

Arabidopsis thaliana and Its Pathogens – T(h)ales From the Wild

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<http://weigelworld.org>



@PlantEvolution



Disclaimers



weigelworld

plant biology, developmental genetics
and evolutionary genomics.



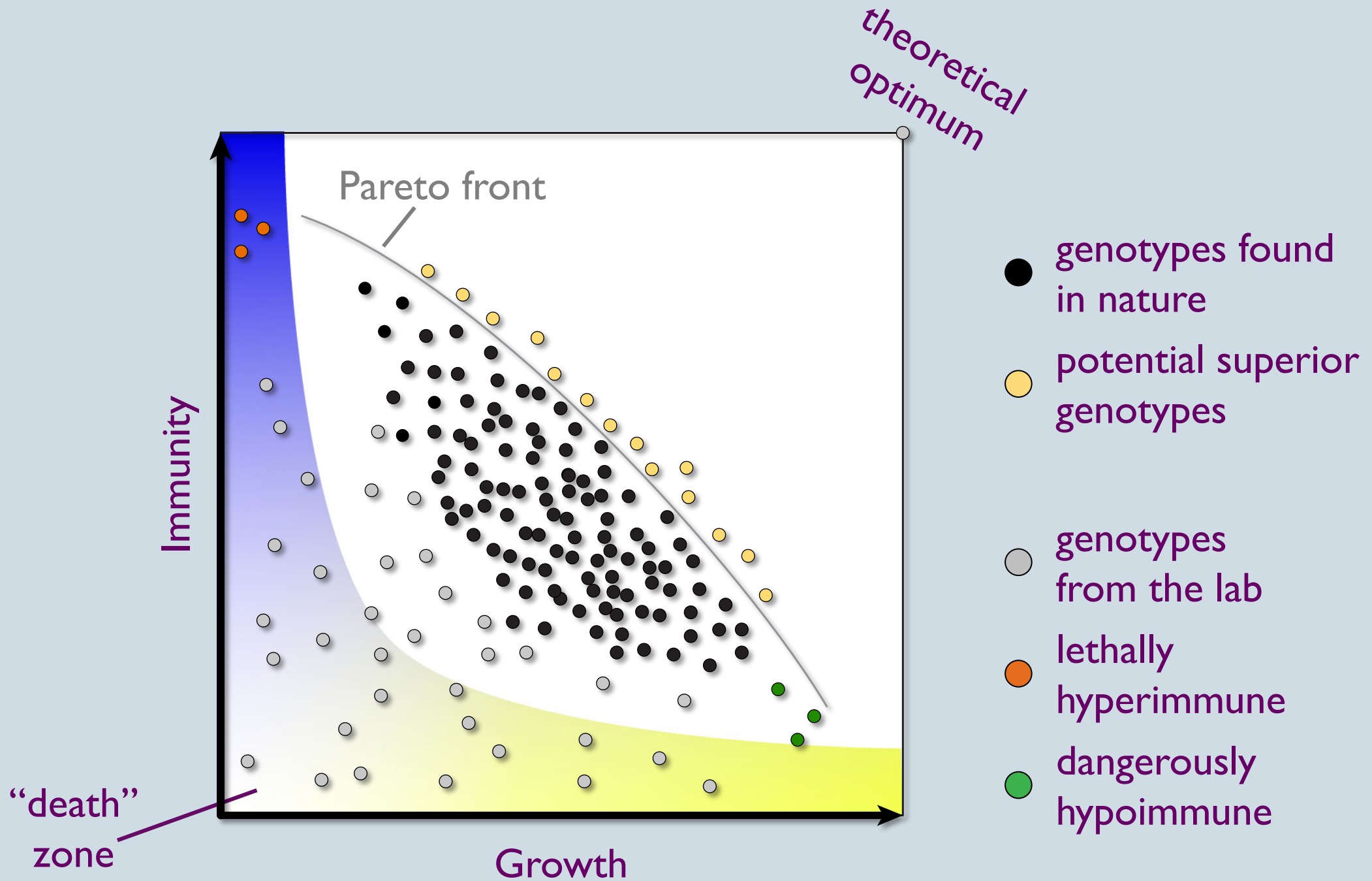
Talia Karasov • Lei Li
Derek Lundberg • Manuela Neumann
Julian Regalado • Michael Thelen
Wangsheng Zhu

Roosa Laitinen (now Golm)
Marco Todesco (now UBC)
Maricris Zaidem (now NYU)

Eric Kemen (Univ. Tübingen)
Juliana Almario (Univ. Tübingen)



Complex Trade-offs Between Immunity & Growth



Complex Trade-offs Between Immunity & Growth



Weigel Lab (immigrated 19... · 22h ▾

Leaving today for two exciting days discussing the intersection of plant development & immunity
#WDMSP When development meets stress: Understanding developmental reprogramming upon pathogenesis in plants

@I_Rubio_Somoza @CRAGENOMICA
bdebate.org/en/forum/when-...

#WDMSP

**When development meets stress:
Understanding developmental
reprogram**
in plants

September 3rd
CosmoCaixa Barc

Scientific lead

Ignacio Rubio Somoza
Nuria Sanchez Coll
Paloma Mas
Centre for Research in



Ignacio Rubio Somoza

@I_Rubio_Somoza ▾

Replying to @SpicyBotrytis @PlantEvolution
and @CRAGENOMICA

yup!...that is something that indeed
needs to be revisited

[9/2/18, 6:22 PM](#)



Daniel J Kliebenstein

@SpicyBotrytis ▾

Replying to @PlantEvolution @I_Rubio_Somoza
and @CRAGENOMICA

Hopefully you will debate the
foundation of the argument, is it
really a trade-off in the context
most people think? Not much
evidence for an energy trade off at
all.

[9/2/18, 6:13 PM](#)



Daniel J Kliebenstein

@SpicyBotrytis ▾

Replying to @I_Rubio_Somoza @PlantEvolution
and @CRAGENOMICA

I also love how growth is a key
defense in ecology as evasion or
over-compensation and defense is
key to development, trichomes and
nectaries, etc. maybe the
dichotomy is in our science and not
in the plant.

[9/2/18, 6:41 PM](#)

Microbes in and on *A. thaliana*:

- Who is there?
- How much is there?

Quantitative microbiome profiling links gut community variation to microbial load

Doris Vandeputte^{1,2,3*}, Gunter Kathagen^{1,2*}, Kevin D'hoel^{1,2,3*}, Sara Vieira-Silva^{1,2*}, Mireia Valles-Colomer^{1,2}, João Sabino⁴, Jun Wang^{1,2}, Raul Y. Tito^{1,2,3}, Lindsey De Commer¹, Youssef Darzi^{1,2}, Séverine Vermeire⁴, Gwen Falony^{1,2§} & Jeroen Raes^{1,2§}

Current sequencing-based analyses of faecal microbiota quantify microbial taxa and metabolic pathways as fractions of the sample sequence library generated by each analysis^{1,2}. Although these relative approaches permit detection of disease-associated microbiome variation, they are limited in their ability to reveal the interplay between microbiota and host health^{3,4}. Comparative analyses of relative microbiome data cannot provide information

Supplementary Table 3). Association analyses confirmed several previously reported FGFP genus–metadata associations, including the covariation of stool consistency with *Akkermansia* and *Methanobrevibacter*^{15,16} (Supplementary Table 4).

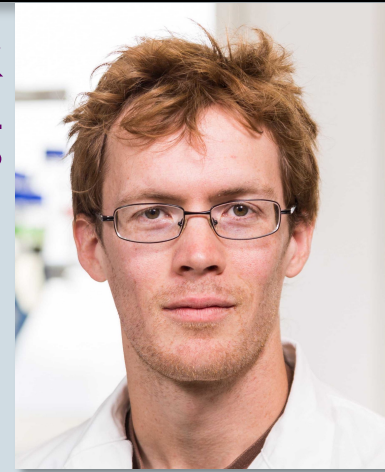
Next, we determined total microbial cell counts in faecal samples using flow cytometry. Because microbiome analyses often begin with frozen material and freeze–thaw cycles can affect cell integrity¹⁷

Foundational Data: Microbe Population in the Wild

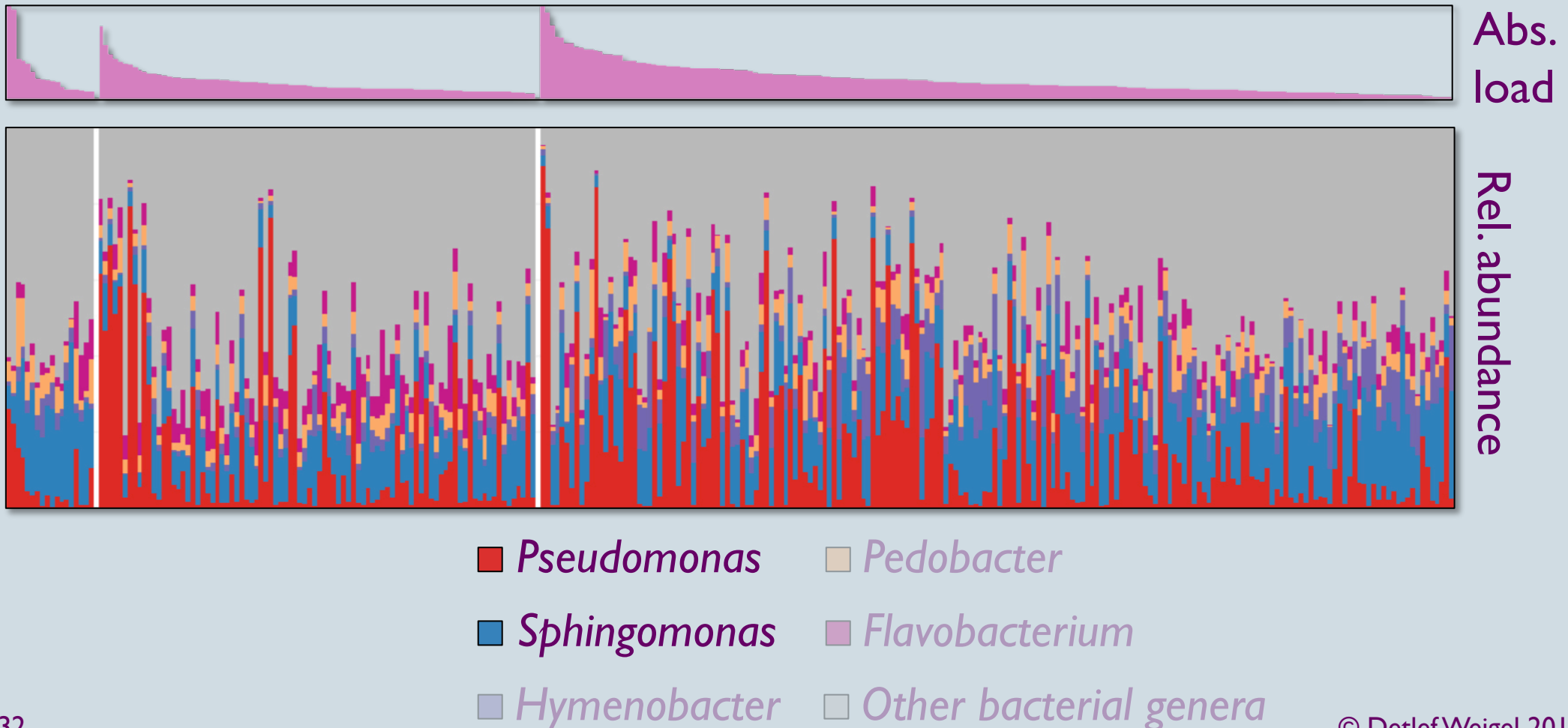


Julian
Regalado

Derek
Lundberg



Whole genome shotgun sequencing
of washed rosettes from wild *A. thaliana* plants

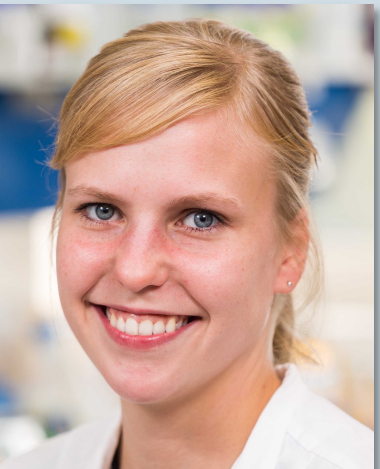


What Biomass Can *Pseudomonas* Achieve in the Lab?

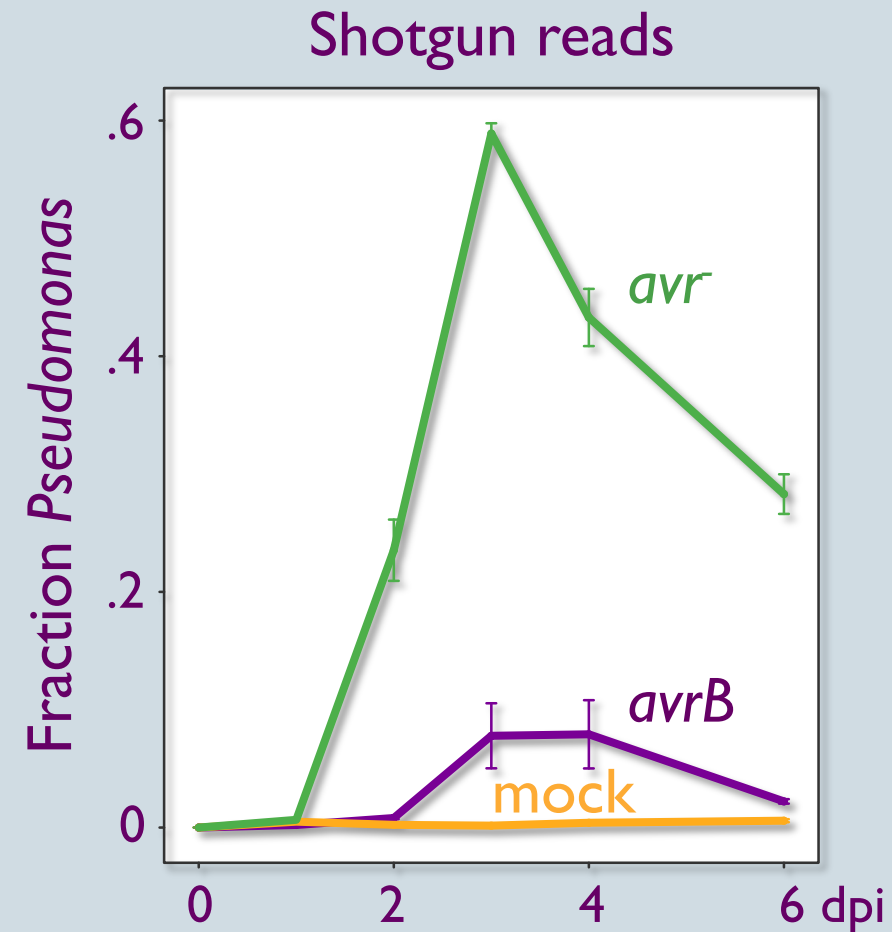
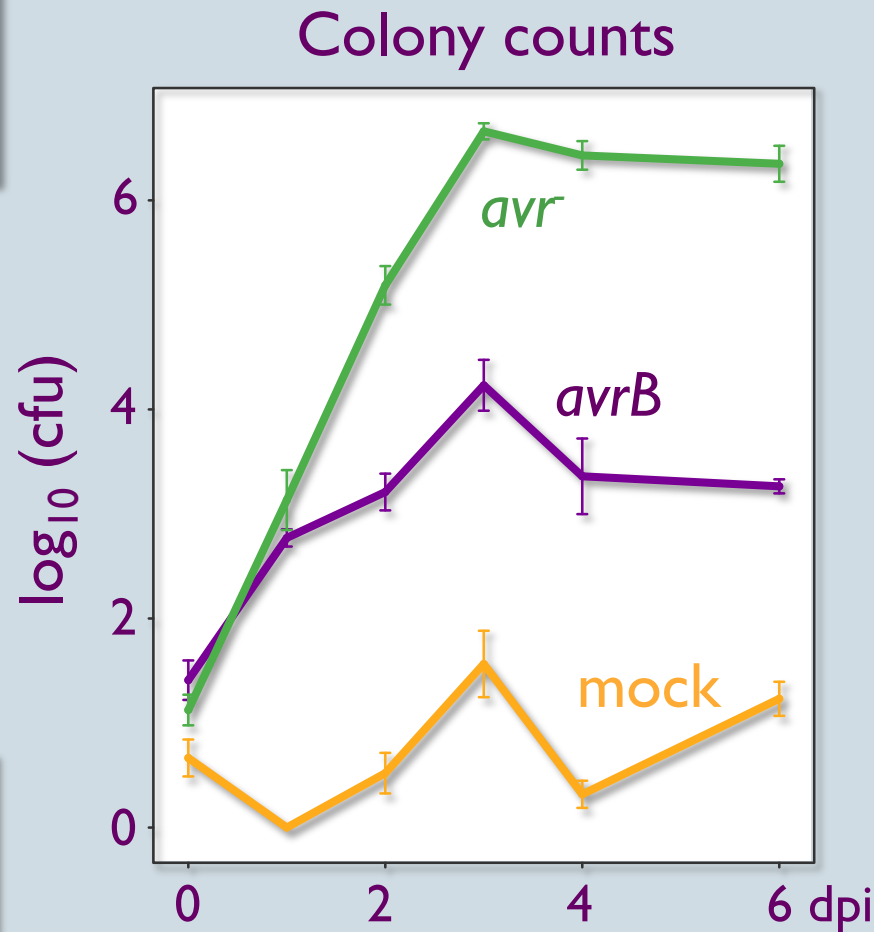


Talia
Karasov

Manuela
Neumann



Laboratory infection with *Pst* DC3000

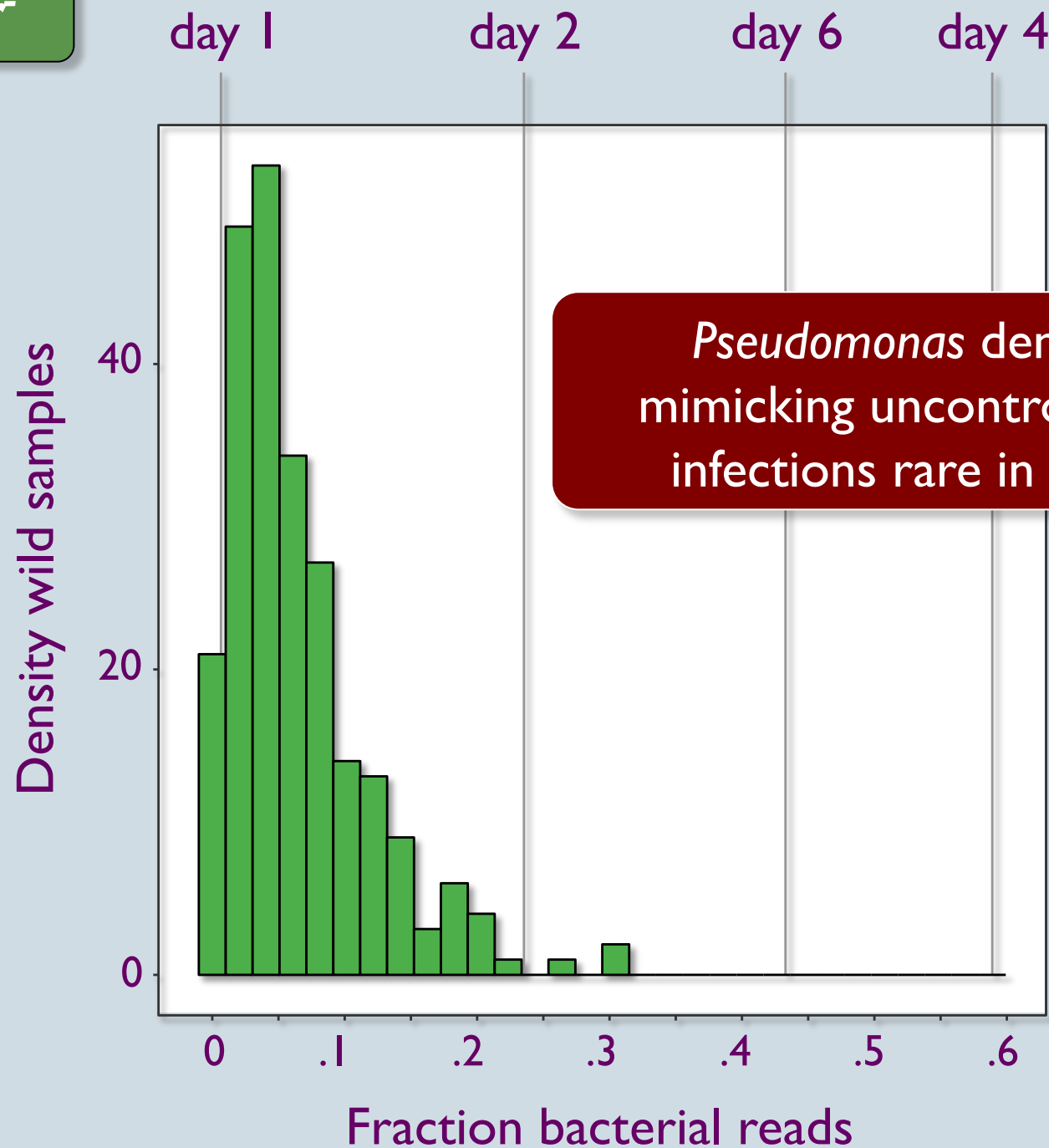


10% *Pseudomonas* reads = 500 bacteria/mm² leaf

How Does It Compare to Microbial Load in the Wild?



Lab infection *avr*

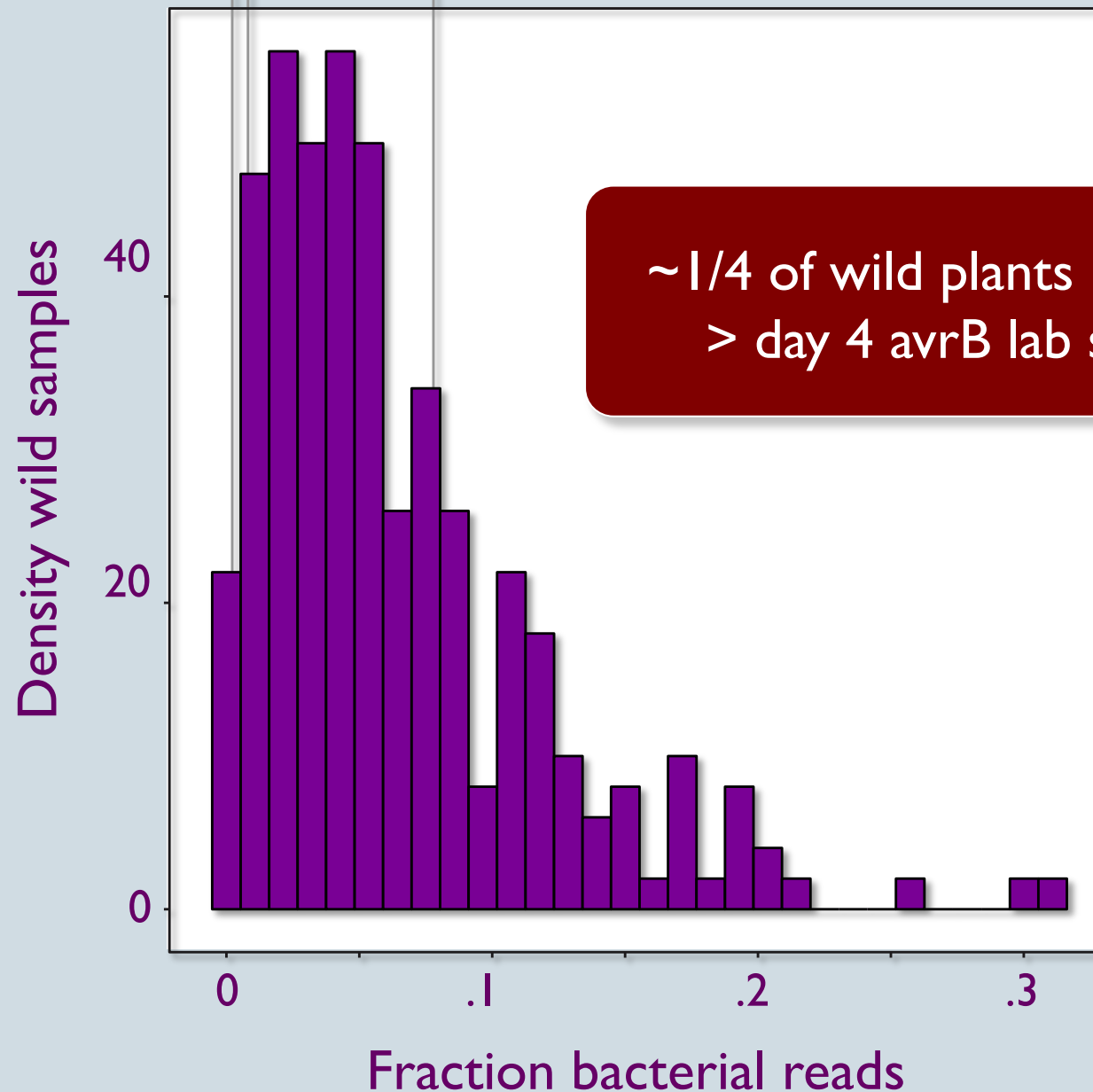


How Does It Compare to Microbial Load in the Wild?



Lab infection *avrB*

day 1 day 2 day 4



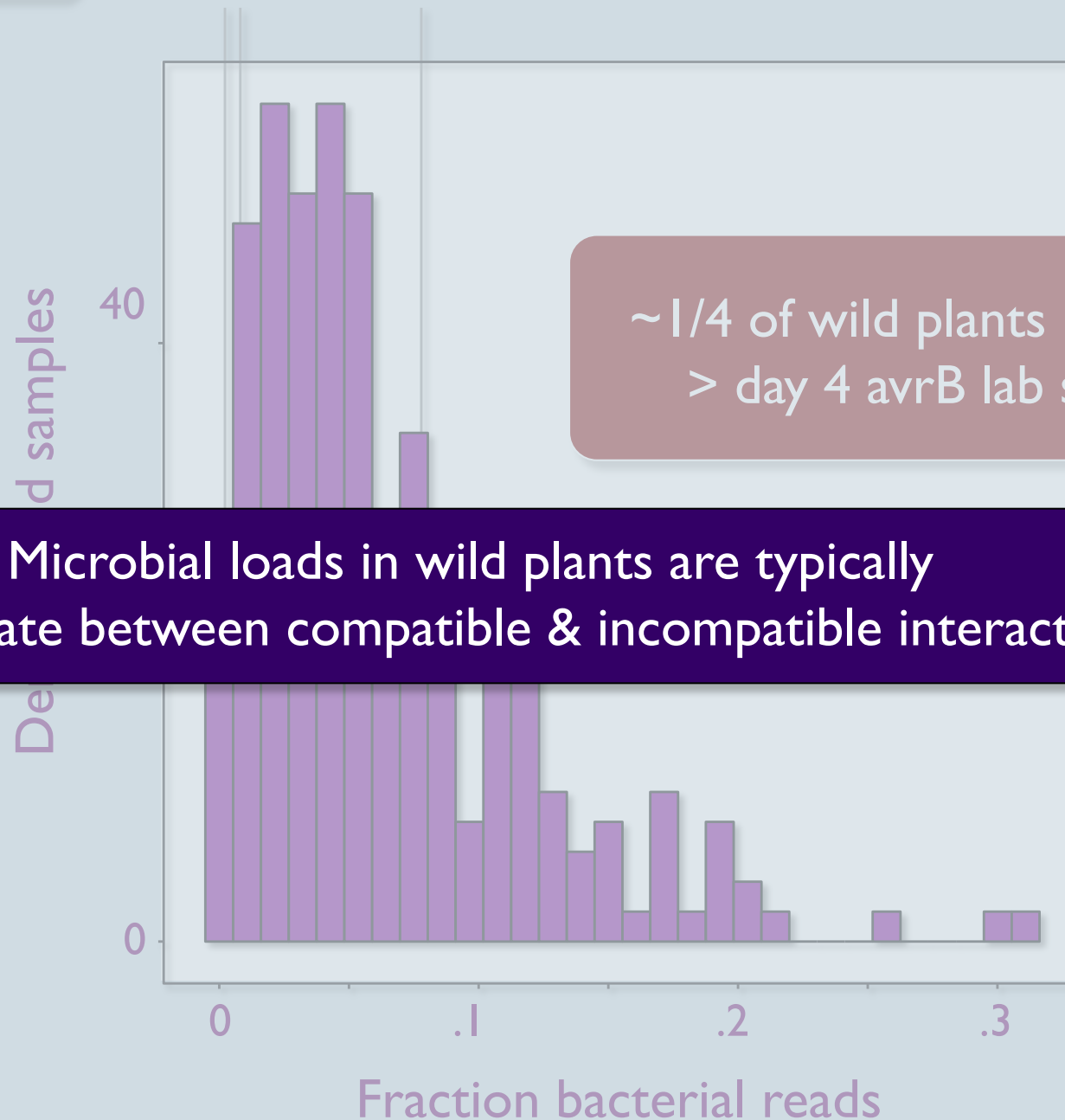
~ 1/4 of wild plants have loads
> day 4 *avrB* lab samples

How Does It Compare to Microbial Load in the Wild?



Lab infection *avrB*

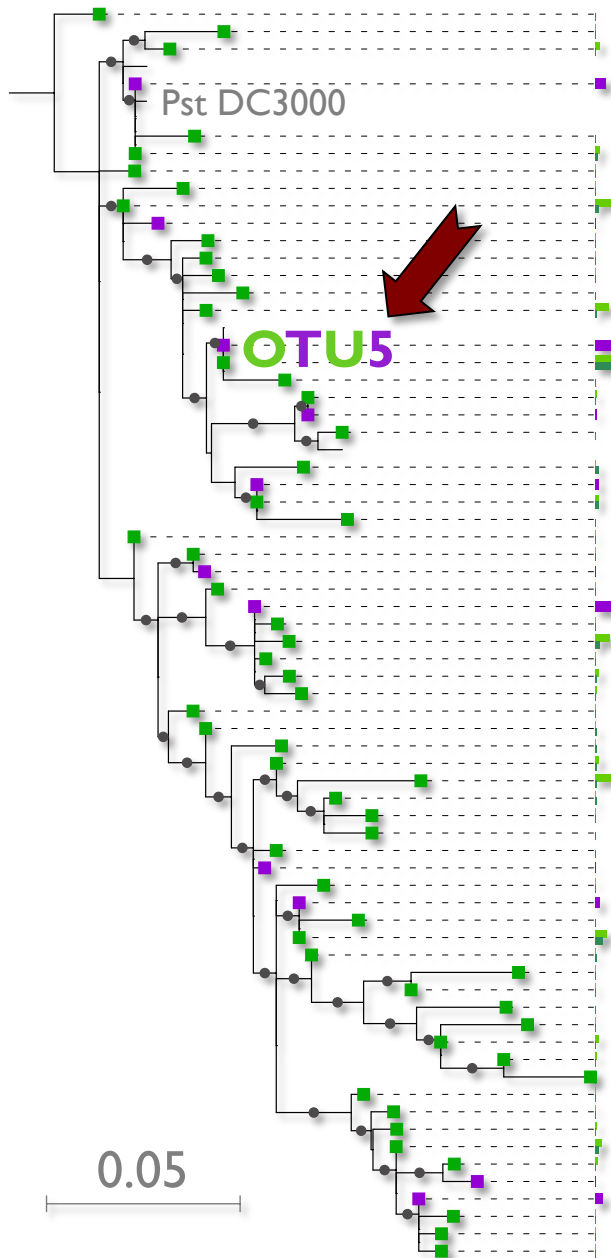
day 1 day 2 day 4



~ 1/4 of wild plants have loads
> day 4 *avrB* lab samples

Microbial loads in wild plants are typically
intermediate between compatible & incompatible interactions

Is This Due to *Pseudomonas* Diversity in the Wild?



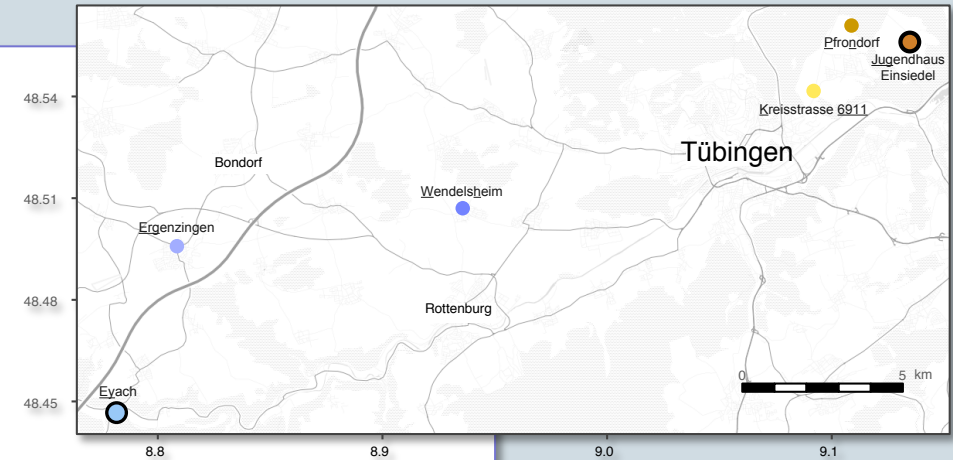
Genome survey

■ isolates (counts)

16S survey

■ endophytic compartment

■ epiphytic compartment



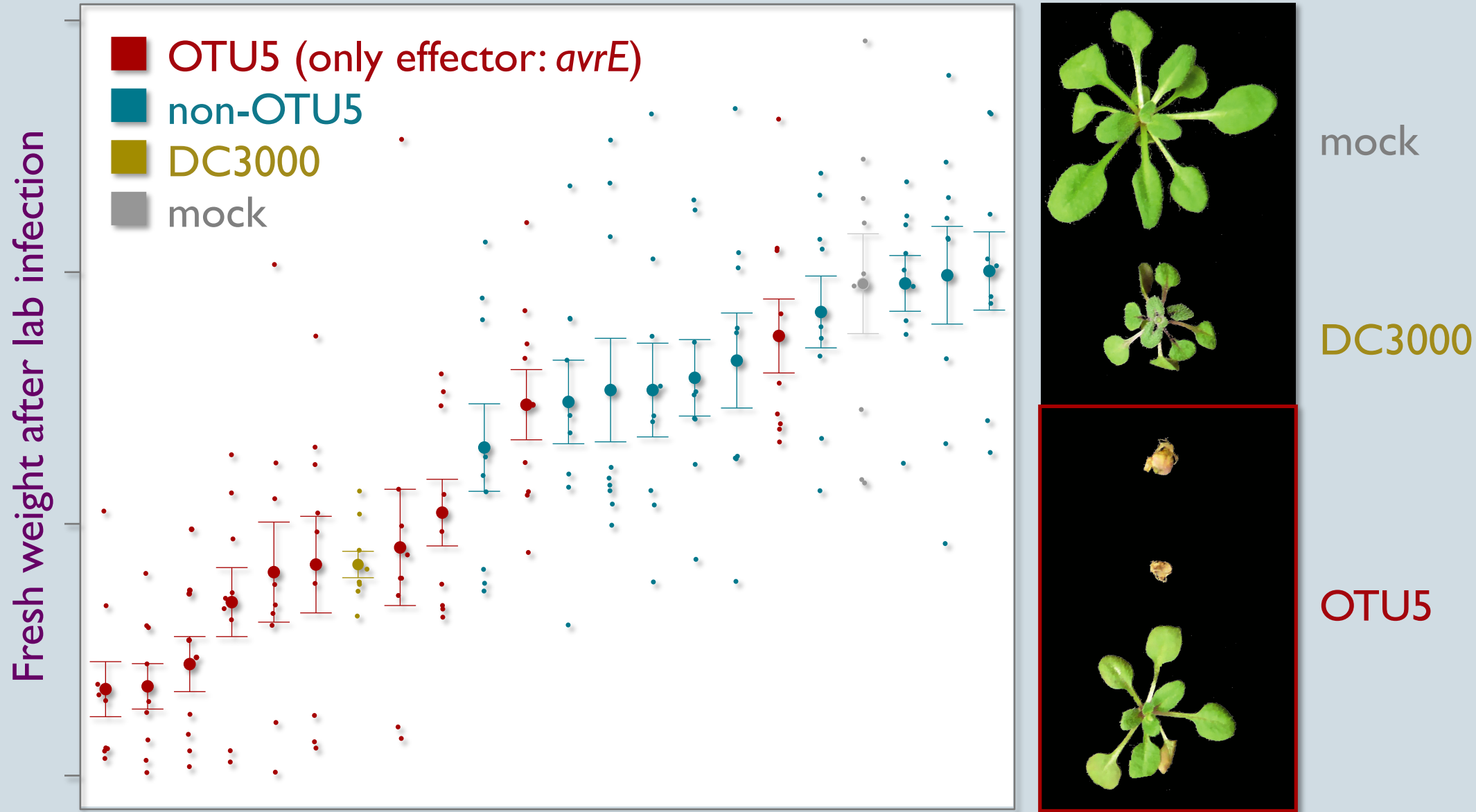
With
Kemen
lab:

Juliana
Almarino

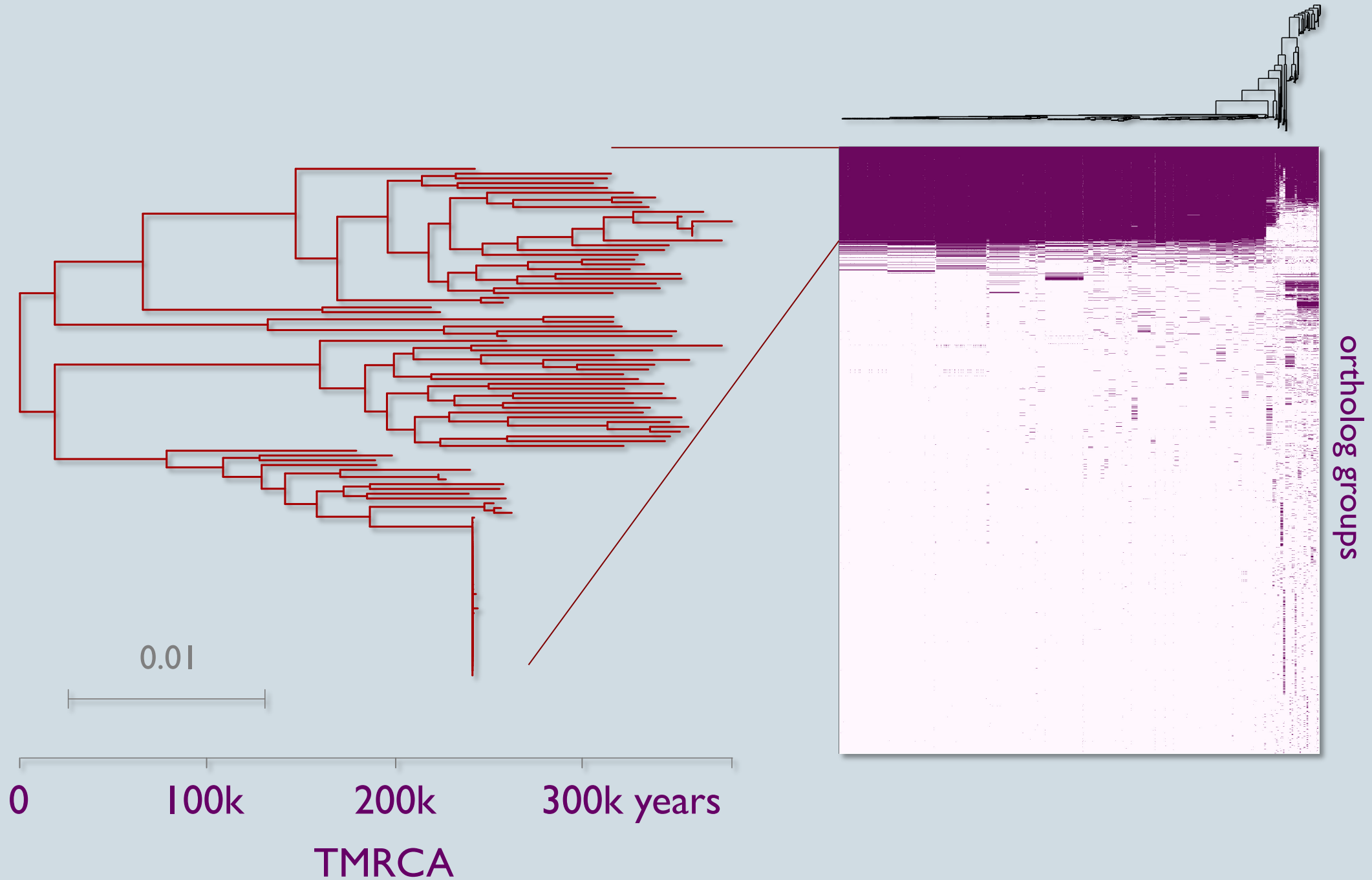
PMID: 30001519

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Locally Common *Pseudomonas* OTU5 Is Often Pathogenic



Pseudomonas OTU5 Has Been Around For a Long Time

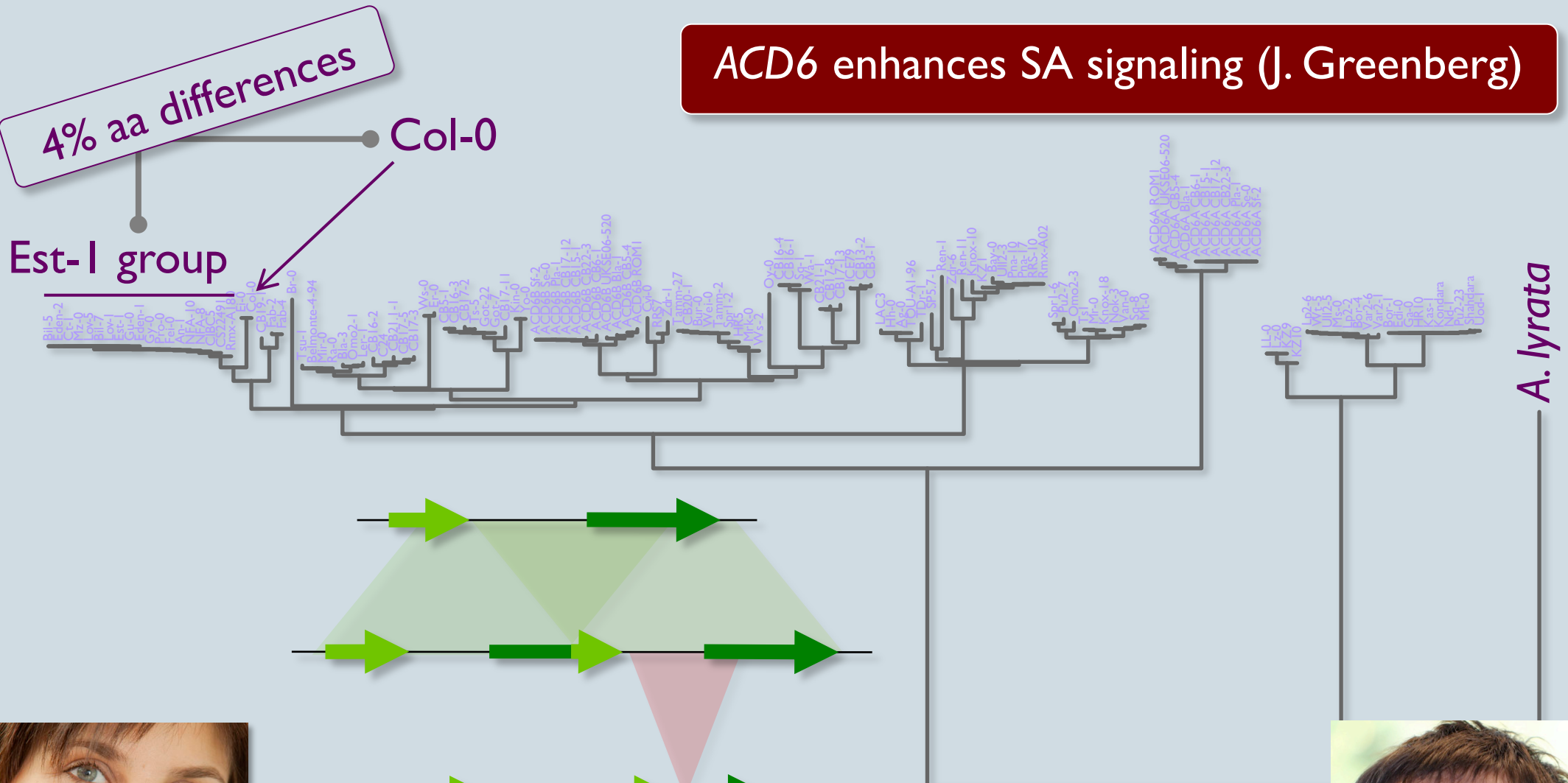


**Does *Arabidopsis thaliana* have similarly old
broad-spectrum resistance genes?**

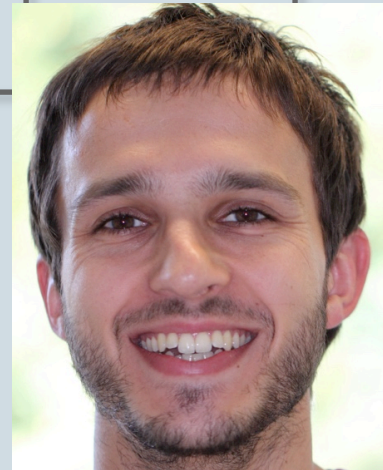
NLR-like Sequence Diversity at ACD6



ACD6 enhances SA signaling (J. Greenberg)



Roosa
Laitinen
(now
MPI Golm)



Marco
Todesco
(now
UBC)

Divergent ACD6 Alleles Are Common and Co-occur



Field in NE Spain (Costa Brava)



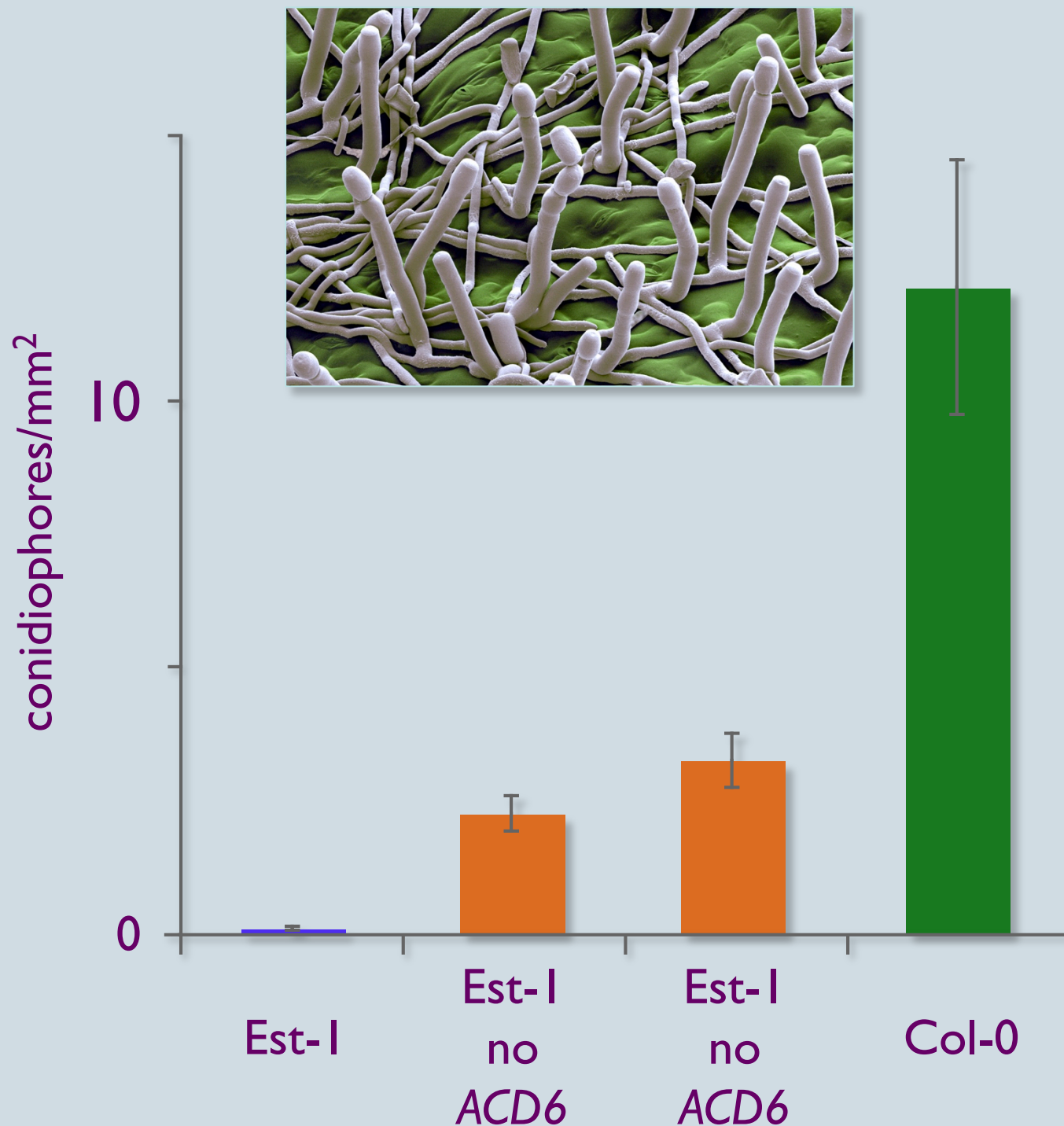
- CB21.1-1 | Mir-0-like class III
- CBI7-3 |
- Se-0
- Bla-1
- CBI7-2 | Mir-0-like class IV
- CBI3-2 |
- Ren-1
- Sq-8
- CBI6-4
- Est-1
- CBI9-1
- KZI0
- other hybrids
- Mir-0 class III x Se-0 hybrids



PMID: 25010663

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ACD6-Est Allele Increases Resistance to *G. orontii*

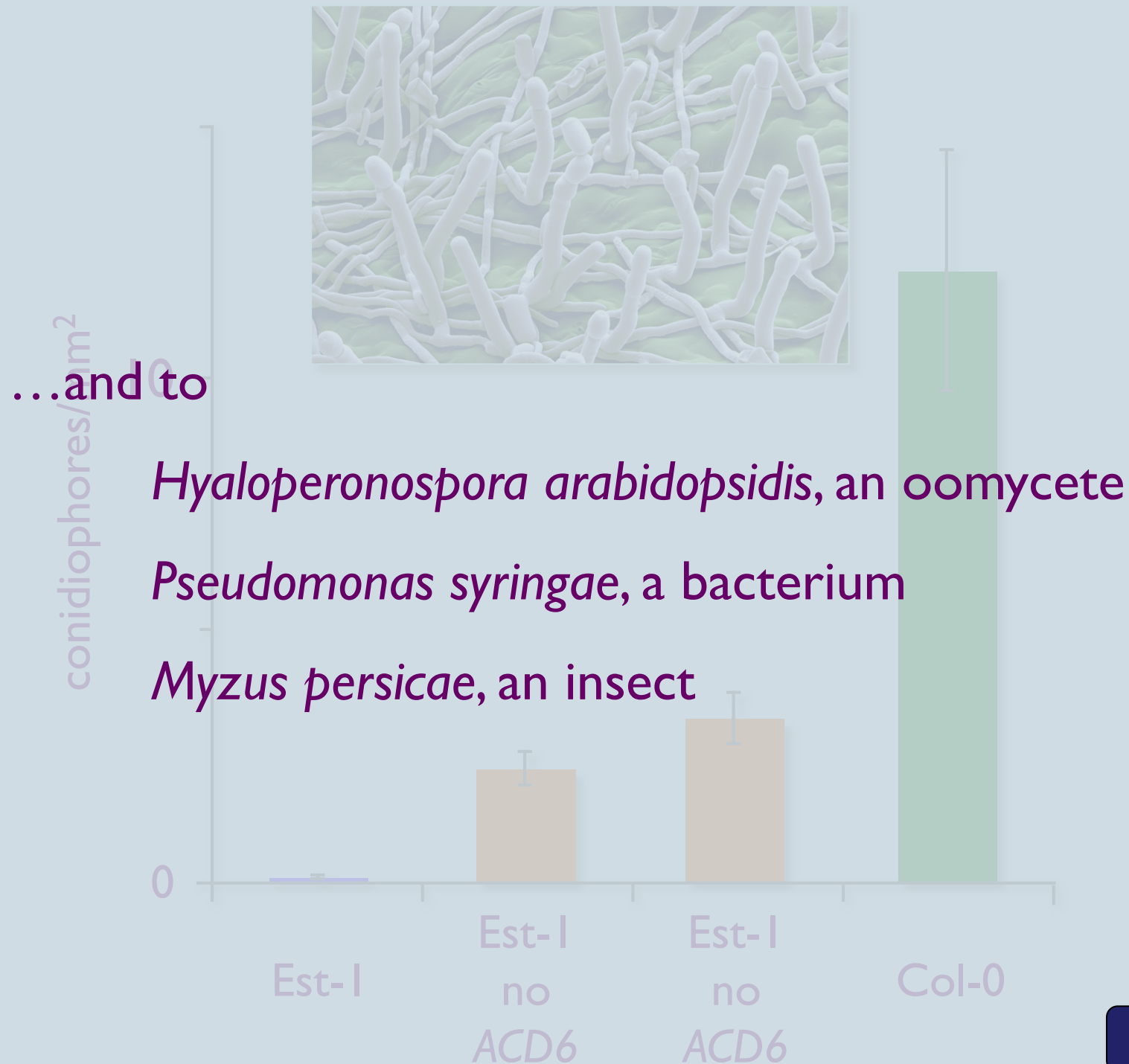


With
Bergelson,
Chory,
Dangl,
Lipka &
Traw labs

PMID: 20520716

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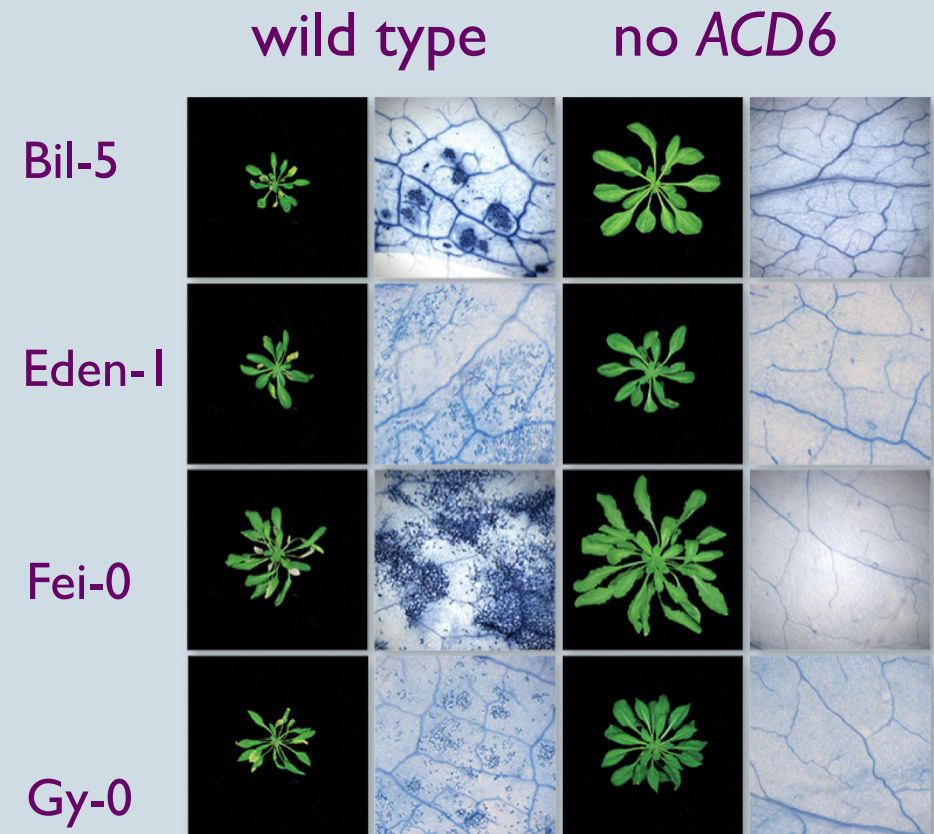
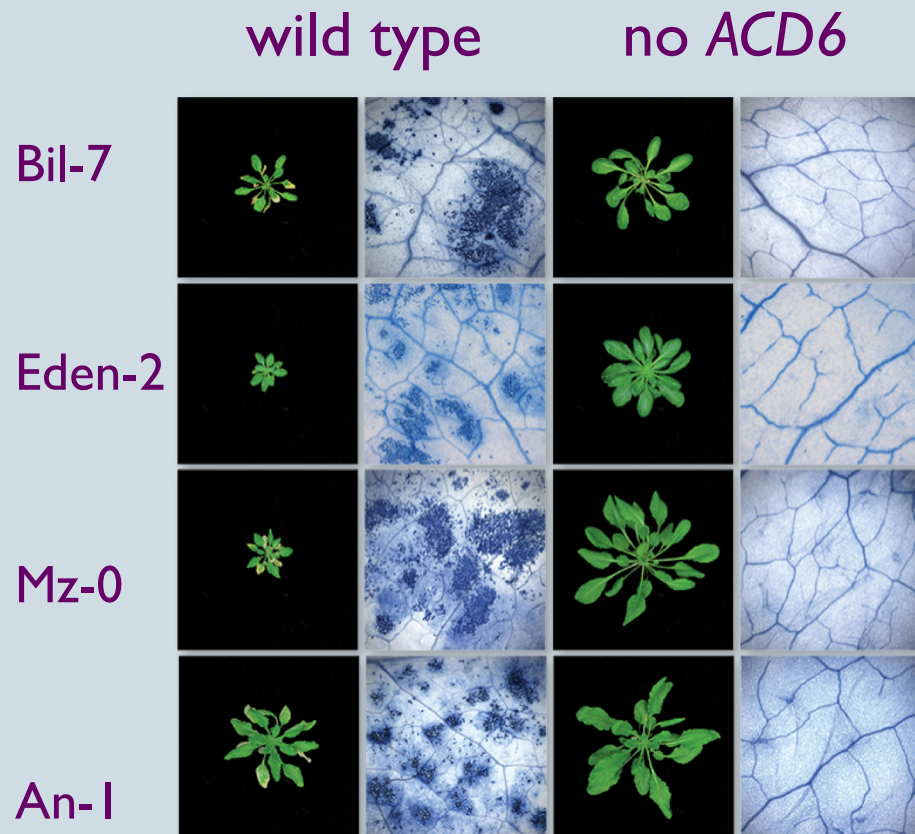
ACD6-Est Allele Increases Resistance to *G. orontii*



With
Bergelson,
Chory,
Dangl,
Lipka &
Traw labs

PMID: 20520716

ACD6-Est Allele Common Cause for Small Size in *A. thaliana*



ACD6-Est Allele Common Cause for Small Size in *A. thaliana*

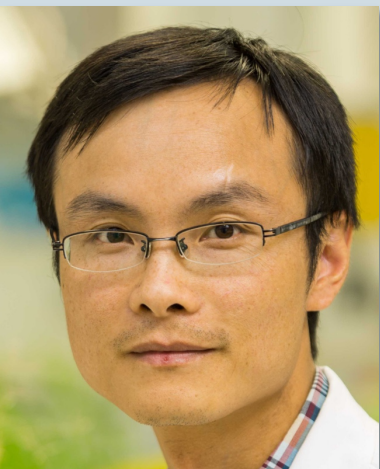


Things Are More Complicated

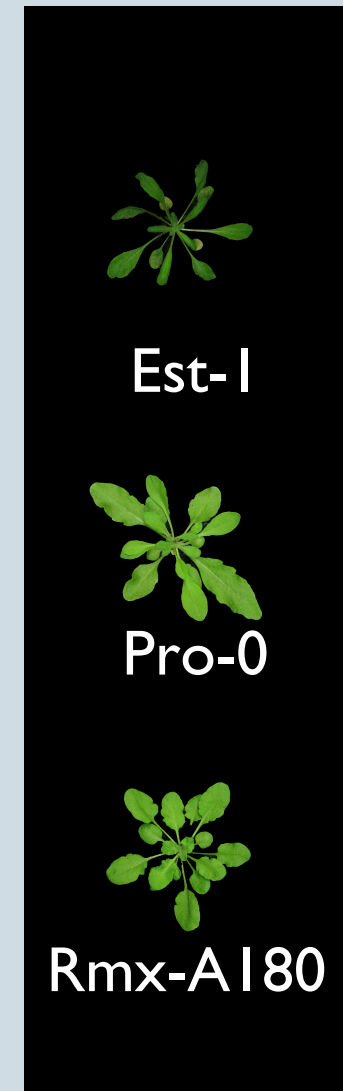
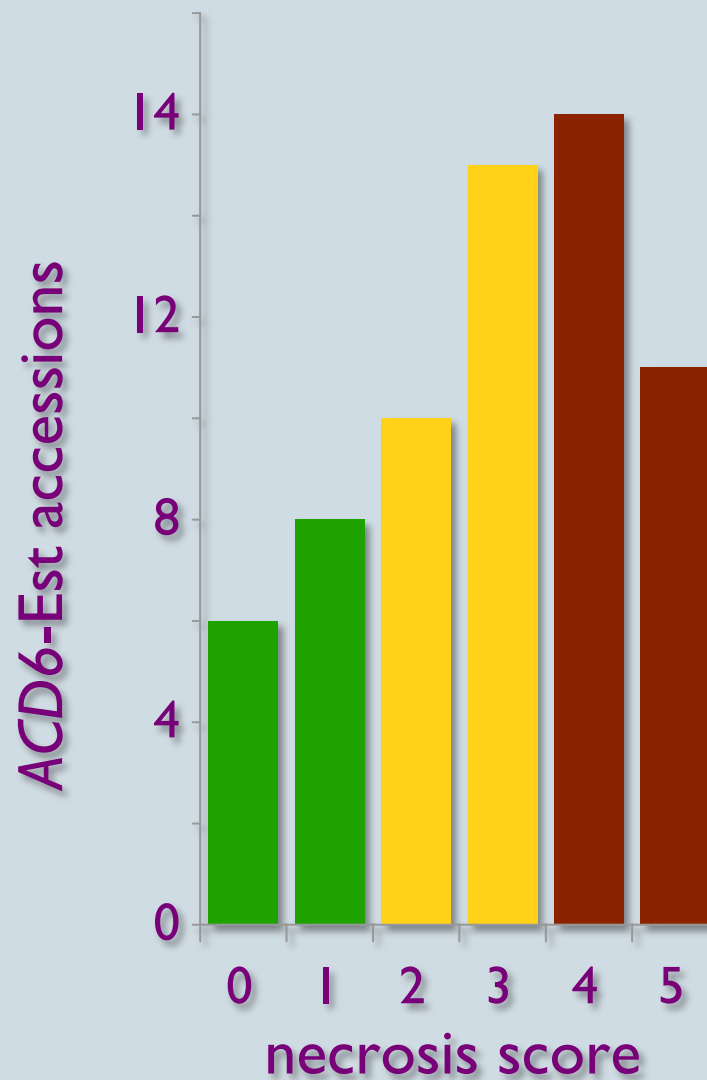


Maricris
Zaidem
(now at
NYU)

Wangsheng
Zhu



ACD6-Est effects depend on genetic background

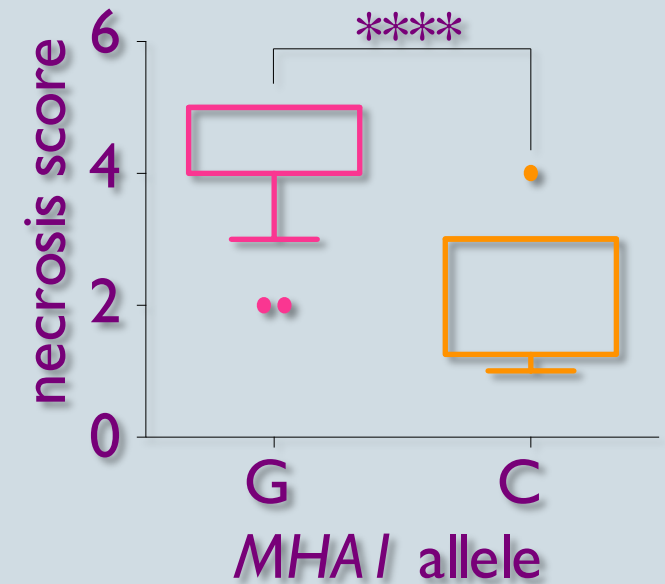
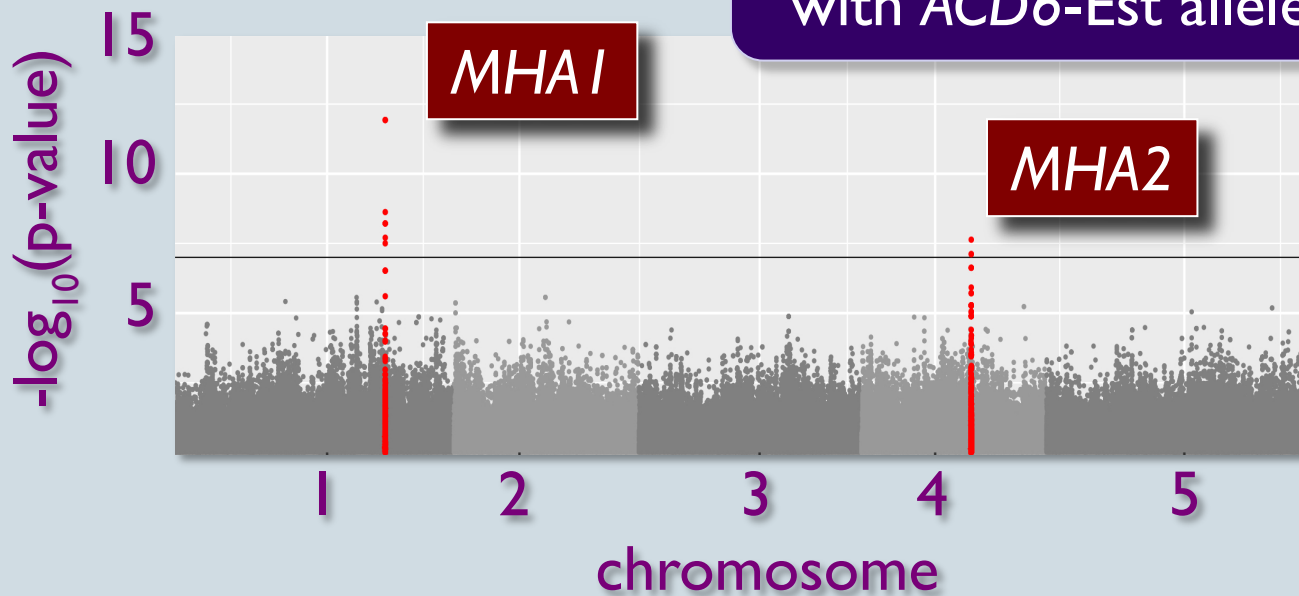


Some ACD6-Est Suppressors Are Common



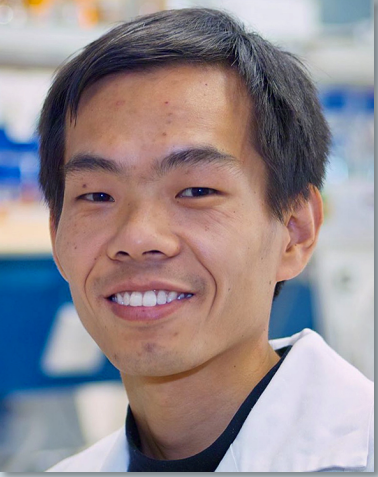
MODIFIER OF HYPERACTIVE ACD6 (MHA)

with only 80 strains
with ACD6-Est allele!



MHA1	Ty-0	MASEAPSWADQWGTGGIGEMPEE	S	TKSKKDAGGKNSGQTKS	---	AKIVDFVSFKWMKNLVHKKK	-	KDSD	-	S
	Est-I	MASEAPSWADQWGTGGIGEMPEE	D	TKSKKDAGGKNSGQTKS	---	AKIVDFVSFKWMKNLVHKKK	-	KDSD	-	S
	Aly	MASEAPSWADQWGTGGIGEMPEE	E	NTKSKKDASGKNSGQNK	---	AKIVDFISLKWMLVQKKK	-	KDSD	-	S
	Cru	MASEAPSWADQWGTGGIGEMAV	D	NTSKKDAGGKNSGQTKS	---	AKIVDLITFKWVKNLVHKKK	-	KDSD	-	S
	Bna	MTSEAPSWADQWGTGGIGEMPEE	D	NTKS---	AGGKKS	SGTTK	---	AKIIDFISFKWMKNLVHKKK	T	KDSN-S
	MAL	MASEAPSWADQWGTGGIGVMAA	E	ETD	GKKDVTGKKSGKTKAGINK	AKIVVFIGVNWMLVQKK	-	KDST	S	S

MHAI-Ty-0 Suppresses ACD6-Est Activity



Lei
Li

Ty-0

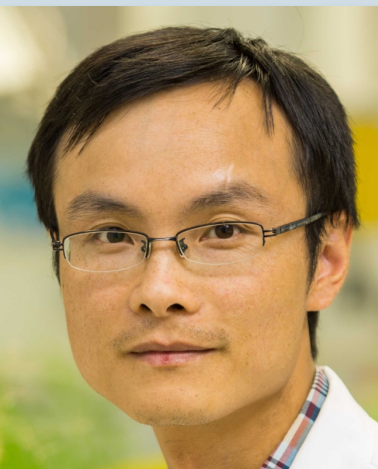


—

mhal-1

mhal-2

Wangsheng
Zhu



Est-1 *mhal*



—

gMHAI-Est-1

gMHAI-Ty-0

But MHA I Homolog MAL Activates ACD6



MHA

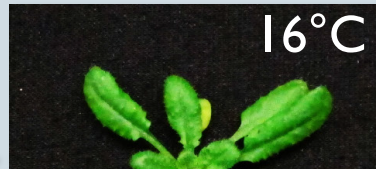
Michael
Thelen



MHA I-Ty-0

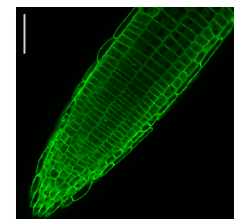


Col-0

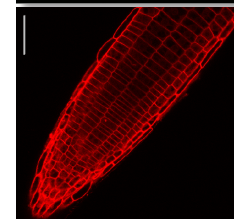


	α-GFP-IP					Input				
ACD6 ^{Col} -FLAG	+	+	+	+	+	+	+	+	+	+
MAL-GFP	+	-	-	-	-	+	-	-	-	+
MAL-N-GFP	-	+	-	-	-	-	+	-	-	-
MAL-C-GFP	-	-	+	-	-	-	-	+	-	-
MHA I ^{Col} -GFP	-	-	-	+	-	-	-	-	+	-
α-GFP										
α-Flag										

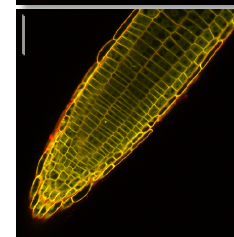
	α-GST			Input		
MBP-His	+	-	-	+	-	-
MHA I-MBP-His	-	+	-	-	+	-
MAL-MBP-His	-	-	+	-	-	+
ANK ^{Col} -GST	-	+	+	-	+	+
α-GST						
α-PolyHis						



MHA I-
GFP

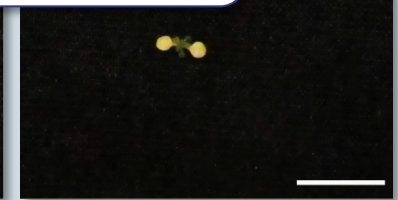


PI



Overlay

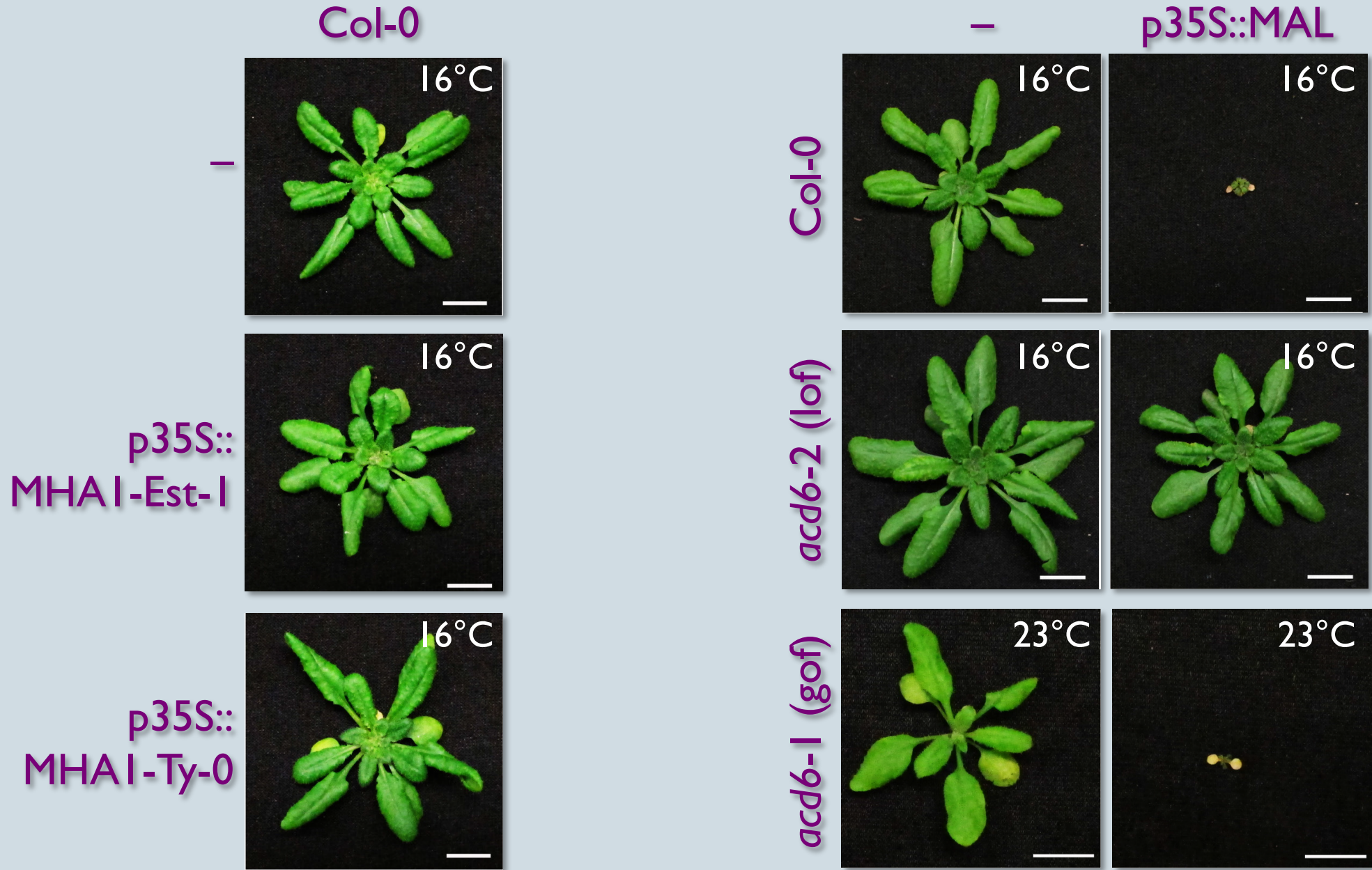
acd6-1



16°C

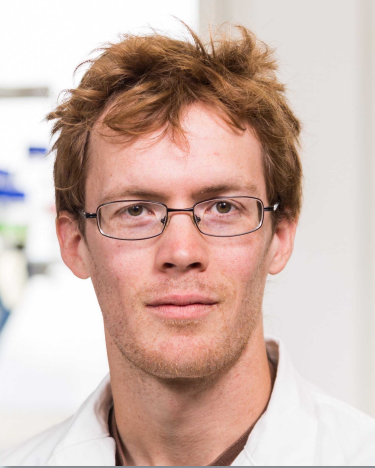
23°C

But MHA I Homolog MAL Activates ACD6



- Functionally very different alleles at *ACD6*
 - Divergent alleles are common
 - Also common variation at modifier loci
- Everything points to *ACD6* as an important immune regulator in natural populations

So What does ACD6-Est Do Outdoors?



Derek
Lundberg

- Greenhouse & field / same soil
- Field plants started 10/16 & 10/17
- Greenhouse plants started 02/17 & 02/18
- Imaged until bolting → harvest



green-
house



field

So What does *ACD6*-Est Do Outdoors?



greenhouse

field

HIF *ACD6*-Est

HIF *ACD6*-Col

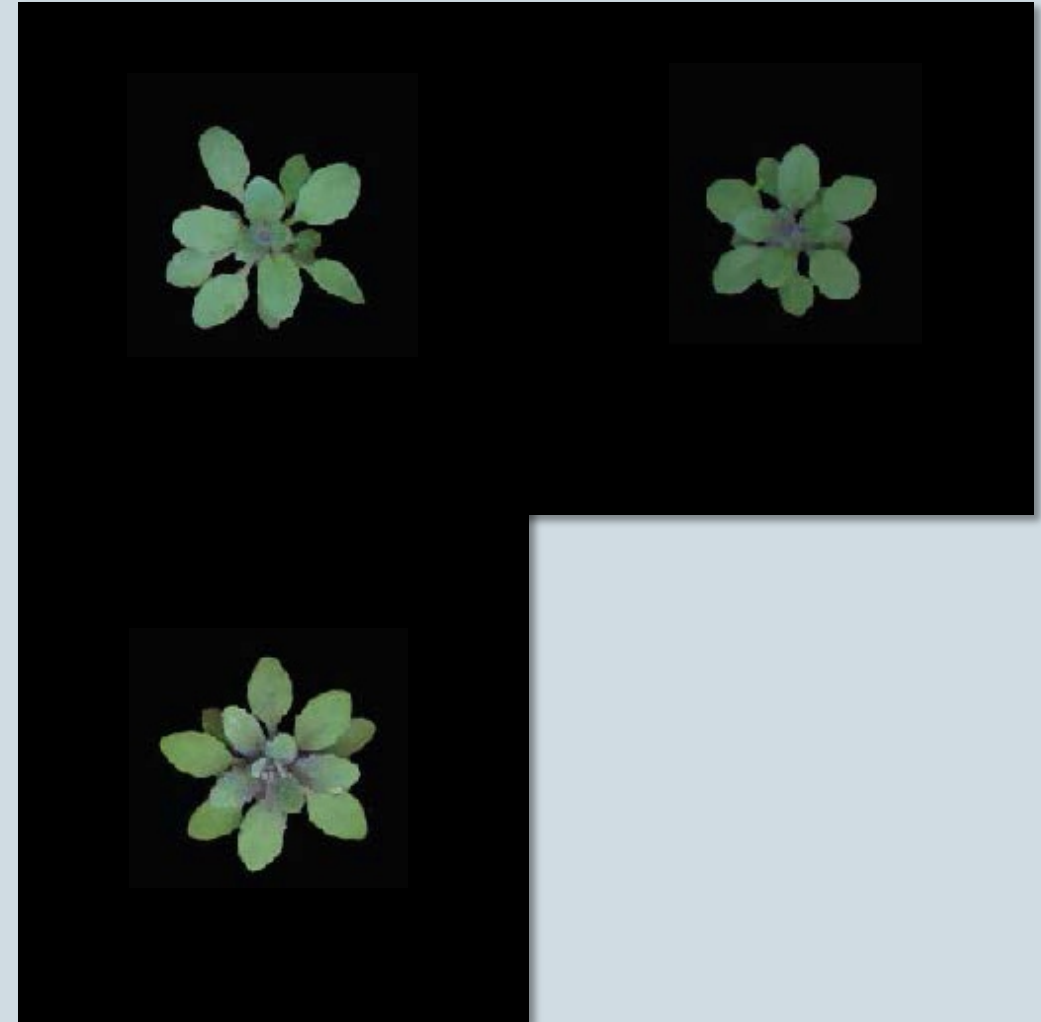
HIF *ACD6*-Est

HIF *ACD6*-Col



Est-1

Est-1 *acd6*



Est-1

So What does ACD6-Est Do Outdoors?



greenhouse

field

HIF ACD6-Est

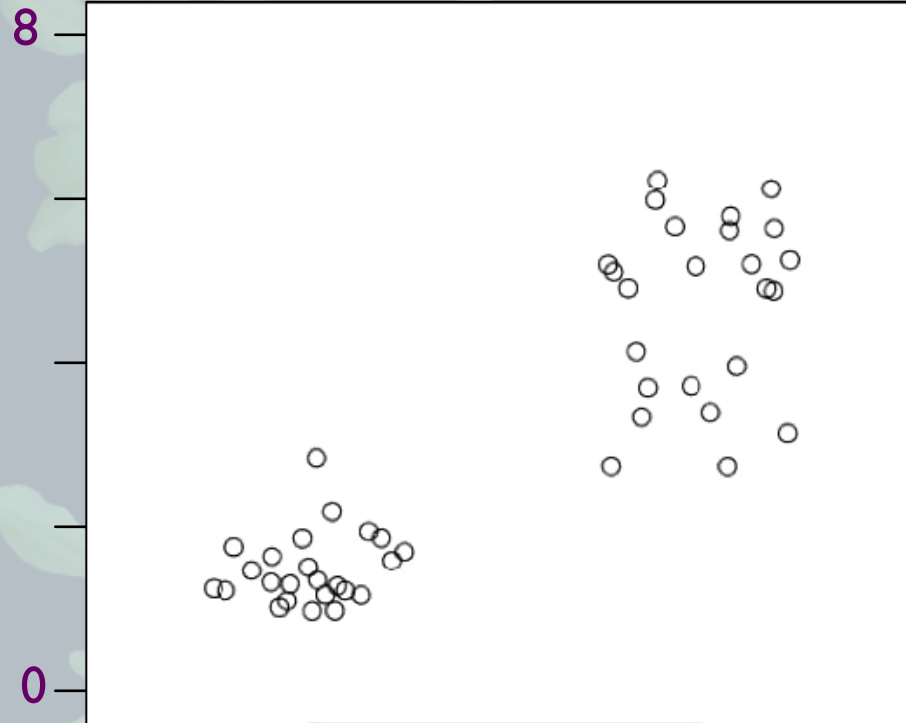
HIF ACD6-Col

HIF ACD6-Est

HIF ACD6-Col

Microbial load

% non-plant shotgun reads



greenhouse

field

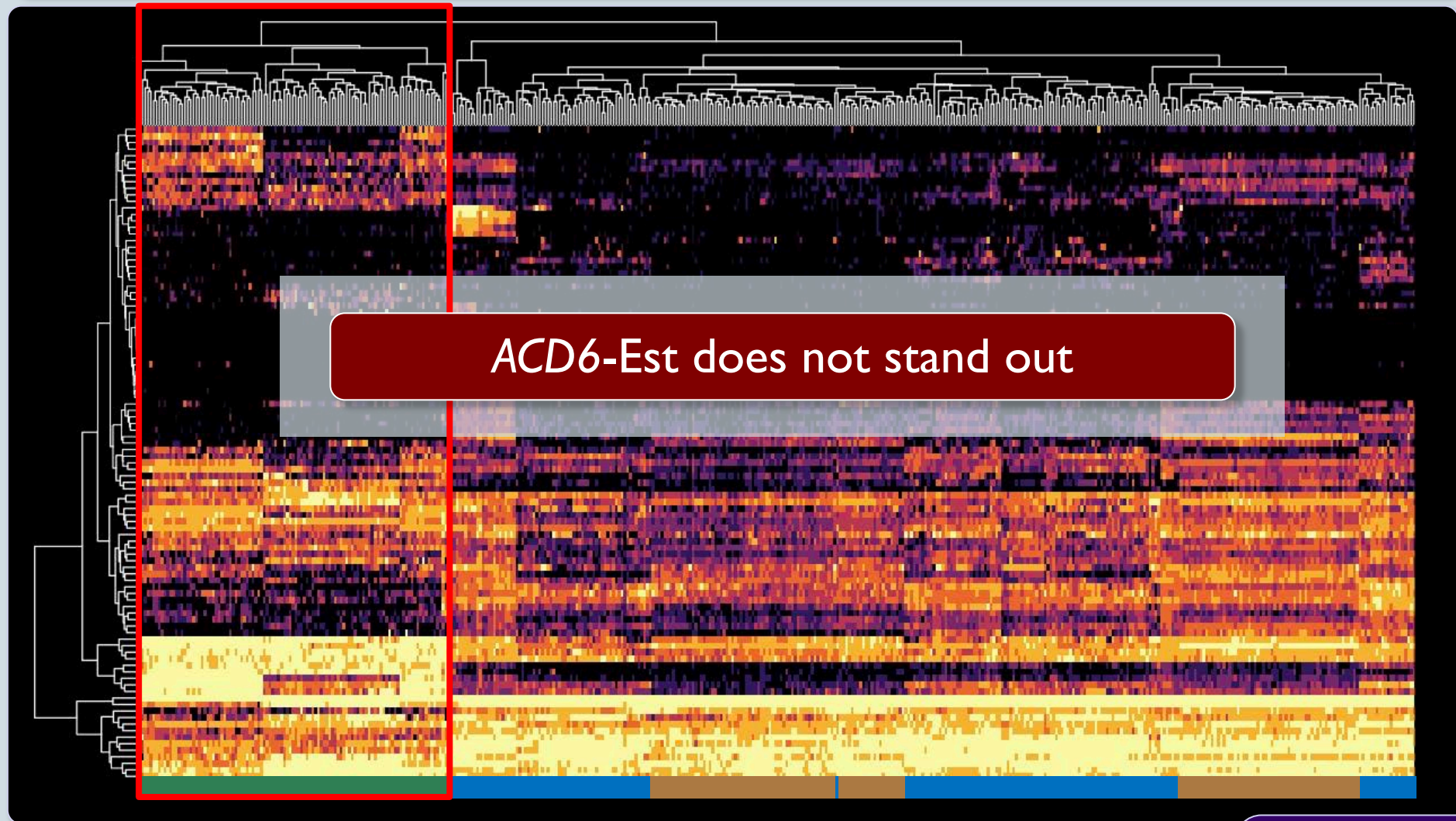
Est-I

Est-I *acd6*

Est-I



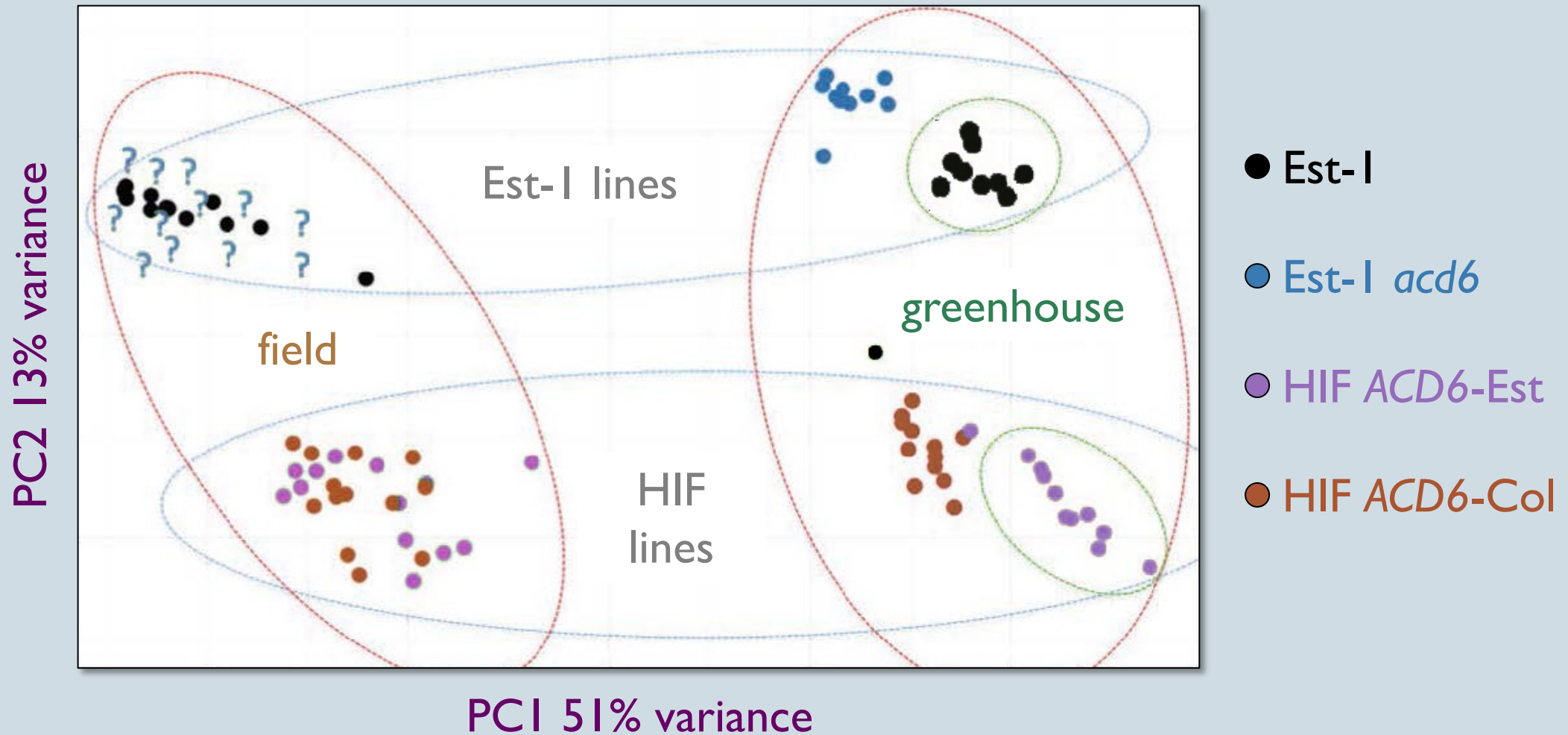
16S rDNA 2017 & 2018 season



■ greenhouse ■ field ■ wild

similar results
with ITS (fungi)

Transcriptome Differences Disappear in the Field



***ACD6*-Est distinct only in the greenhouse**

same applies
to SA differences

Fitness Difference Only Obvious in the Greenhouse



control



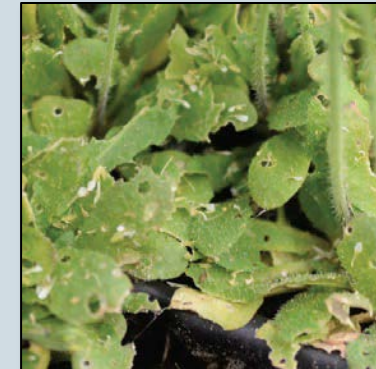
greenhouse



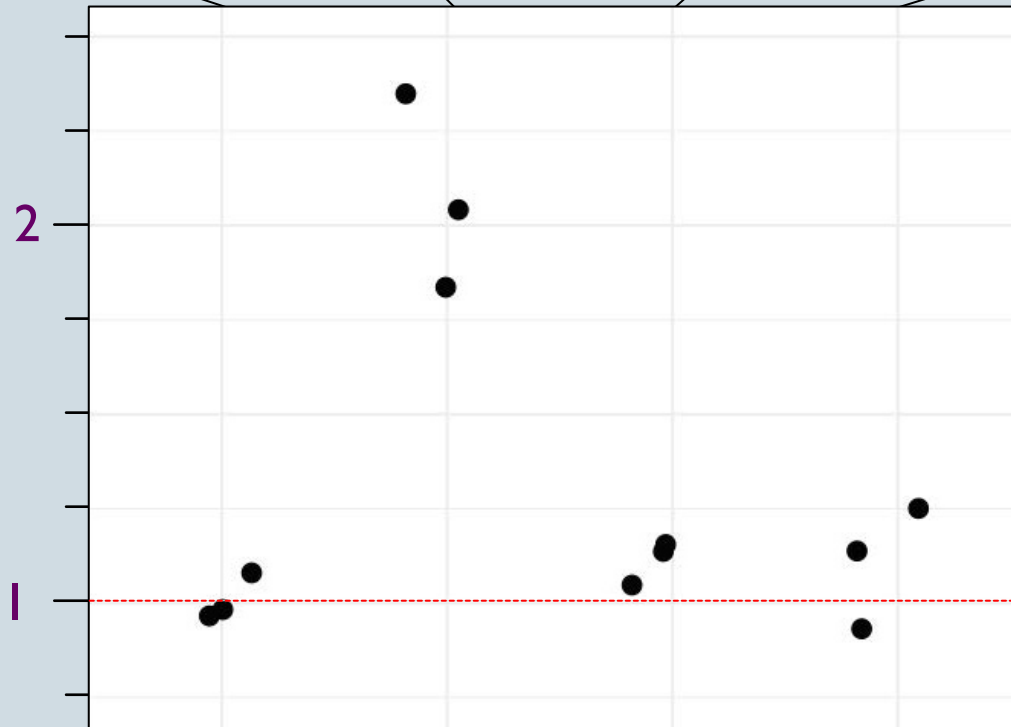
field



wild



ACD6-Col / ACD6-Est allele



allele quantification
in progeny



- Natural variation reveals new aspects of the plant immune system
- Whole-genome shotgun sequencing to measure microbial loads
- Wild plant pathosystems differ from crop and lab pathosystems
- Trade-offs differ between greenhouse and field

