fbs per mix)

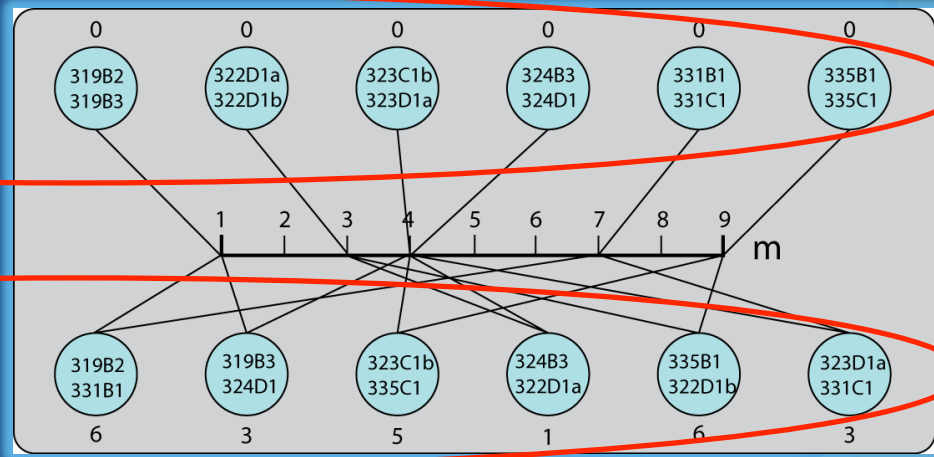
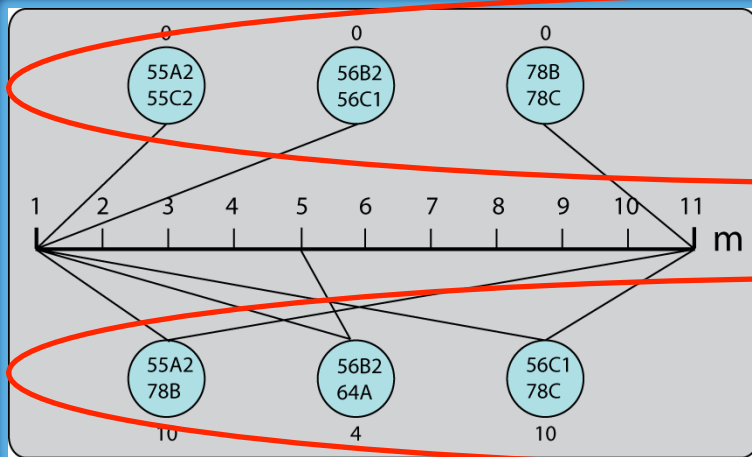


Clones used from Bald Knob, VA

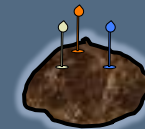
Transect 1 : Sep 25, 2000

Transect 2: Oct 15, 2000

mm-scale mixes



meter-scale mixes

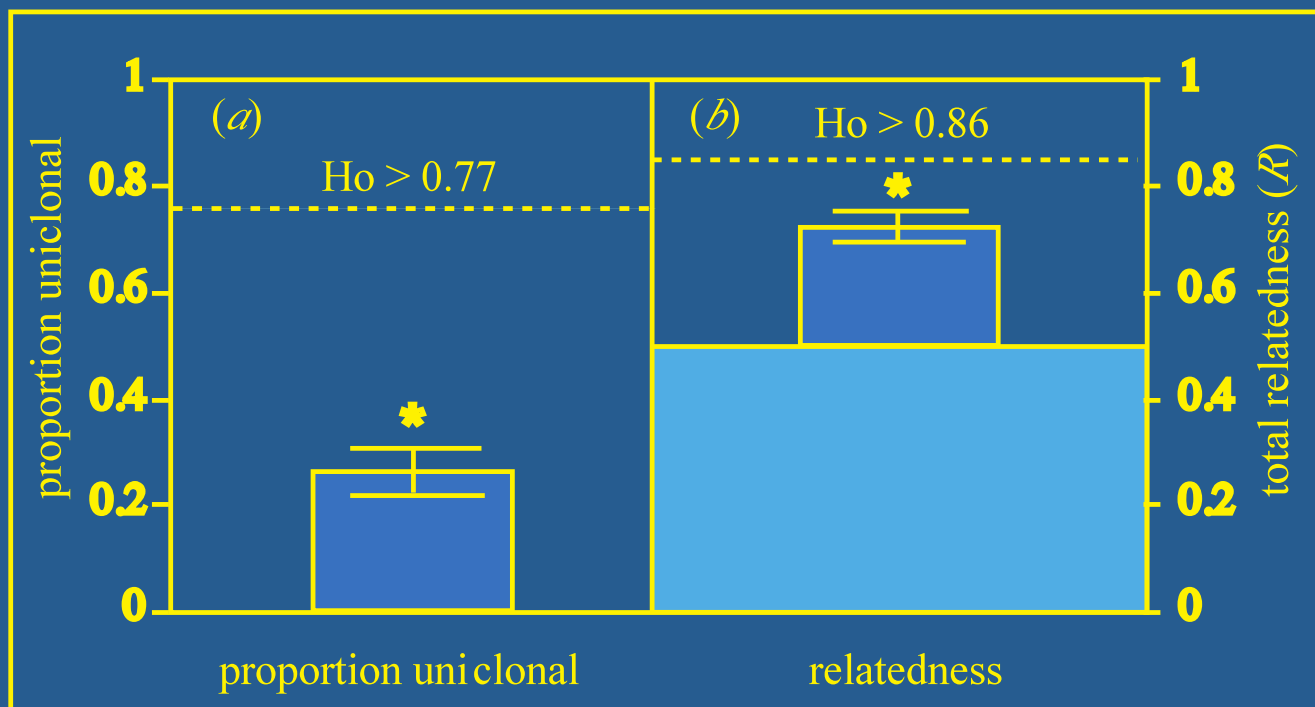


Relatedness between clones

Locus	Chromosome	No. of alleles here
<i>Dict398a.AAT</i>	1	9
<i>Dict404.AAT</i>	1	6
<i>Dict25.AAC</i>	1	9
<i>Dict505e.AAT</i>	2	6
<i>Dict506e.AAT</i>	2	9
<i>Dict511.AAT</i>	3	8
<i>Dict513e.TAA</i>	3	6
<i>Dict518.AAT</i>	3	7
<i>Dict604.AAT</i>	4	6
<i>Dict13.CAT</i>	4	7
<i>Dict19.AAC</i>	4	6
<i>Dict406a.AAT</i>	5	7
<i>Dict414'.TTA</i>	5	11
<i>Dict414a'.TTA</i>	5	4
<i>Dict417.AAT</i>	6	5
<i>Dict418.TTA</i>	6	6

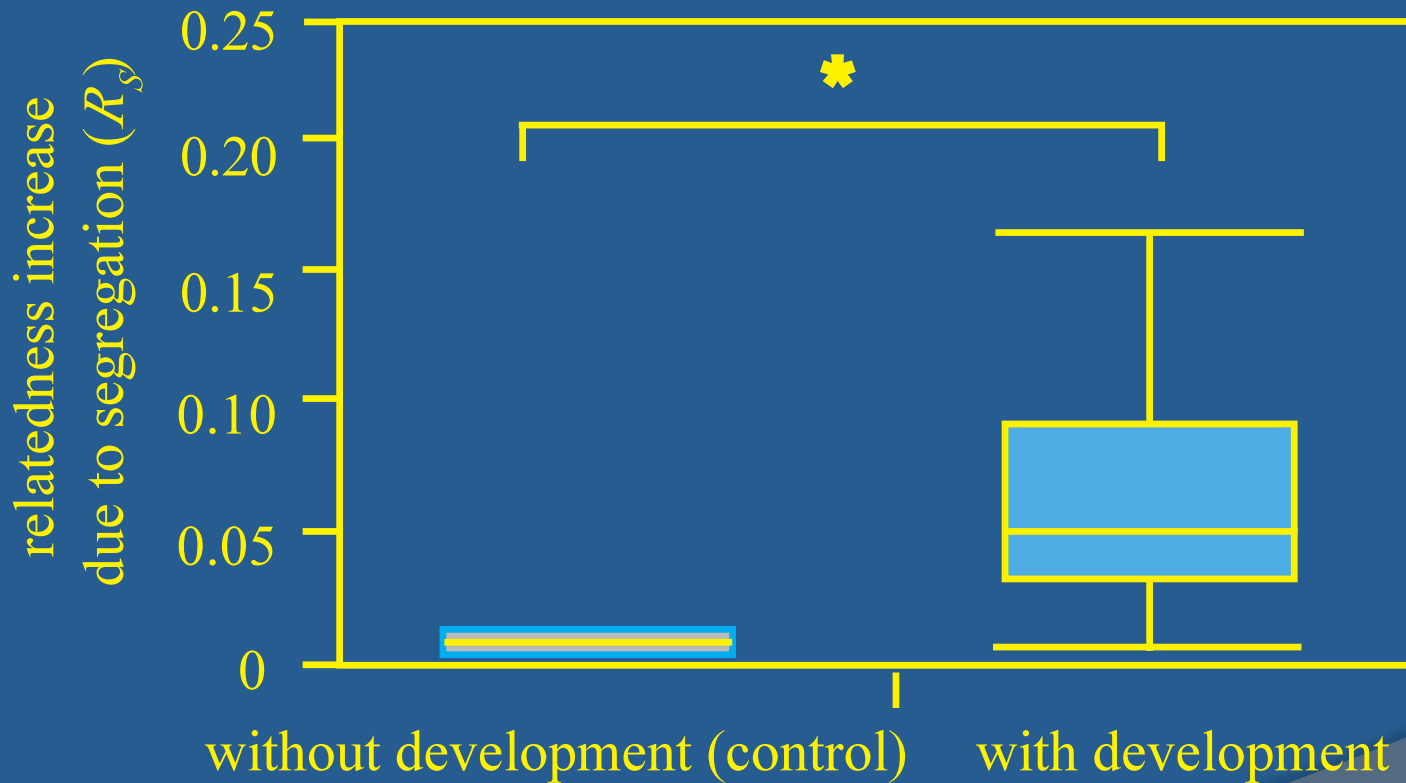
- Clones genotyped for 16 polymorphic microsatellite loci
- All 6 chromosomes represented
- Relatedness estimated using *Relatedness 5.0.8*
- Avg. *R* not sig. different from zero.

Results



*one-tailed t -test, $p < 0.001$; comparison to lower estimate from nature

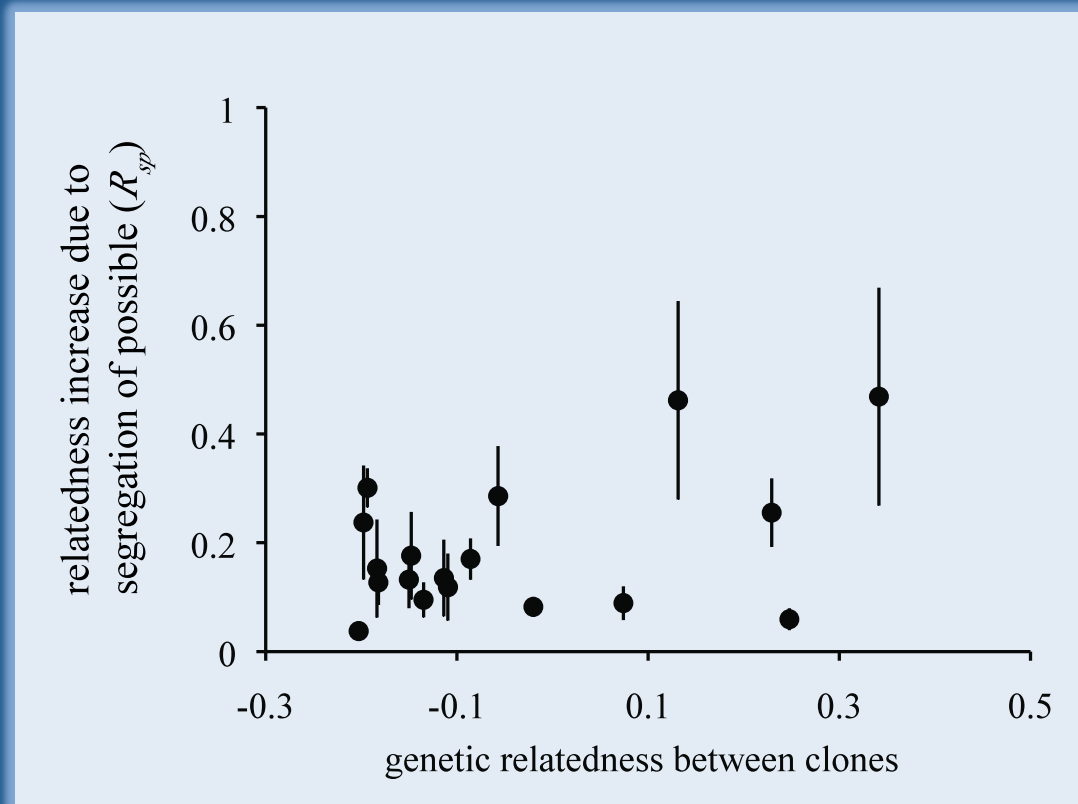
Control shows some segregation



* Wilcoxon rank-sum, $P < 0.0001$

Gilbert *et al.* (2012)

No correlation with R

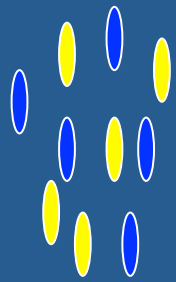


ANCOVA: Effect of R , $P = 0.22$

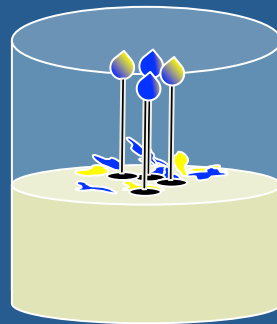
Gilbert *et al.* (2012)

Control 1: Experiment also without soil on second day

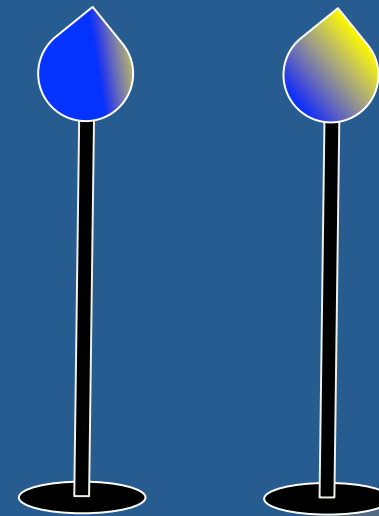
Mix Spores at High Density



50:50



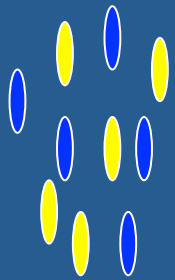
Genotype Individual Fruiting Bodies



$n = 18$ mixes

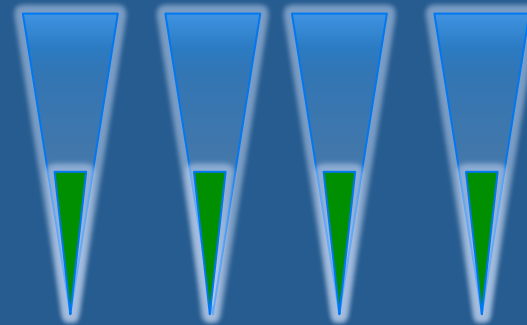
Control 2: Genotyping method

Mix Spores at known proportions



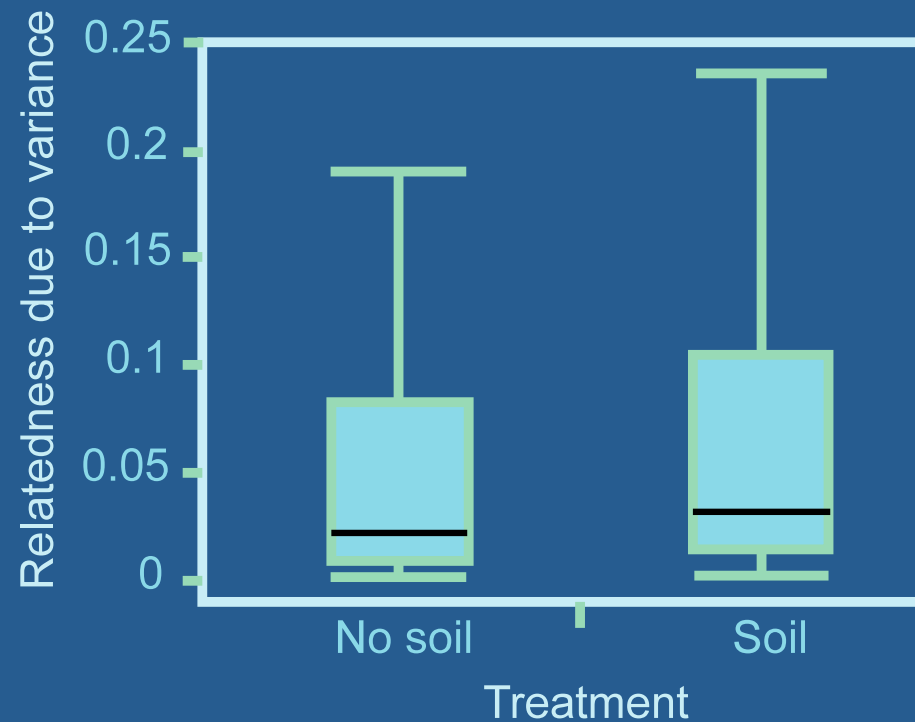
05:95, 10:90,
25:75, 50:50,
75:25, 90:10,
95:05

Genotype 4 aliquots
of each proportion



- 1a. Control for random variation between genotyping wells
- 1b. Measure sensitivity to rare clones
- 1c. Control for PCR bias

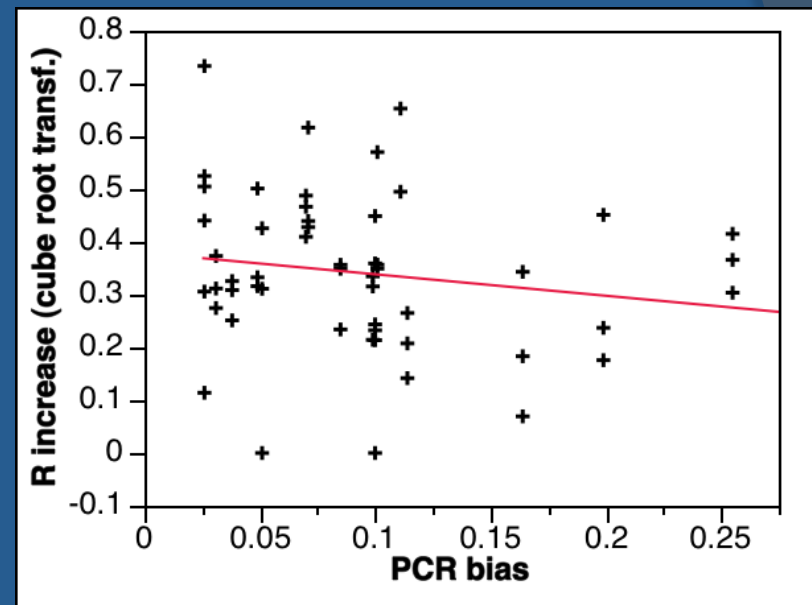
Control 1: Experiment without soil



**Ho not rejected, Wilcoxon test, $P = 0.44$, $n = 17$

Control 2: PCR bias

- Rare clone detectable @ 5%
- PCR bias not predictor of relatedness increase due to variance



(R square= 0.027, P = 0.24)

Overall contribution of kin discrimination



Structure for talk

- ⦿ Introduction to the problem.
- ⦿ Review of means that it has been addressed.
- ⦿ Future work.

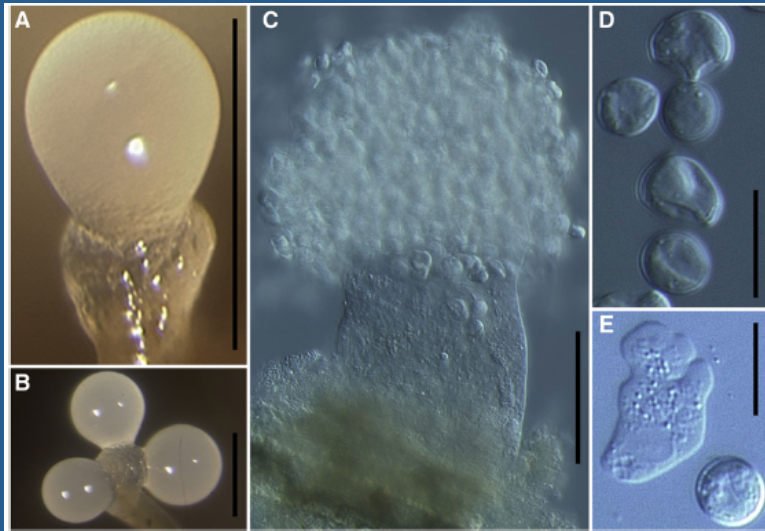
Structure for talk

- ⦿ Introduction to the problem.
- ⦿ Review of means that it has been addressed.
- ⦿ **Future work.**

Questions

- ⦿ What structures populations?
- ⦿ How important is kin discrimination?
- ⦿ How important are different types of cheating (obligate vs. facultative)?
- ⦿ How do traits of microbes map to habitats and functions?

Much remains to be discovered

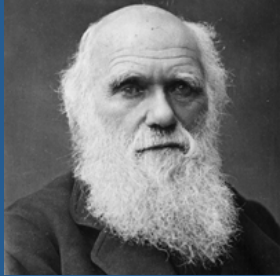


Brown *et al.* (2012)



Credit: Trance Gemini

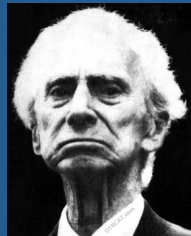
Last thoughts



“Looking back, I think it was more difficult to see what the problems were than to solve them.”



“We are apt to fall into the error of thinking that the facts are simple because simplicity is the goal of our quest.”

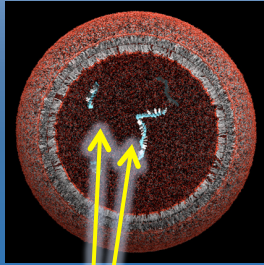


“When a man tells you that he knows the exact truth about anything, you are safe in inferring that he is an inexact man.”

The Origin of Organisms

Cellular organisms

Protocell

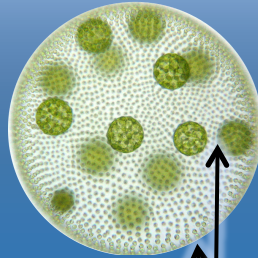


Credit: J. Iwasa

Cooperative replicators

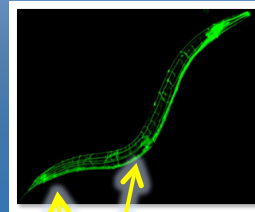
Multicellular organisms

V. carteri



Credit: A. Nedelcu

C. elegans



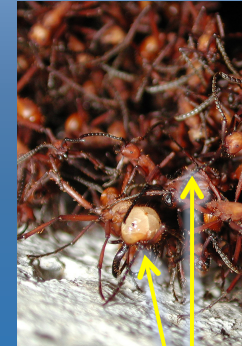
Credit: J. Bessereau

Cooperative cells

Colonial organisms

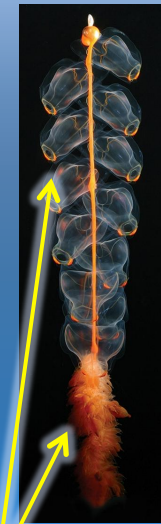
Siphonophore

E. hamatum



Credit: L. Gilbert

Credit: K. Raskoff



Cooperative Individuals

Thank You!



- Wray-Todd graduate fellowship
- NSF



