

Aphid communities, symbionts and barcodes

Charles Godfray

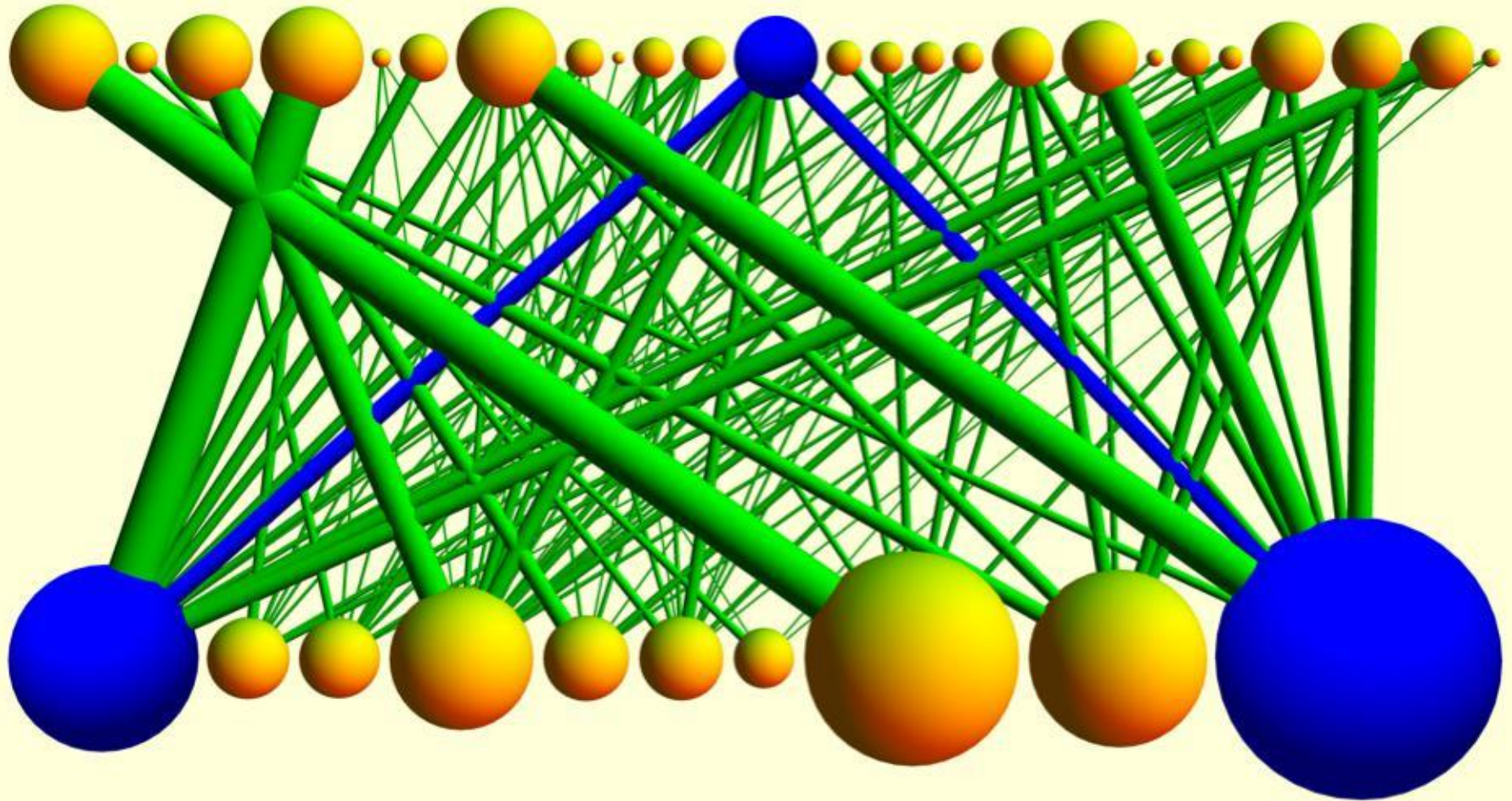
Department of Zoology, Oxford University



This talk

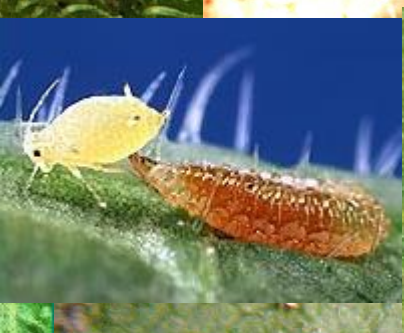
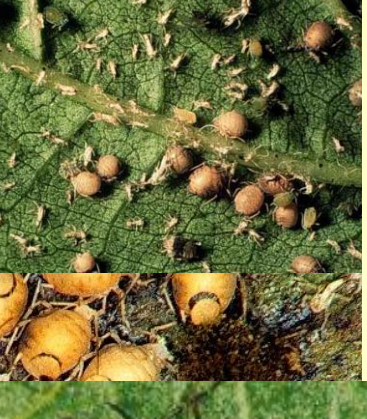
- Canter through some of our work on aphid communities: their natural enemies and their bacterial symbionts
- Talk about where we have used barcode techniques and how they might be used more in the future

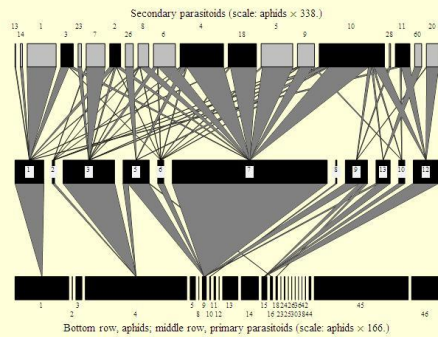
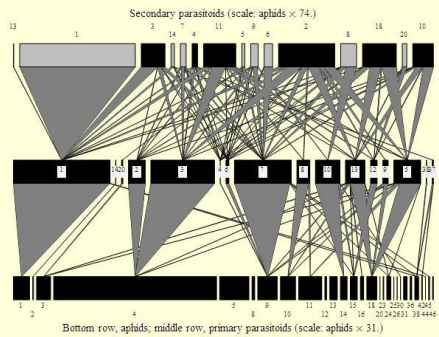
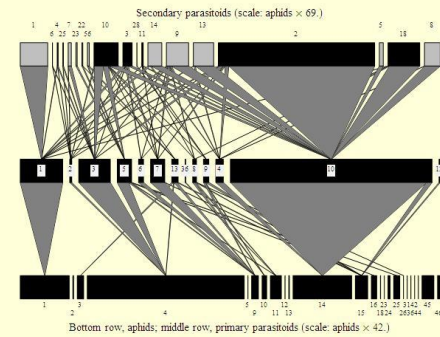
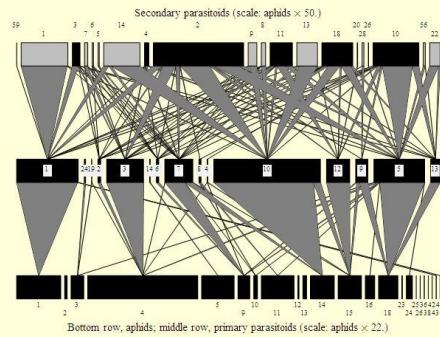
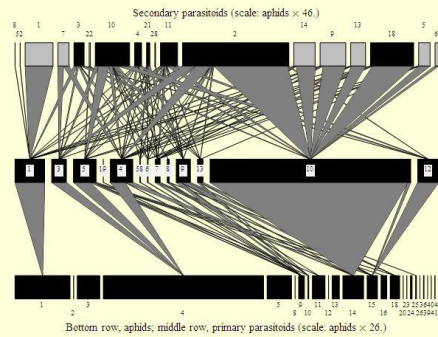
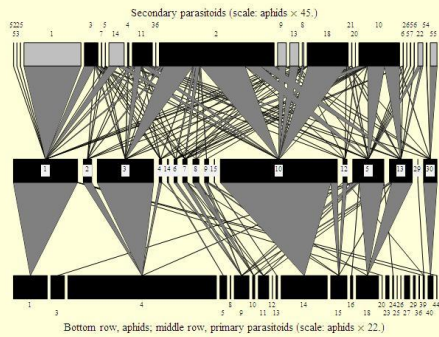
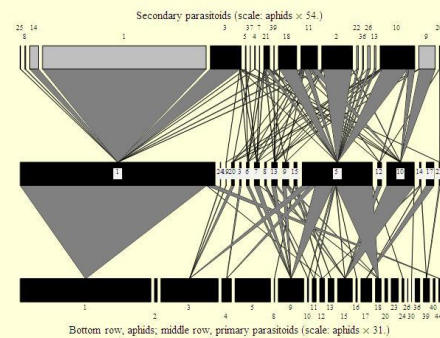
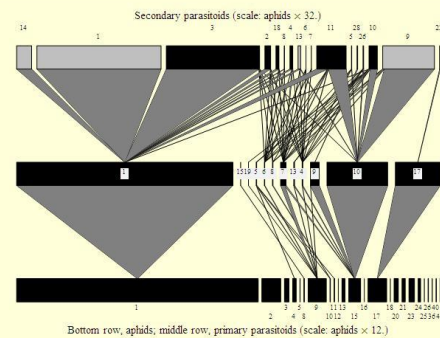
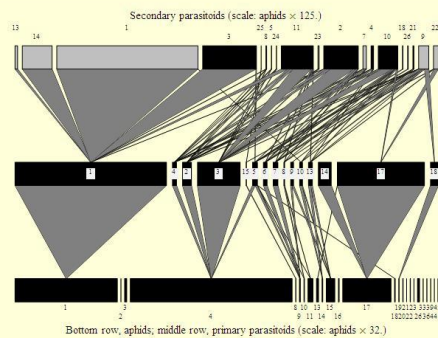
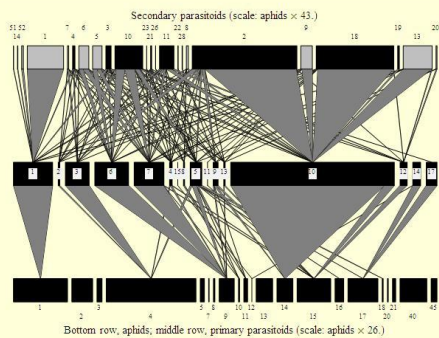
Parasitoids



Hosts



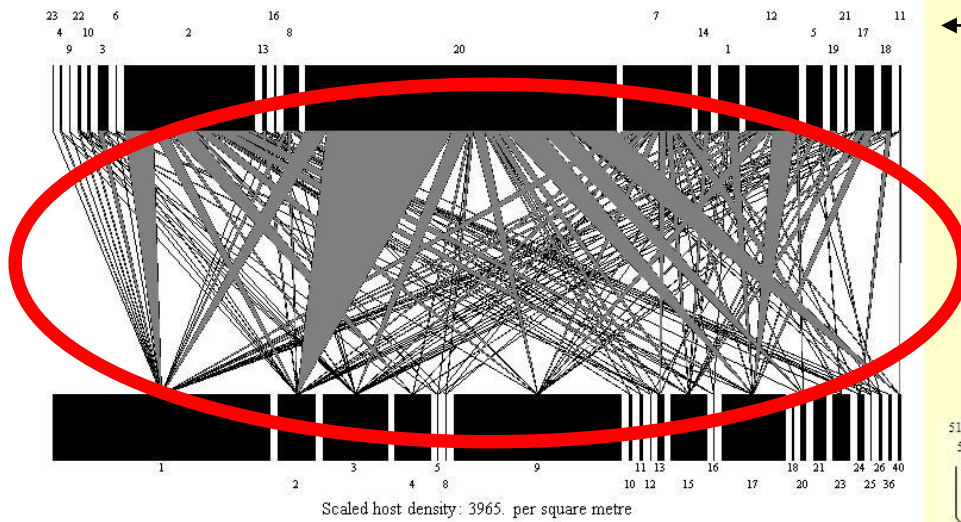




Annual summary food webs

Christine Müller & Frank van Veen

Scaled Predator Density (8.)

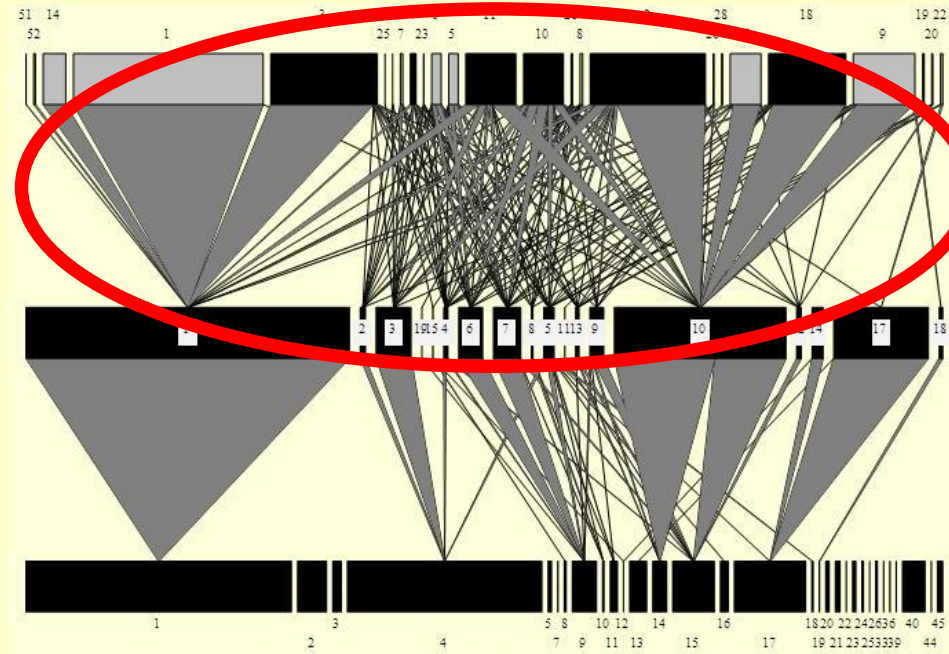


Scaled host density: 3965. per square metre

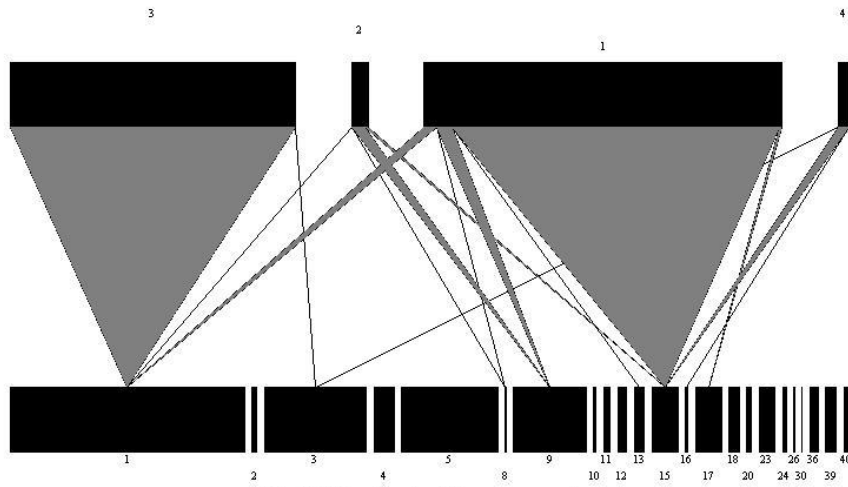
Predators

(scaled for aphid body size and predator consumption)

Parasitoids and hyperparasitoids



Pathogens (scale: hosts times 116.)

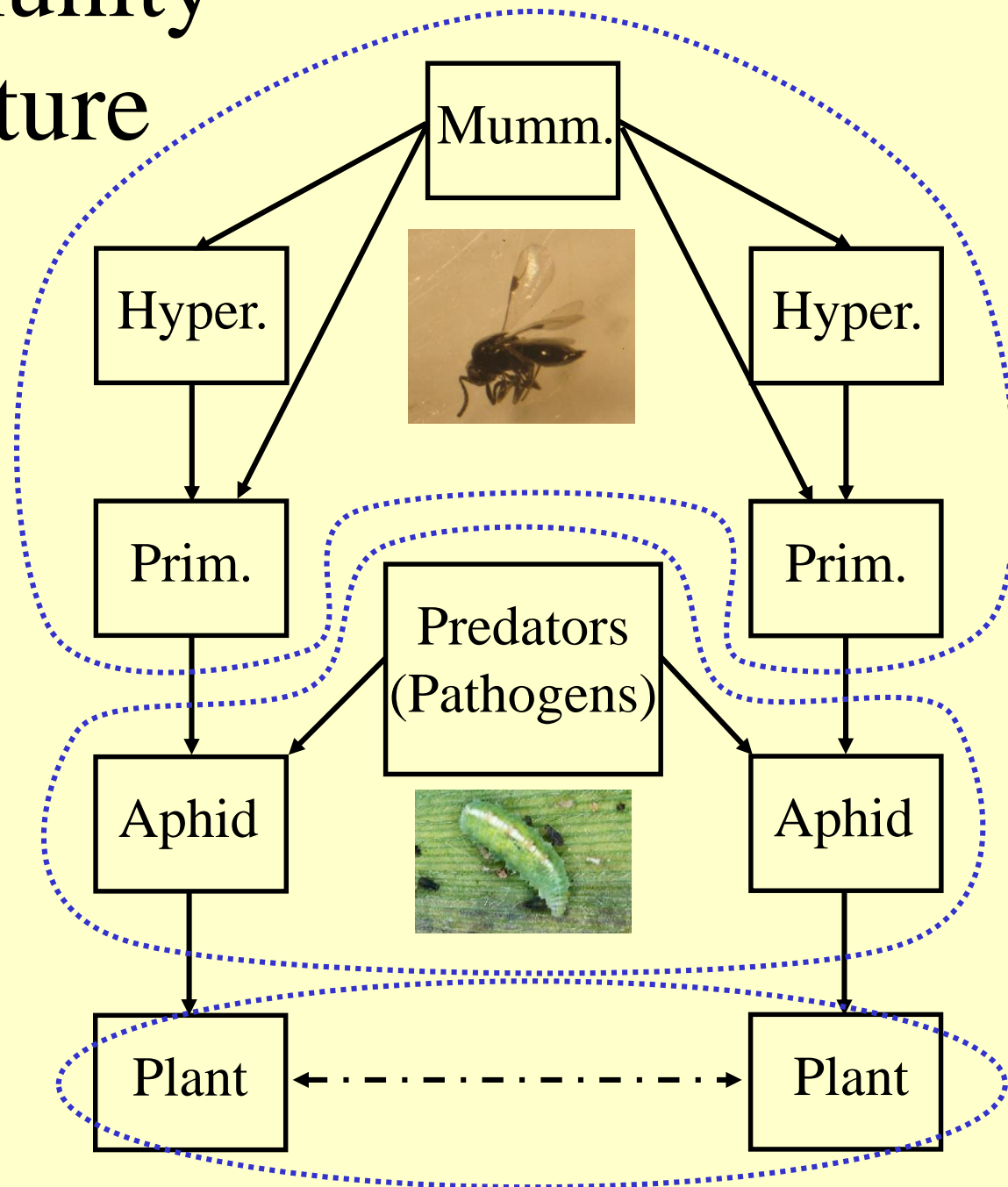


Total 1998 host density: 307. per square metre

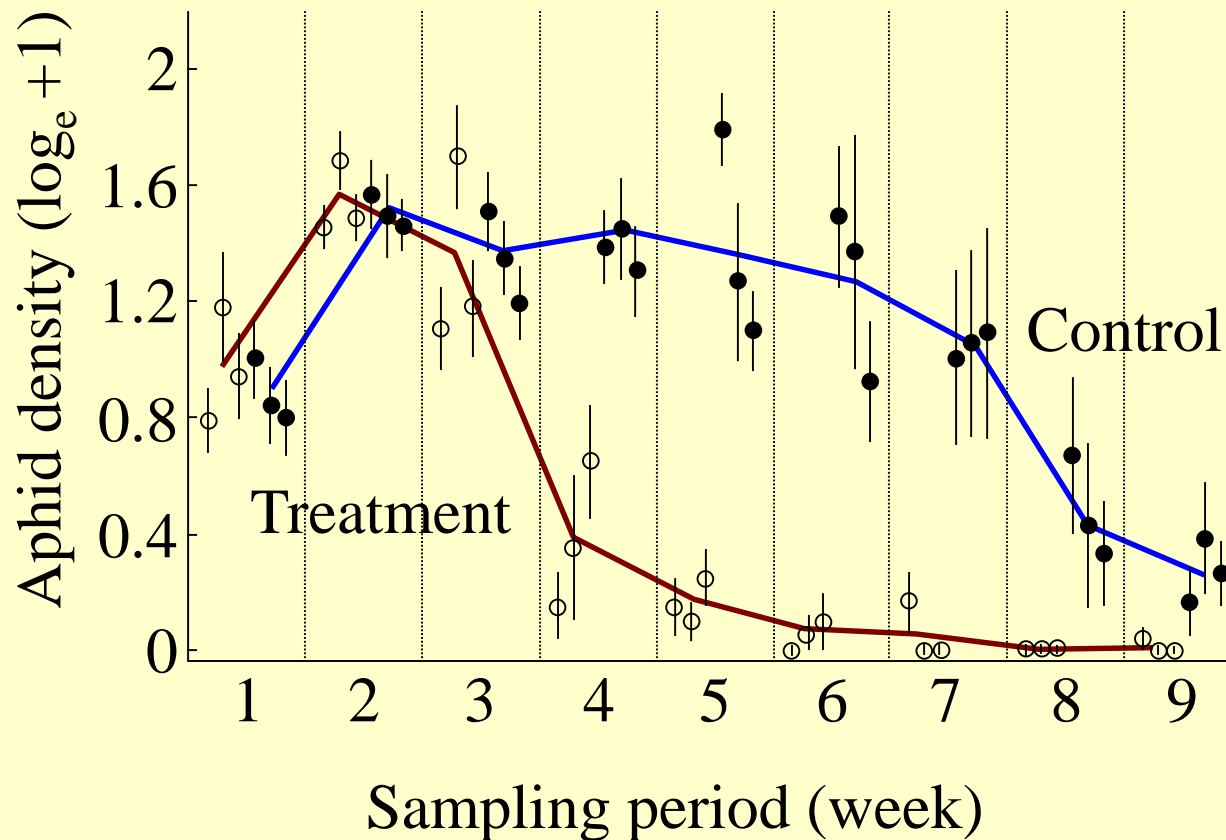
Pathogens

*Frank van Veen, Christine Müller
Richard Cooke, Judy Pell*

Community structure



Aphids via natural enemies

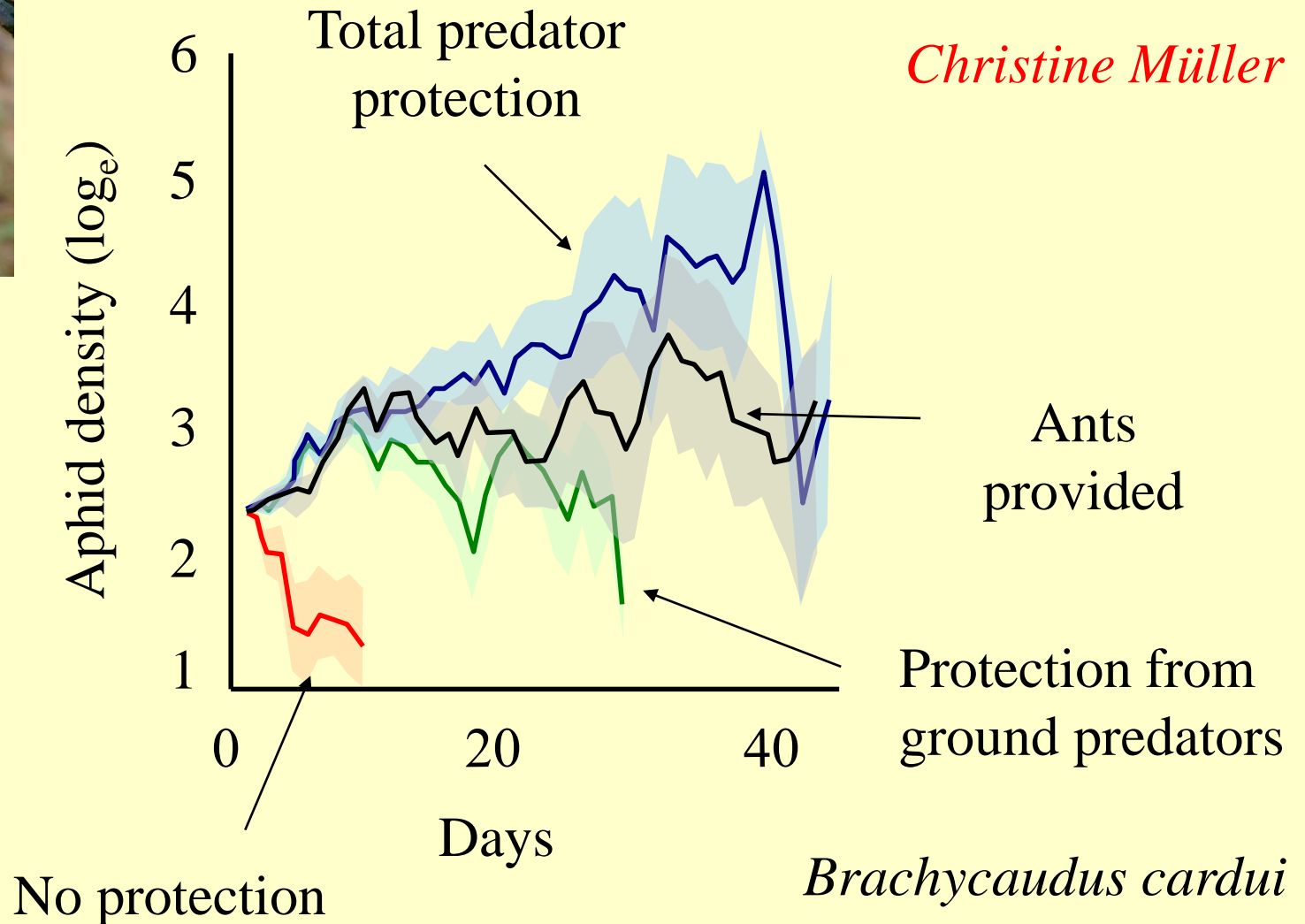


Christine Müller



Community composition

Christine Müller



Pea Aphid and its natural enemies



Acyrtosiphon pisum:
pea aphid



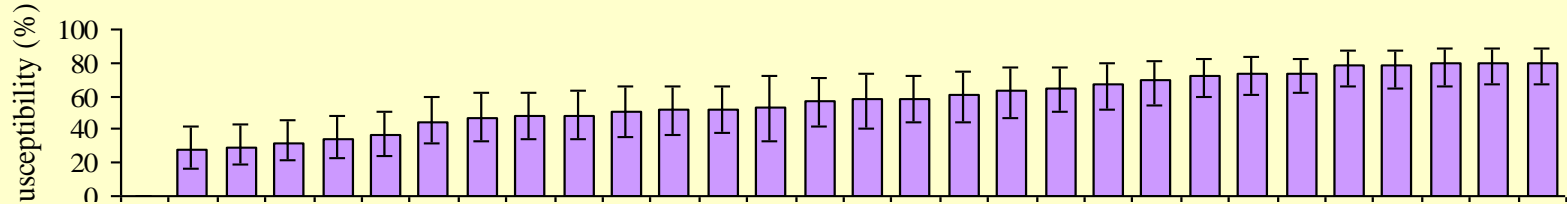
Aphidius ervi (& *eadyi*): braconid wasps



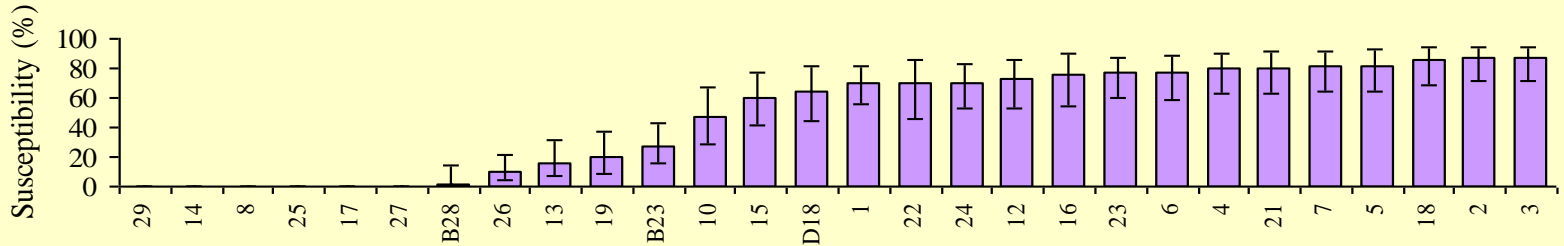
Erynia neoaphidis:
entomopathogenic
fungus

Clonal variability in resistance

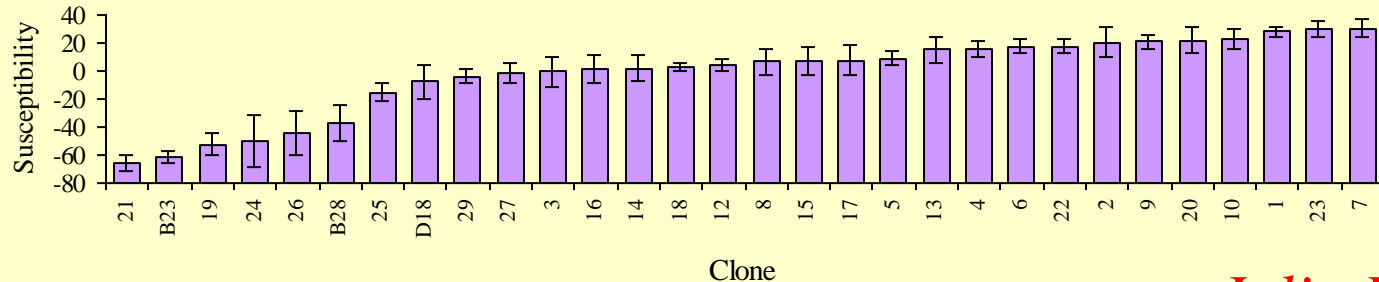
Susceptibility to *A. ervi*



Susceptibility to *A. eadyi*



Susceptibility to *E. neoaphidis*



Julia Ferrari

Facultative bacterial symbionts in aphids confer resistance to parasitic wasps

Kerry M. Oliver*, Jacob A. Russell†, Nancy A. Moran†, and Martha S. Hunter**

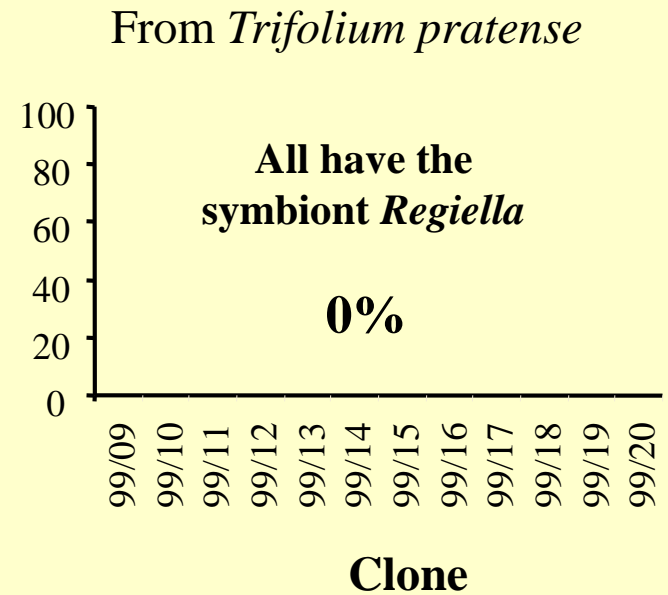
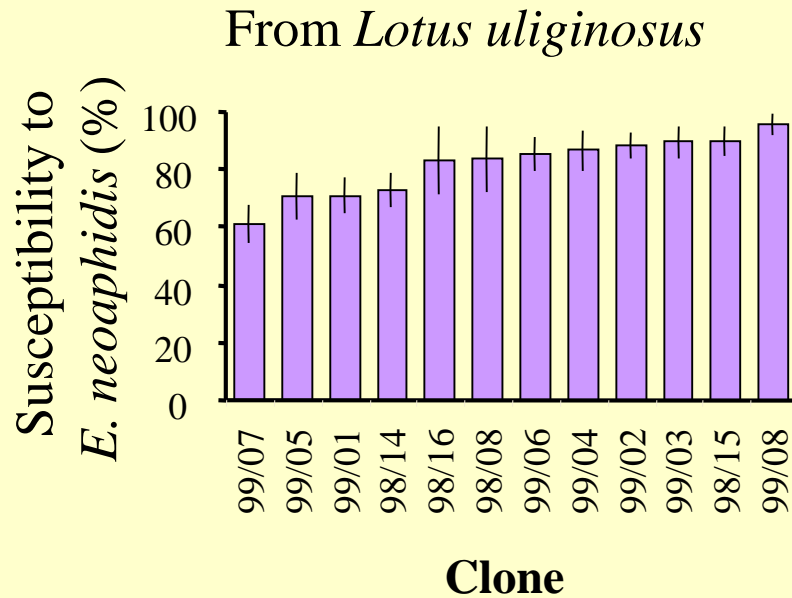
Departments of *Entomology and †Ecology and Evolutionary Biology, University of Arizona, Tucson, AZ 85721

Edited by Lynn Margulis, University of Massachusetts, Amherst, MA, and approved December 16, 2002 (received for review August 28, 2002)

Symbiotic relationships between animals and microorganisms are common in nature, yet the factors controlling the abundance and distributions of symbionts are mostly unknown. Aphids have an obligate association with the bacterium *Buchnera aphidicola* (the primary symbiont) that has been shown to contribute directly to aphid fitness. In addition, aphids sometimes harbor other vertically transmitted bacteria (secondary symbionts), for which few benefits of infection have been previously documented. We carried out experiments to determine the consequences of these facultative symbioses in *Acyrtosiphon pisum* (the pea aphid) for vulnerability of the aphid host to a hymenopteran parasitoid, *Aphidius ervi*, a major natural enemy in field populations. Our results show that, in

A. pisum clones vary greatly in their resistance to *A. ervi* development following oviposition. To determine the possible contribution of SS to this variation, we established genetically uniform aphid lineages that differed only in their SS infection status. To eliminate any effects of genetic variation of the aphids in resistance to parasitism, we inoculated an uninfected *A. pisum* clone with SS from body fluids of clones harboring each of the γ -3 proteobacteria SS types, thus creating three genetically uniform lineages of aphids that differed from the original only by the presence of a particular SS. These lineages were used in experiments to determine the consequences of these facultative symbioses for aphid vulnerability to an important hymenopteran

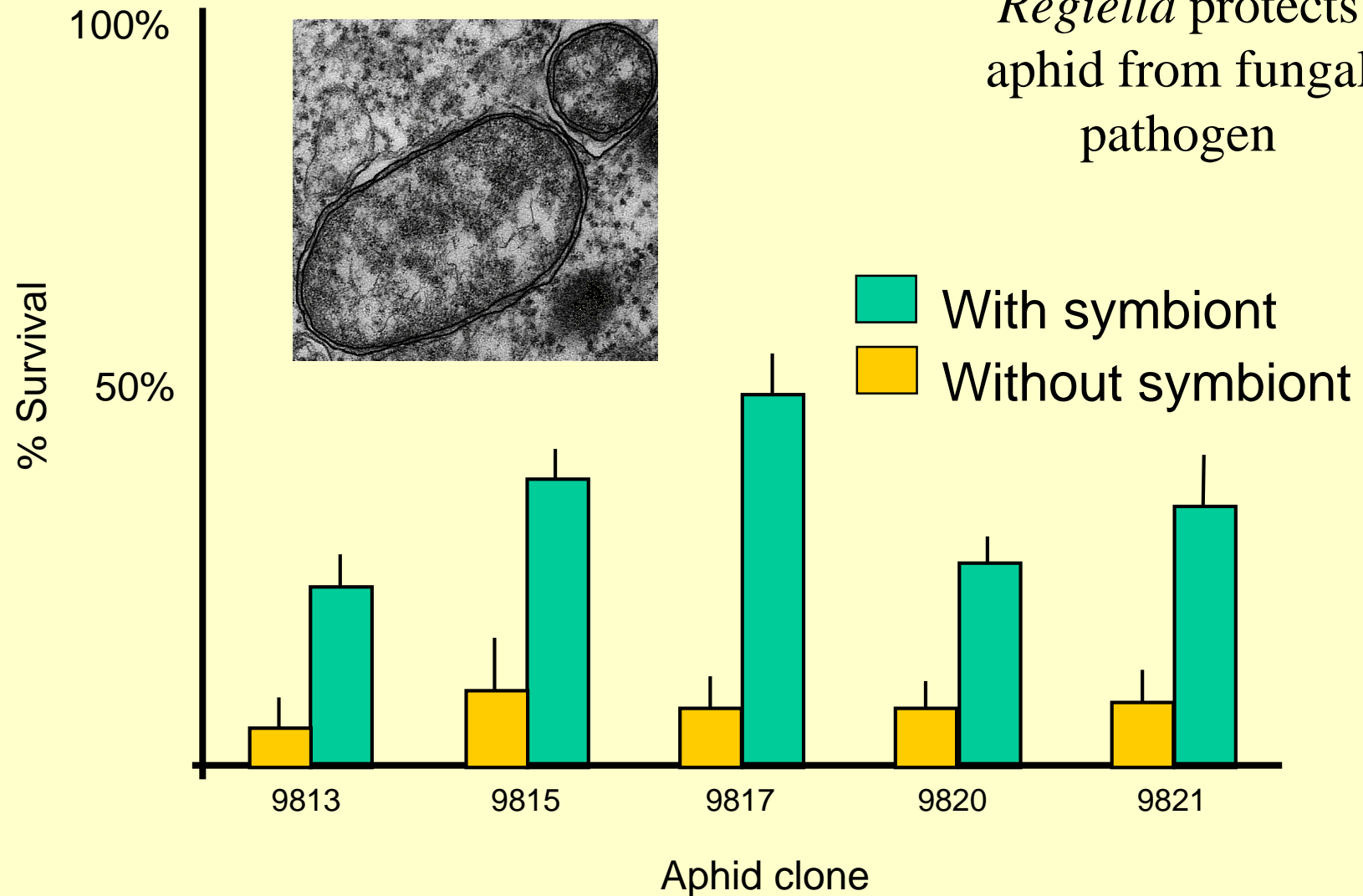
Fungus resistance correlated with host plant



Julia Ferrari

Aphid Secondary Symbionts

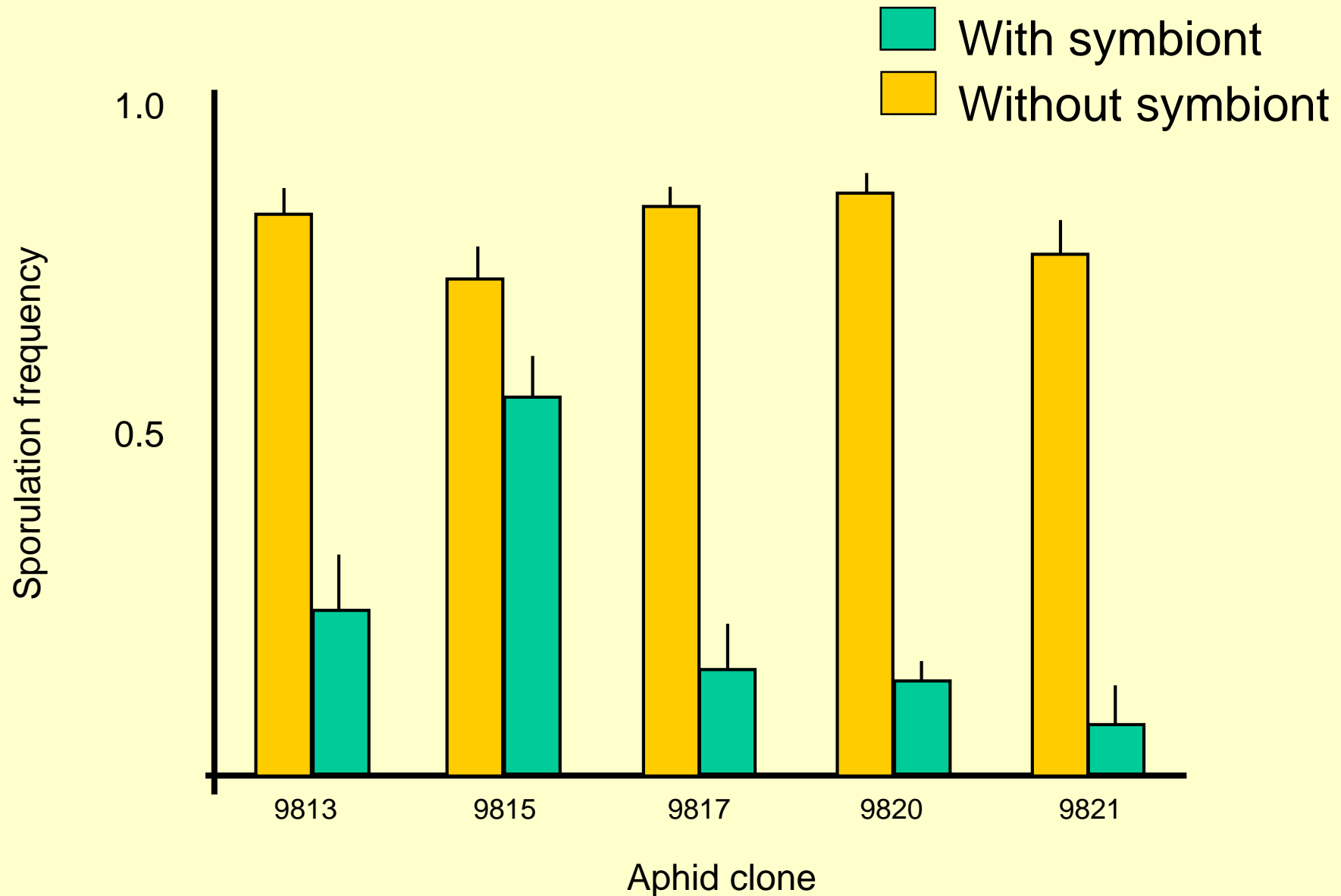
Regiella protects
aphid from fungal
pathogen



Claire Scarborough & Julia Ferrari

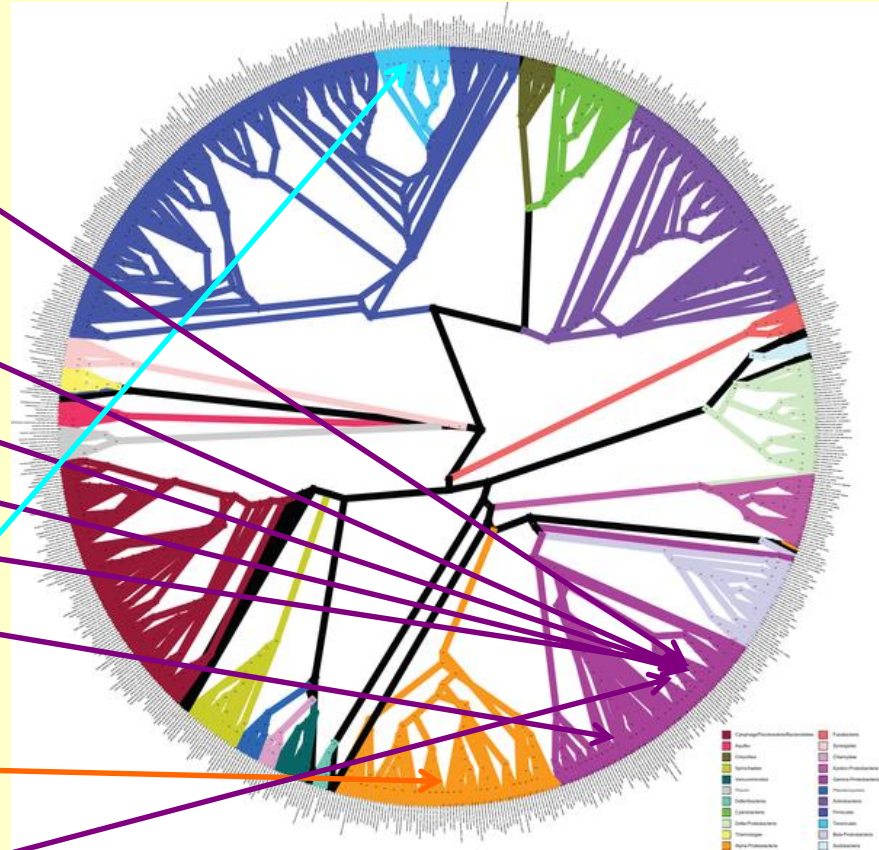


Aphid Secondary Symbionts



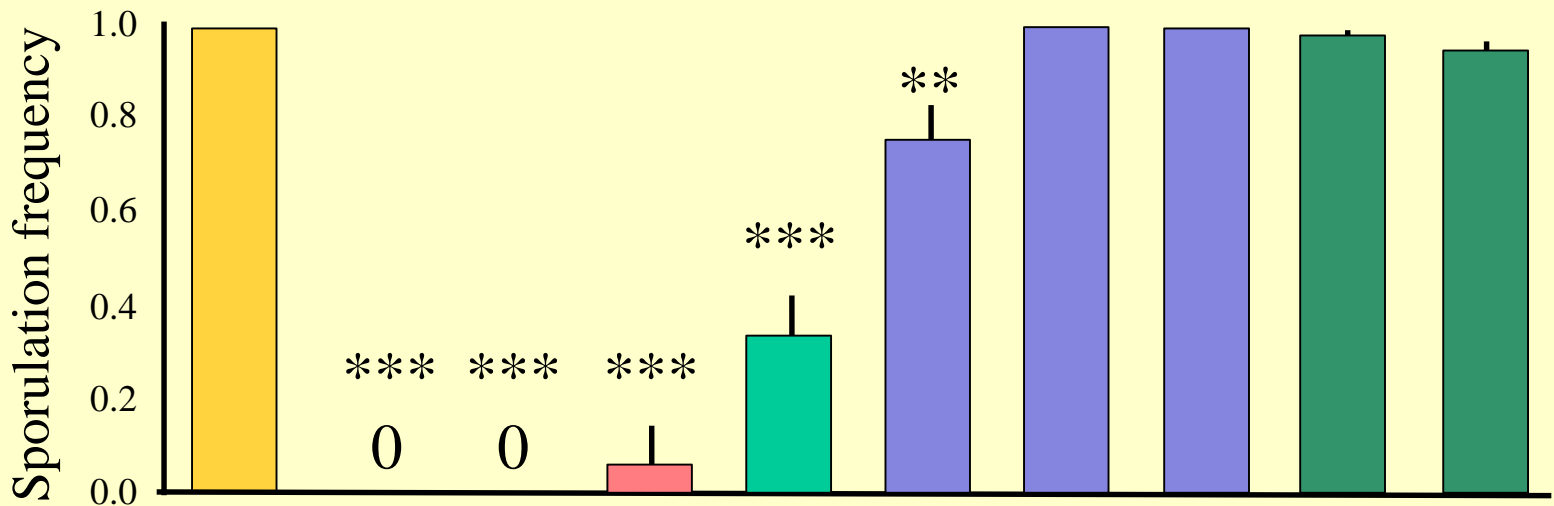
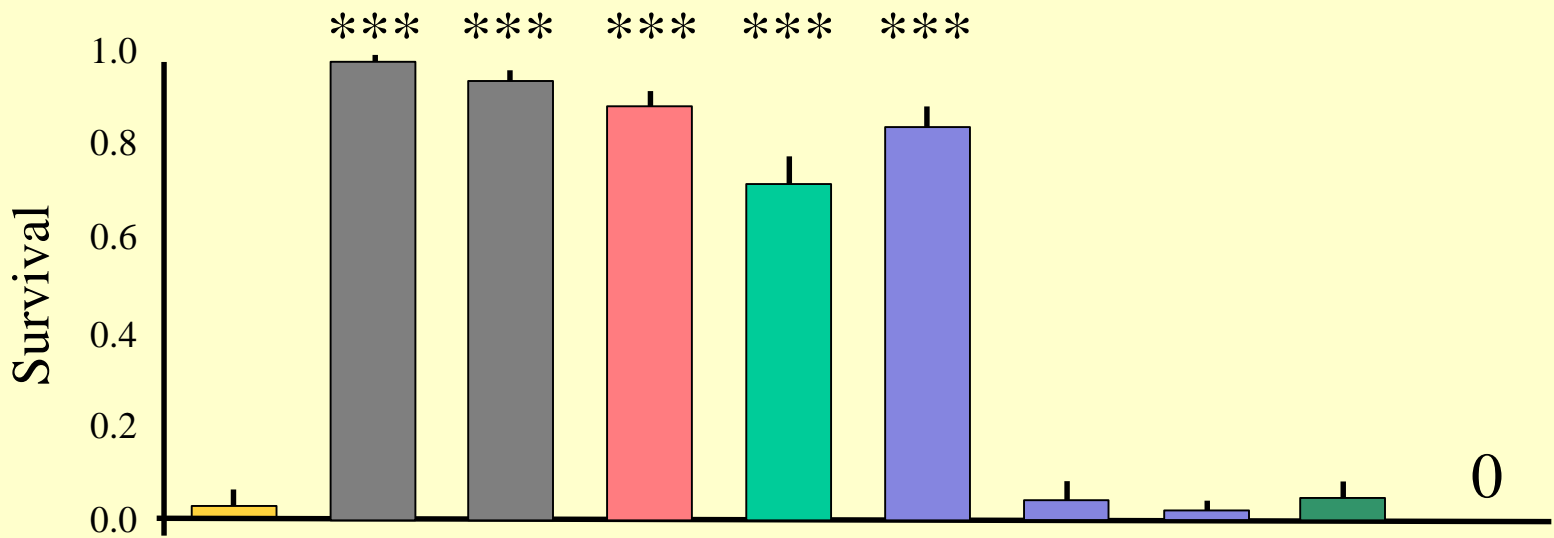
Aphid symbionts

- Primary symbiont
 - *Buchnera aphidicola*
- Secondary symbionts
 - *Hamiltonella defensa*
 - *Regiella insecticola*
 - *Serratia symbiotica*
 - X type
 - *Rickettsia*
 - *Spiroplasma*
 - *Rickettsiella*
 - [*Arsenophonus*, *Wolbachia*]



Lang JM, Darling AE, Eisen JA (2013) *PLoS ONE* 8(4): e62510

Transmission?



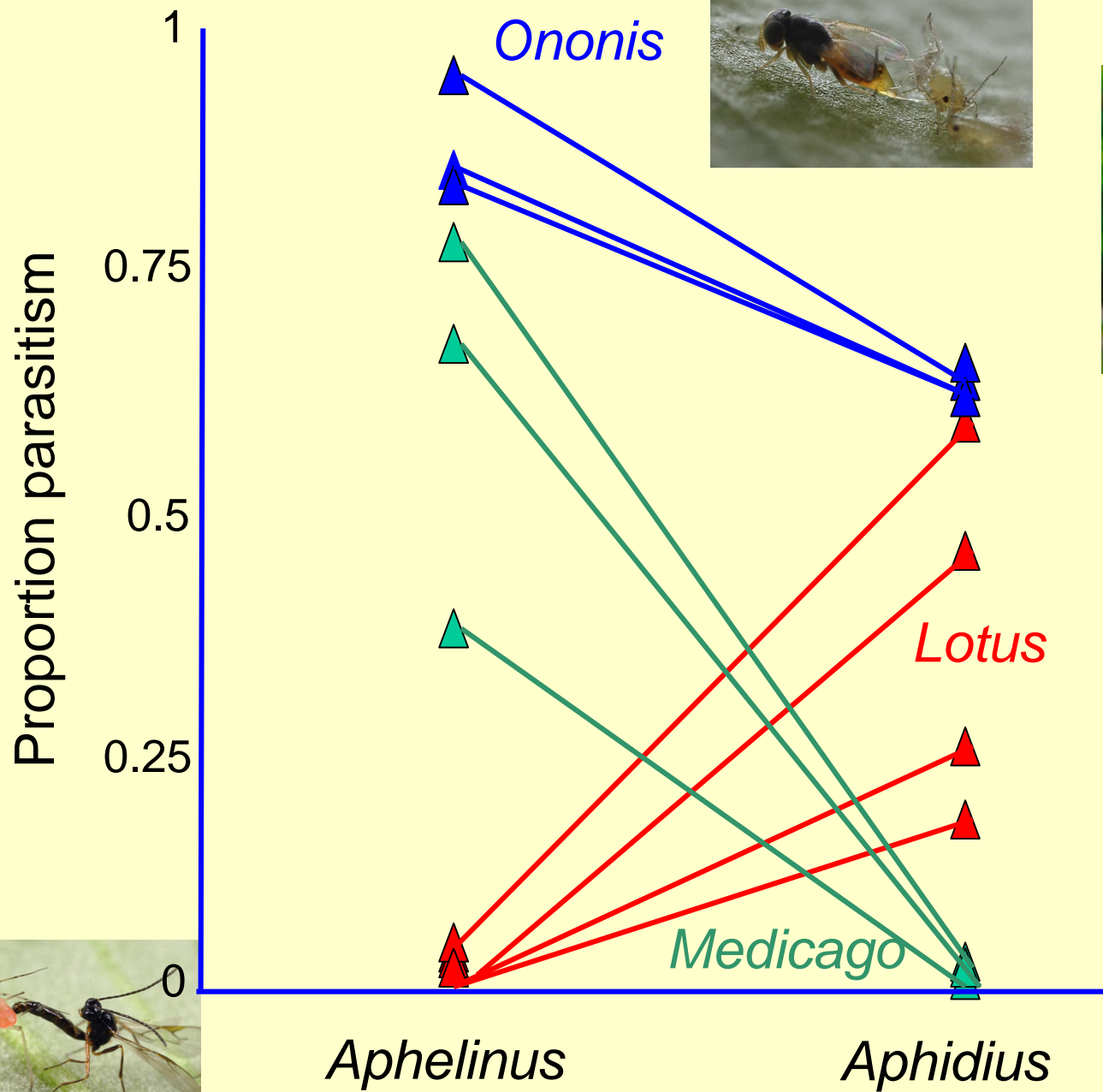
none *Rickettsia* *Rickettsiella* *Regiella* *Spiroplasma* *Hamiltonella*



Aphidius ervi
(Ichneumonoidea:
Braconidae)

Aphelinus abdominalis
(Chalcidoidea:
Aphelinidae)





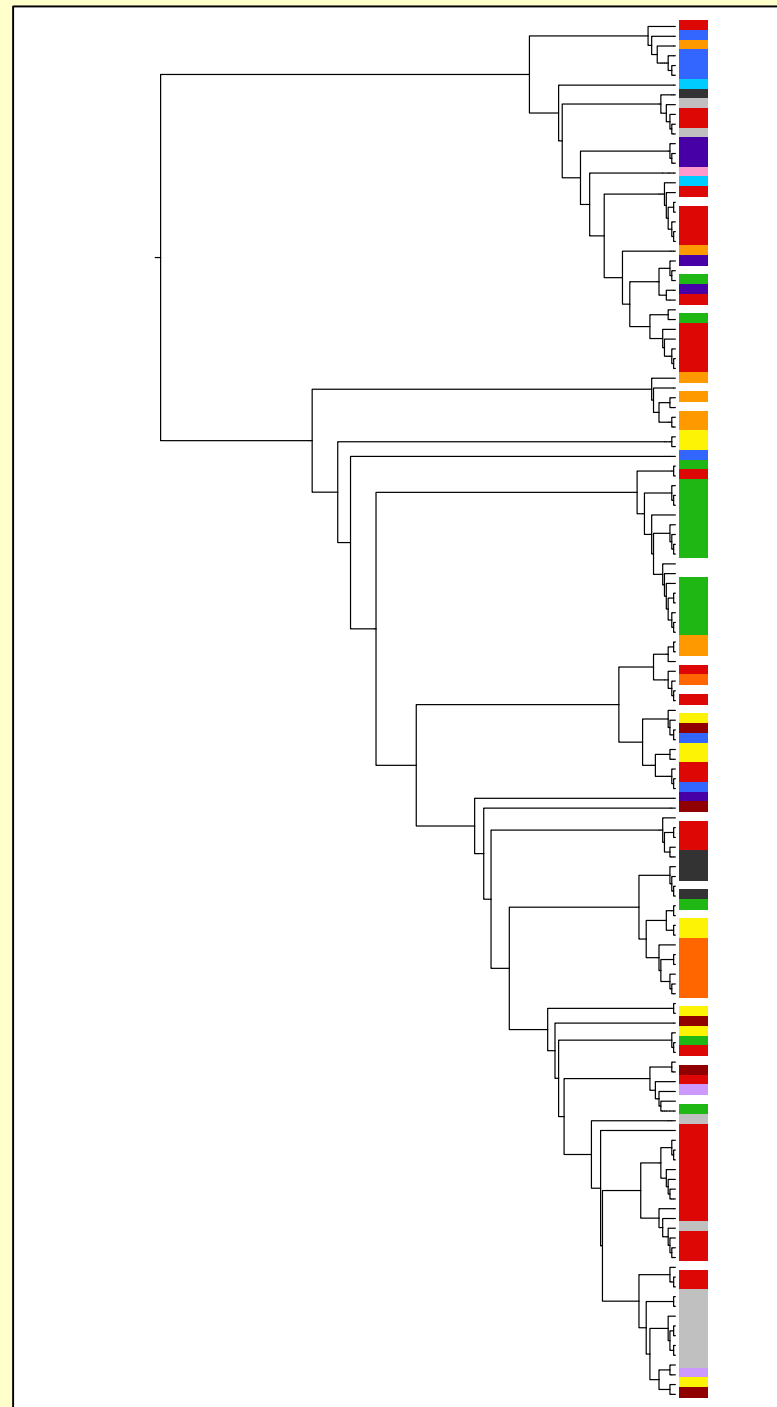
Ailsa McLean

Symbionts and natural enemies

- Secondary symbionts important in defence against parasitoids and fungi
 - *Hamiltonella*; & phage delivery (Moran, Hunter, Oliver labs)
- Different symbiont species protect against the same natural enemy
- Specialist defence within symbiont species

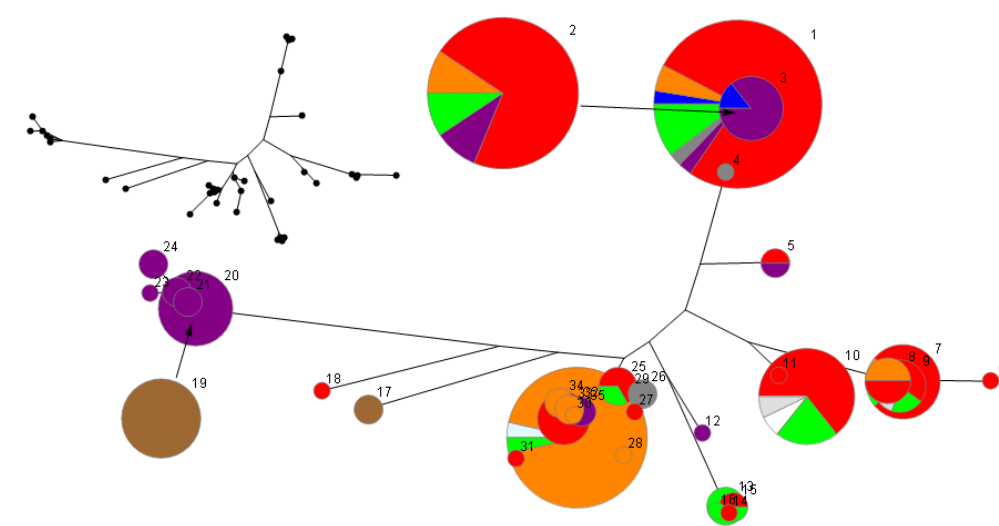


Population structure 1100 pea clones

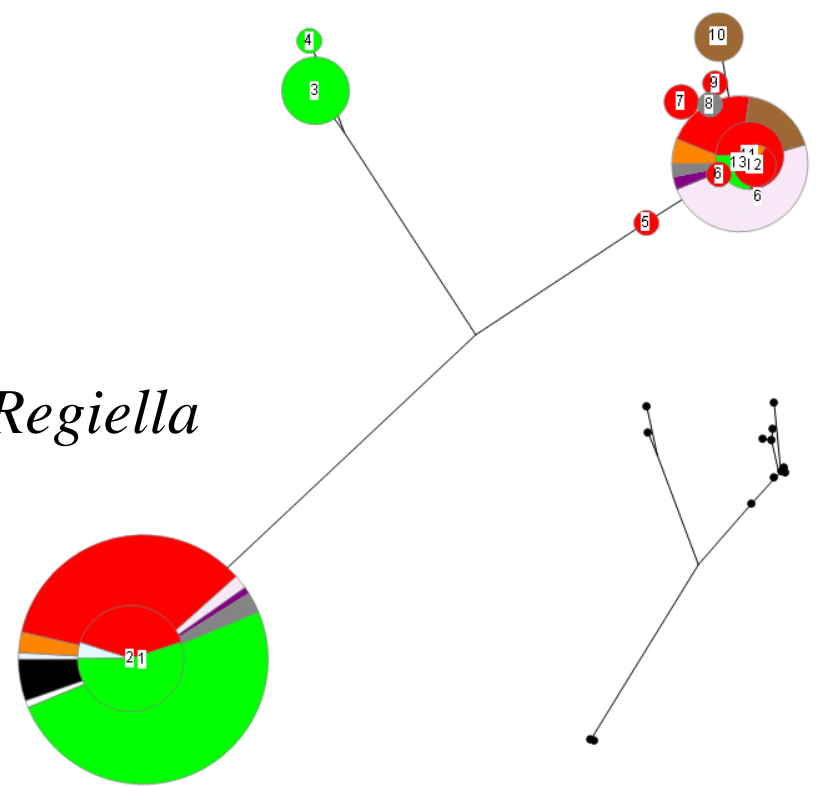


Lee Henry

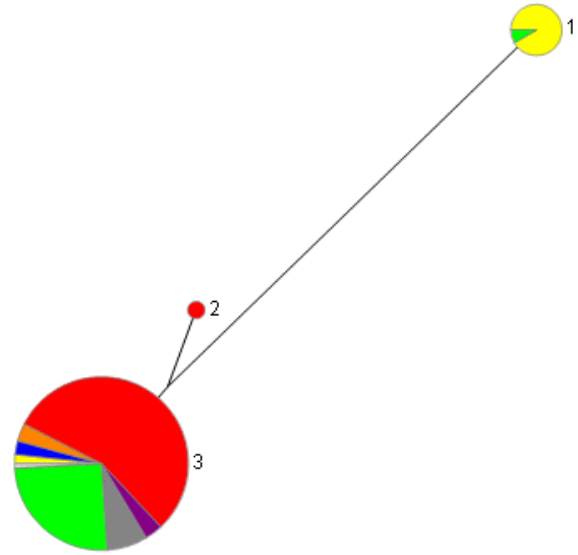
Hamiltonella



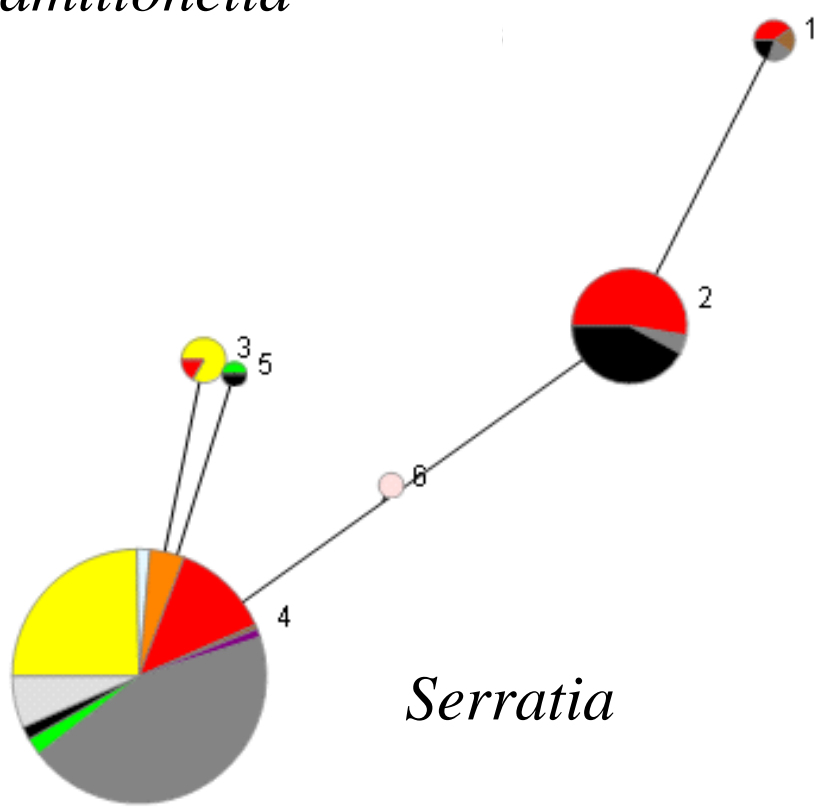
Regiella



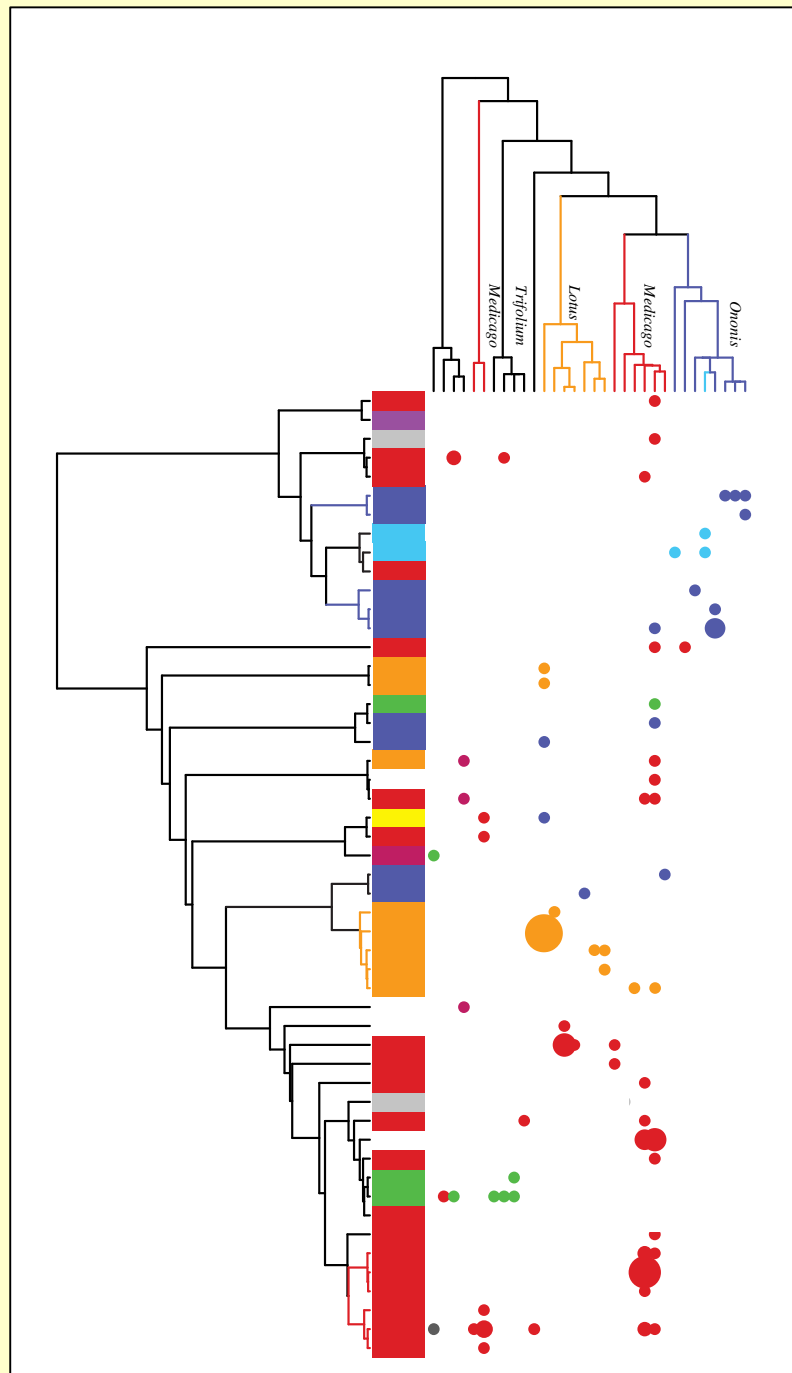
X-type



Serratia



Pea aphid



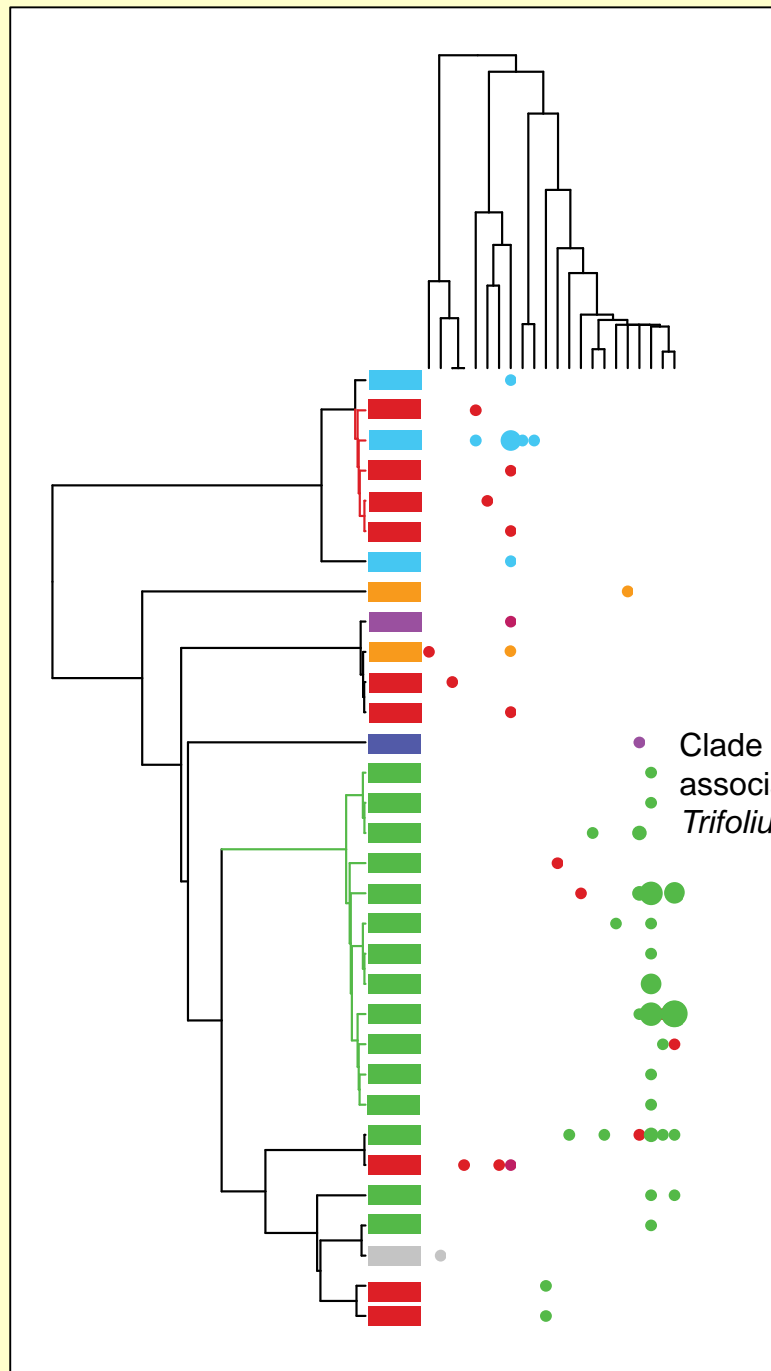
Hamiltonella

- Cytisus scoparius*
- Lathyrus pratensis*
- Lotus corniculatus*
- Lotus pedunculatus*
- Medicago sativa*
- Medicago lupulina*
- Melilotus officinalis*
- Unknown
- Ononis* spp.
- Onobrychis viciifolia*
- Pisum sativum*
- Securigera varia*
- Trifolium* spp.
- Vicia cracca*

Lee Henry

Pea aphid

Regiella



Clade particularly associated with *Trifolium*

Lee Henry

Population structure

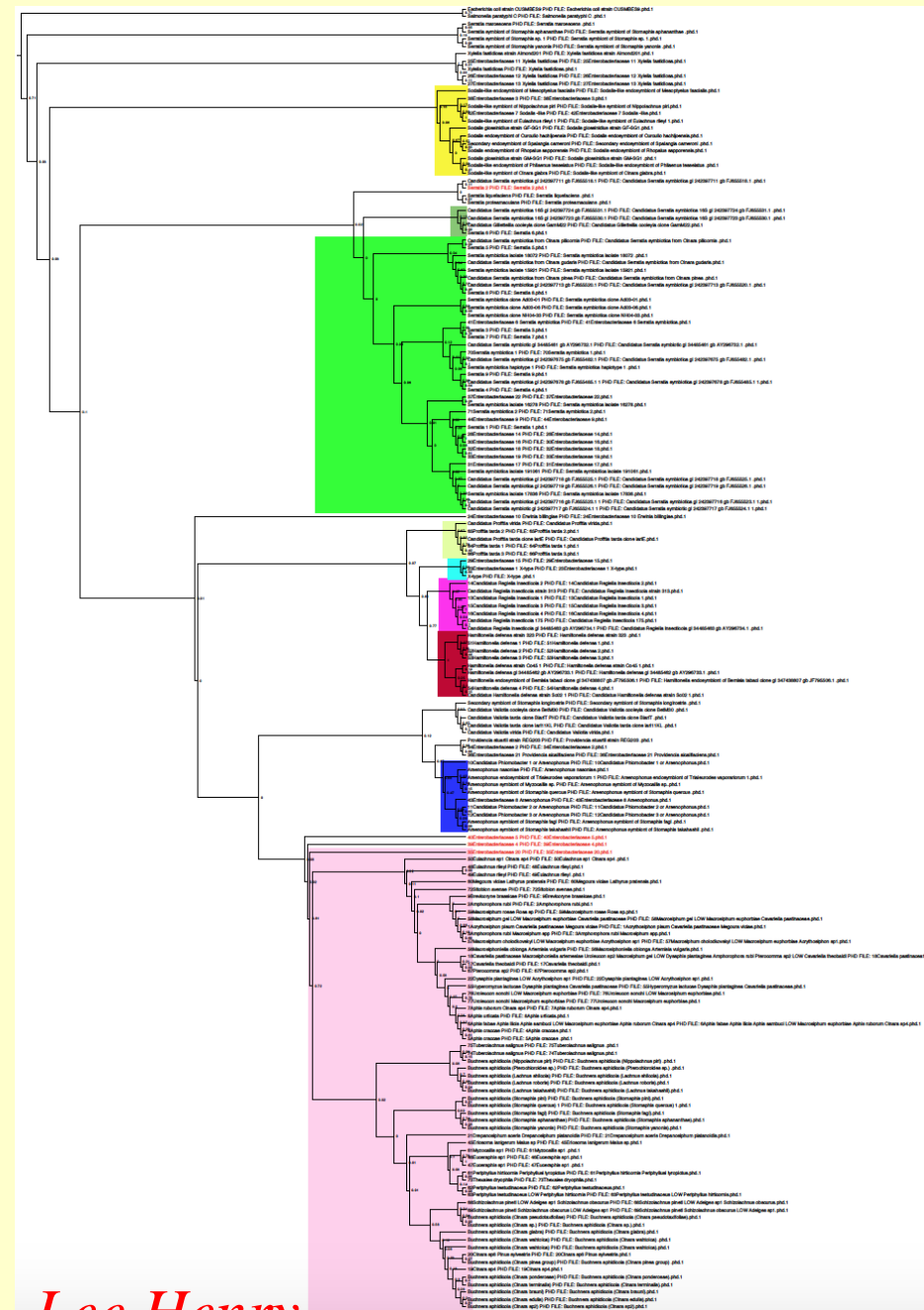
- Ancestral state reconstruction
 - Colonisation of *Lotus/Ononis* more likely with *Hamiltonella*
 - *Trifolium* with *Regiella* (one clade)
 - X-type acquisition more likely if already have *Hamiltonella*
- Major clade ages 0.1 - 0.5 Myr
 - Older than pea aphid host races

[illegible]

Lee Henry

NG Sequencing

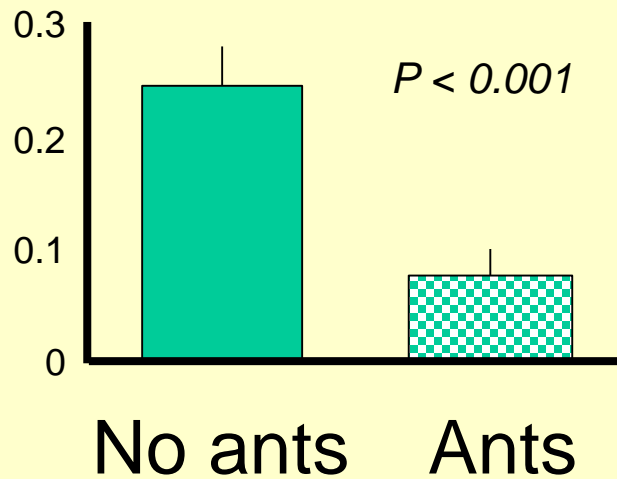
- Pea aphid primers good
- Few new candidate endosymbionts
- Microbiome correlated with relatedness & ecology



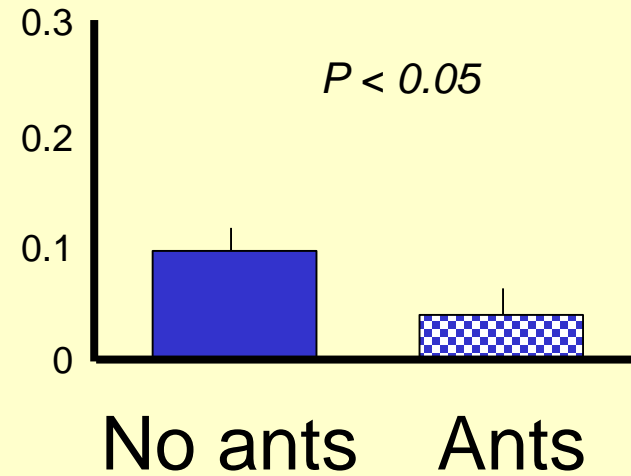
Lee Henry

Probability infected

Hamiltonella



Regiella



Lee Henry

Conclusions

- We didn't know as much about aphids as we thought!
 - And possibly many other eukaryote systems
- Secondary symbionts provide a reservoir of adaptations that can be sampled by aphids
 - A horizontal gene pool
 - Parallels with plasmids and bacteria
- Alternative defence systems

Barcodes 1

- Aphid natural enemy community structure
 - Bulk of this work done before barcodes
 - Would it have affected food web metrics?
 - Experiments that didn't work
- Future
 - Robotic, cheap high-throughput barcoding

Barcodes 2

- Pea aphid-symbiont community structure
 - Below barcode resolution; multilocus sequence typing (MLST) required
- Aphid-symbiont community structure
 - With aphids in UK we could have done it without barcodes but would have been **much** more difficult

An old hobby horse

- Barcoding [etc.] will render obsolete many taxonomy craft skills
- But a barcode bin code or even a name of limited use
- Taxonomy needs to reinvent as the science of biodiversity informatics

Challenges for taxonomy

The discipline will have to reinvent itself if it is to survive and flourish.

H. Charles J. Godfray

Taxonomy, the classification of living things, has its origins in ancient Greece and in its modern form dates back nearly 250 years, to when Linnaeus introduced the binomial classification still used today. Linnaeus, of course, hugely underestimated the number of plants and animals on Earth. As subsequent workers began to describe more and more species, often in ignorance of each others' work, the resulting confusion and chaos threatened to destroy the whole enterprise while still in its infancy. In today's jargon, we might call this the first bioinformatics crisis. Using the tools then available, nineteenth-century taxonomists solved this crisis in a brilliant way that has served the subject well since then. They invented a complex set of rules that determine how a species should be named and associated with a type specimen; how generic and higher taxonomic categories should be handled; and how conflicts over the application of names should be resolved. All these rules revolved around publications in books and scientific journals, and their descendants form the current codes of zoological and biological nomenclature.

But today much of taxonomy is perceived

One reason is that taxonomists lack clearly achievable goals that are both realistic and relevant. Of course it would be great to describe every species of organism on Earth, but we are still monumentally uncertain as to how many species there are (probably somewhere between 4 million and 10 million); this goal is just not realistic at present. There are various projects aimed at listing, for example, all the valid described species of animal in Europe, or butterflies on Earth (see Box 1, overleaf). These aims are eminently achievable and very worthwhile, but the results are like raw, unannotated DNA sequences: unexciting and of relatively little value in themselves to non-specialists. Taxonomists need to agree on deliverable projects that will receive wide support across the biological and environmental sciences, and attract public interest.

A second problem is part of the legacy of more than 200 years of systematics. Many taxonomists spend most of their career trying to interpret the work of nineteenth-century systematicists: deconstructing their often inadequate published descriptions, or scouring the world's museums for type material that is often in very poor condition. A depressing fraction of published systematic research concerns these issues. In some taxonomic groups the past acts as a

commentary



From paper to screen: is it time for taxonomy to break with tradition and unify on the Internet?

being a scientist at this particular time in history is the vast amount of information that is available, essentially free, via one's desktop computer. I once downloaded the

MUSEUM LONDON

Thanks to the
Barcode
Conference

