Epistasis, the Spice of Life (and Evolution)

Lessons from the study of the plant immune system

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for Developmental Biology
Tübingen

http://weigelworld.org

@PlantEvolution

Disclaimers

eLIFE

computomics®

KWS

weigelworld
plant biology, developmental genetics
and evolutionary genomics.

WeigelWorld @IS-MPMI

Derek Lundberg (@DerekSeveri) Wednesday | 15:10 **M1 CS15**
Sphingomonas and *Pseudomonas* in wild *A. thaliana* and neighboring plants

Talia Karasov (@KarasovTalia) Wednesday | 14:50 **Lomond CS14**
Mapping genes in a leaf microbiome responsible for strain-specific pathogenicity

Or Shalev (@orshalevsk) Monday/Tuesday **028-P1**
Host Genotype-dependent Interactions among *Pseudomonas* in *A. thaliana*

Lei Li (@Lei_Li0601) Monday/Tuesday **328-P1**
Autoimmunity activated by atypical R protein RPW8/HR4 and NLR RPP7

Haim Ashkenazy (@Haim_Ashkenazy) Wednesday/Thursday **887-P2**
The evolution of *Arabidopsis thaliana* associated *Pseudomonas*

Wangsheng Zhu (@WangshengZhu) Wednesday/Thursday **888-P2**
Epistatic interactions between immune genes in *Arabidopsis*

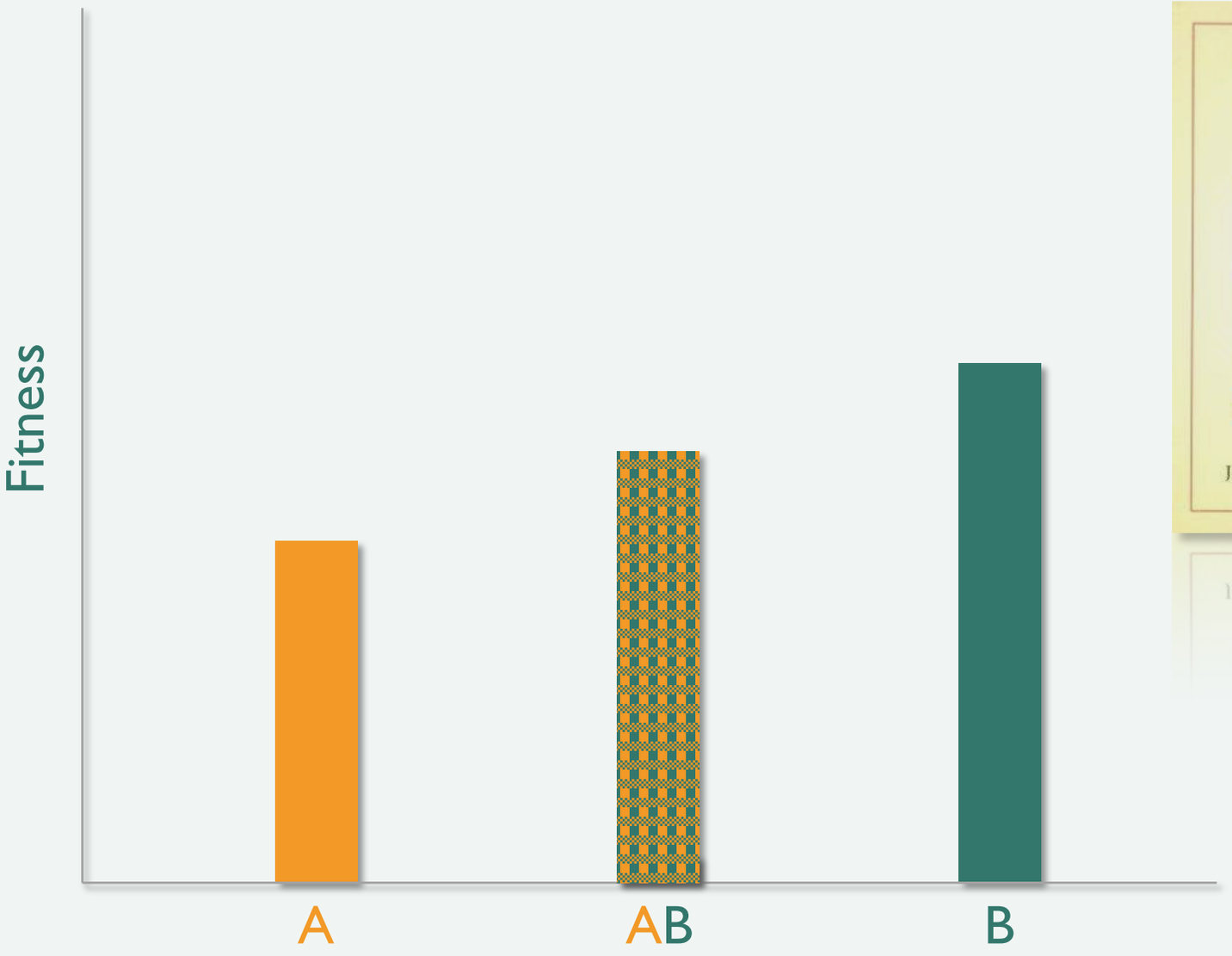
Fiona Paul Wednesday/Thursday **1023-P2**
Population genetics of *Hyaloperonospora arabidopsidis* (*Hpa*)

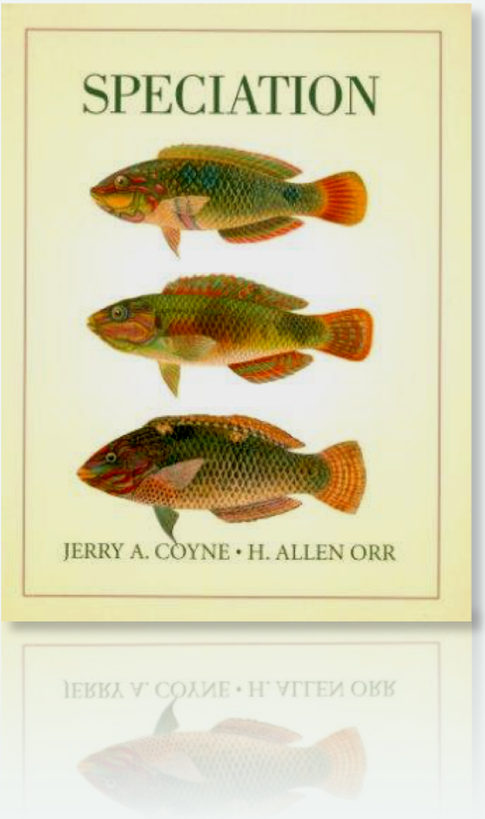
Eunyoung Chae (@EunyoungChae) Monday | 15:30 **Clyde CS4**
RPW8/HR repeats predict NLR-dependent hybrid performance

Epistasis – nonadditive gene action

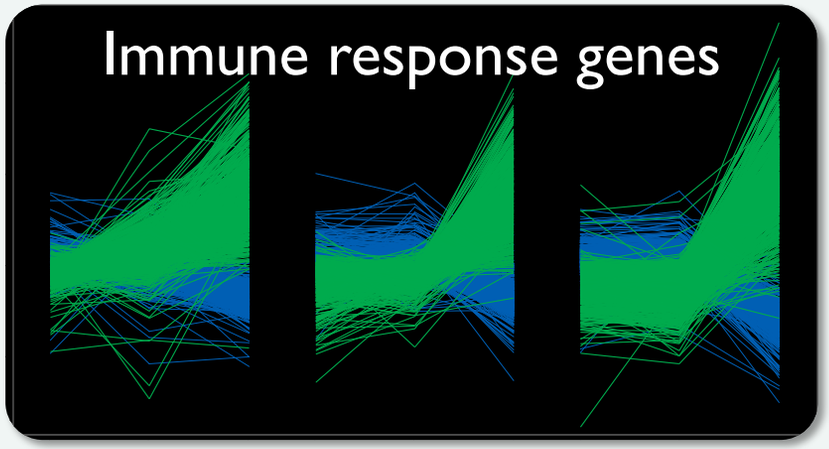
Epistasis as Evolutionary Disaster

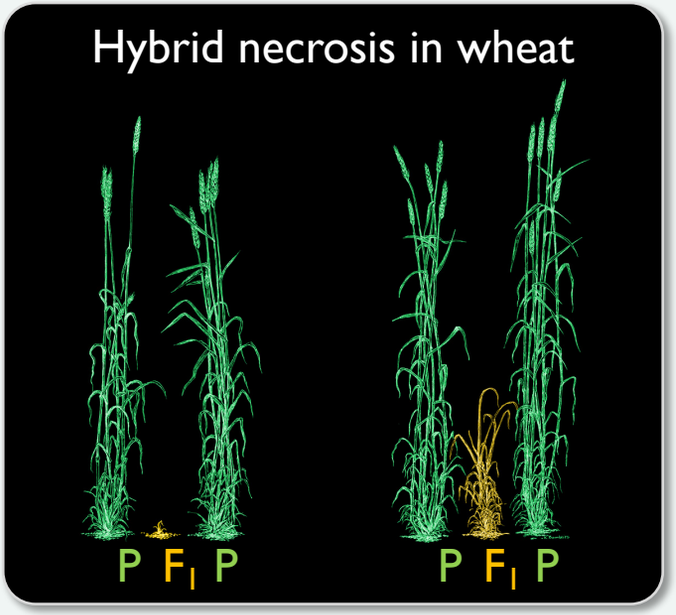
Hybrid weakness – negative heterosis

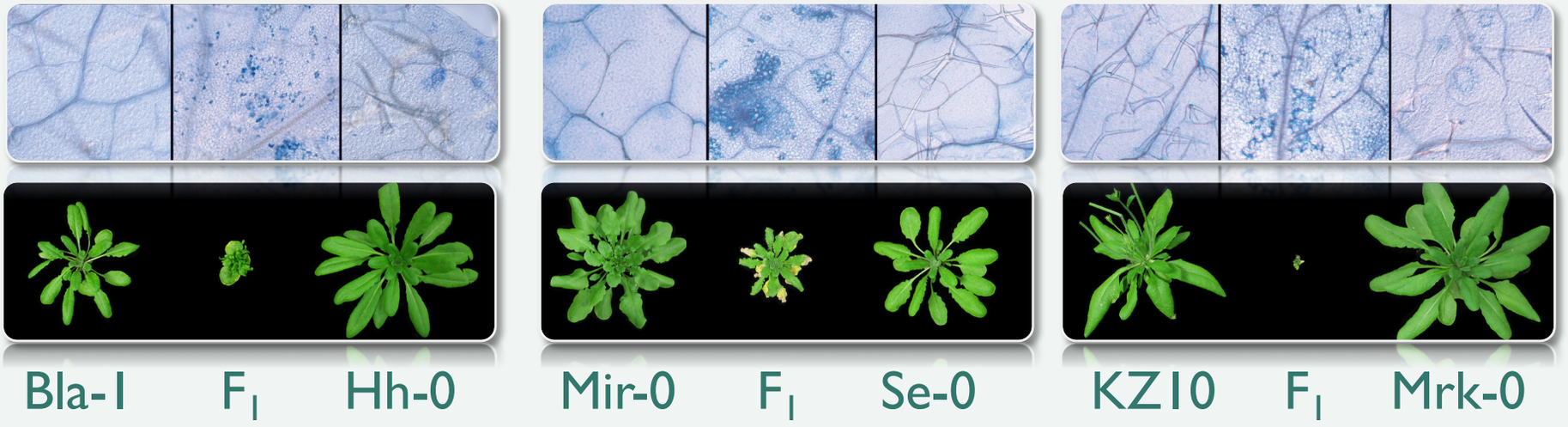




Hybrid Necrosis – Autoimmunity in *A. thaliana* F_1 Hybrids

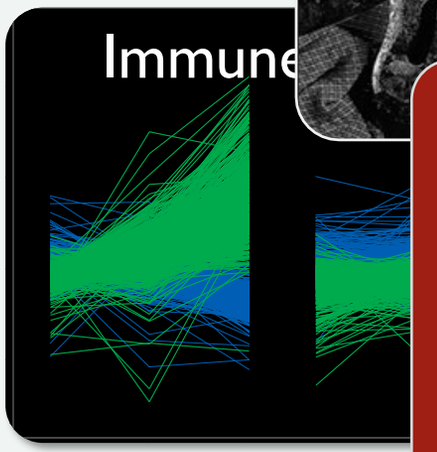


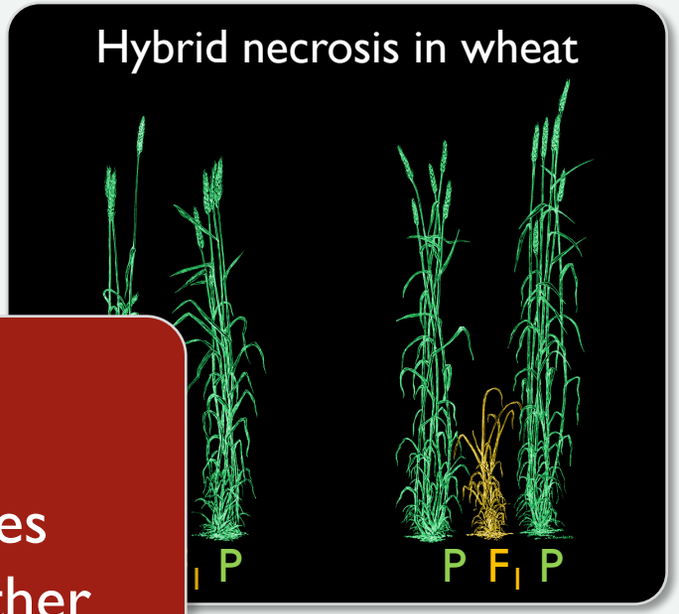




Bomblies et al. (2007)

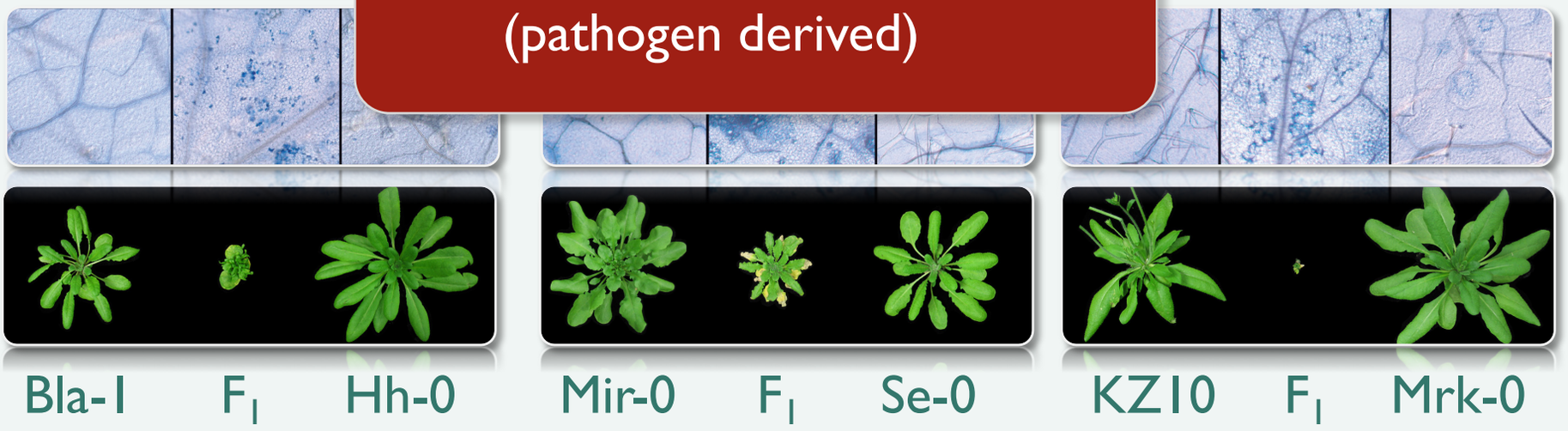
Hybrid Necrosis – Autoimmunity in *A. thaliana* F_1 Hybrids





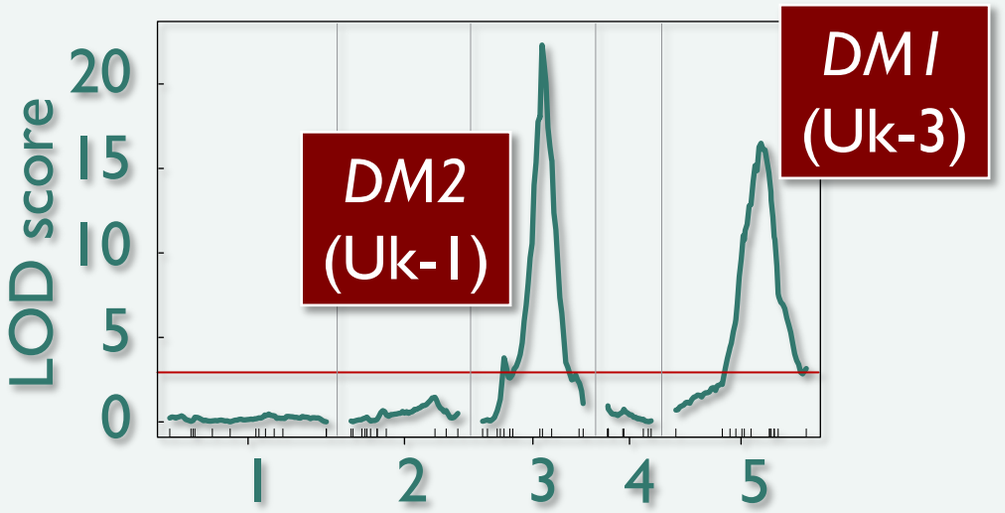
Hypothesis:

One genome recognizes something from the other genome as foreign (pathogen derived)



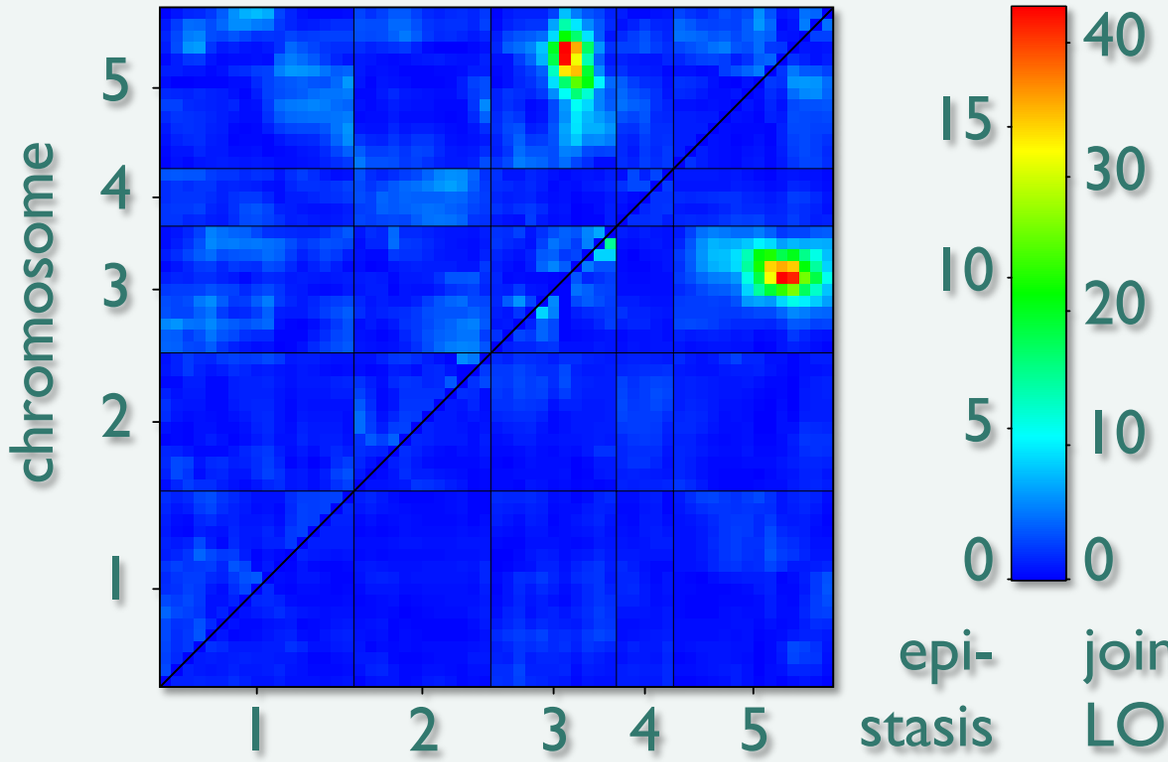
Bomblies et al. (2007)

Simple Genetics of Hybrid Necrosis



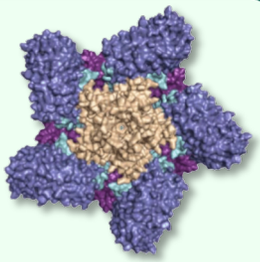
Dangerous Mix (DM)

Conforms to (Bateson-) Dobzhansky-Muller incompatibility

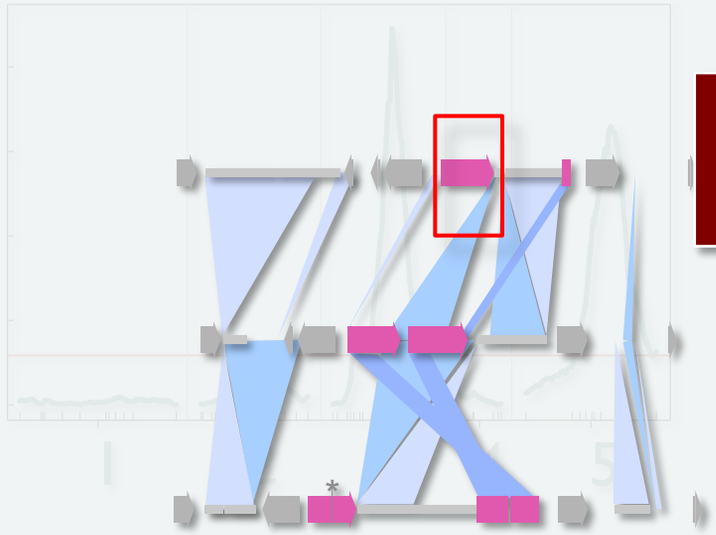


With Dangl lab

DM1 Encodes an NLR Immune Receptor and *DM2* as well!



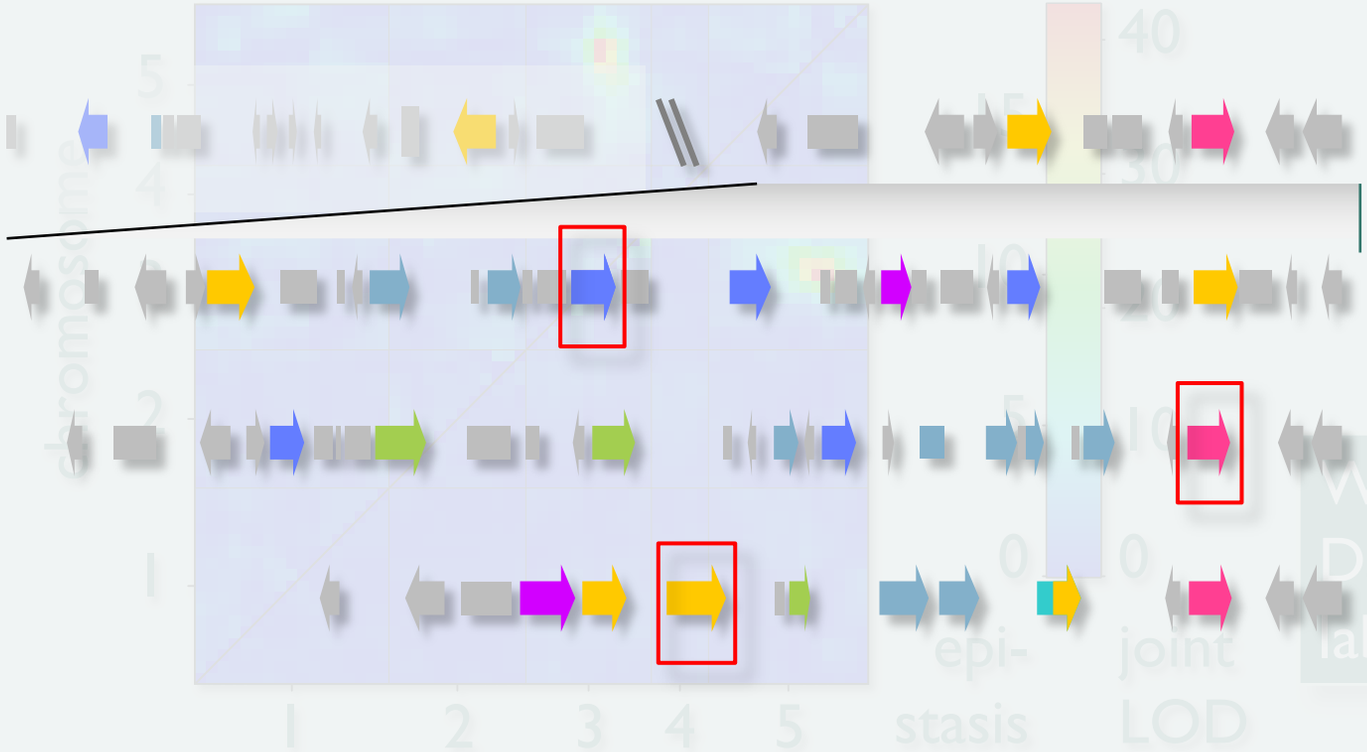
Nucleotide binding site
Leucine rich repeat
Receptor



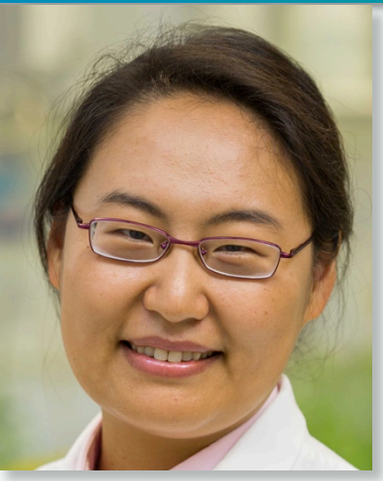
DM1 (Uk-3)

Dangerous Mix (DM)

DM2 (Uk-1)



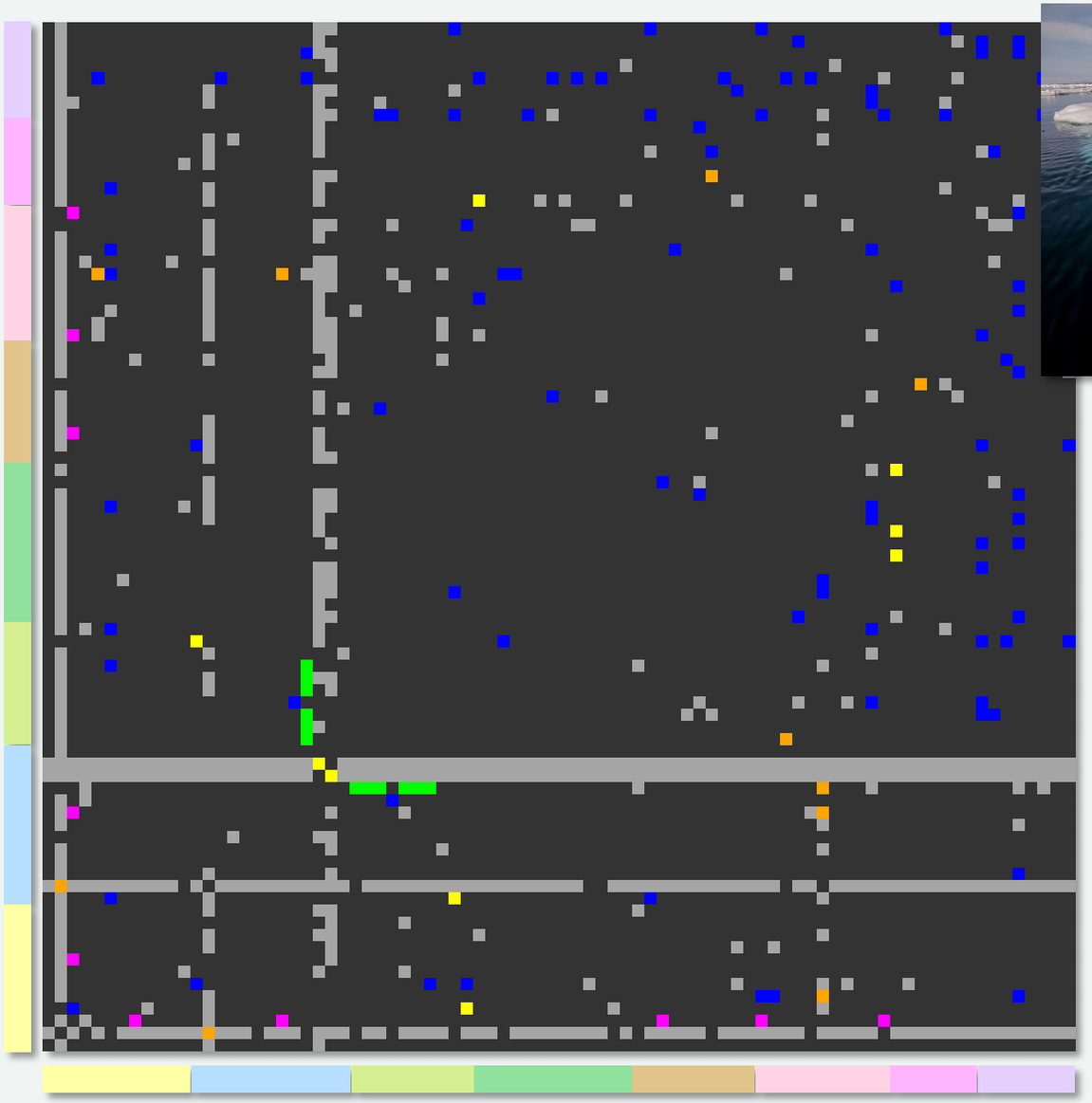
Species-wide Survey of Hybrid Necrosis



Eunyoung Chae (now NUS)

6,409 crosses (3,330 unique combinations)

♀



♂

not tested

hybrid

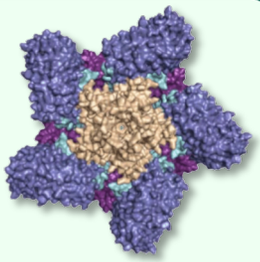
necrosis

classes

geographic origins

Chae et al. (2014)

Specific *R* Gene Loci Overrepresented in Hybrid Necrosis



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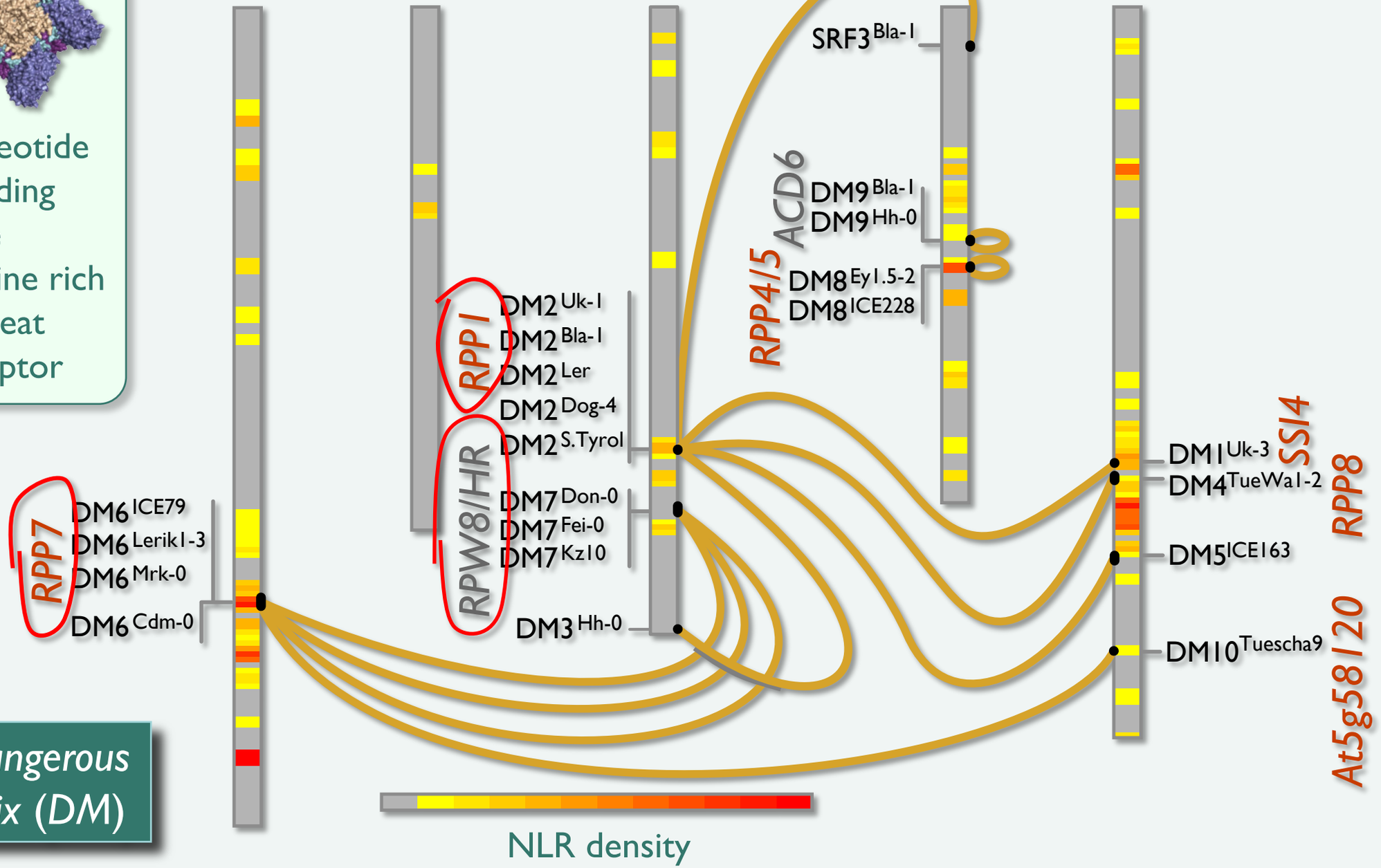
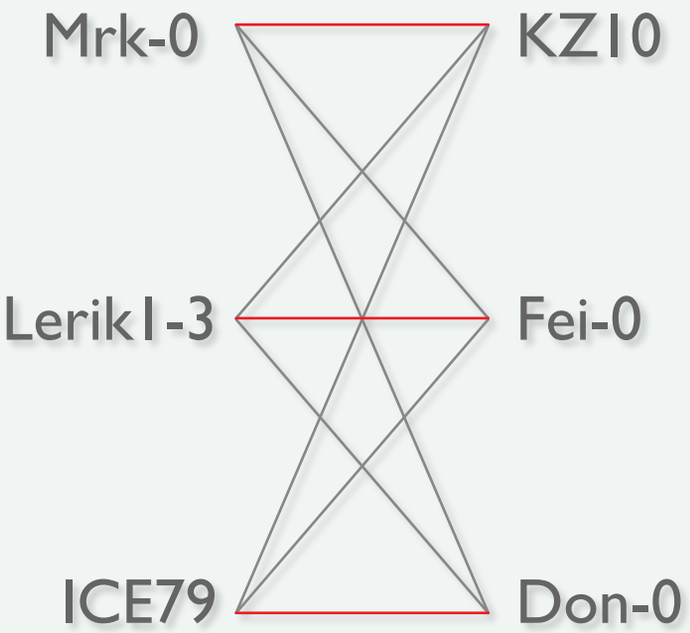


Dangerous Mix (DM)

Multiple Pairs of *RPP7* – *RPW8/HR* Interactions

Cristina Barragan

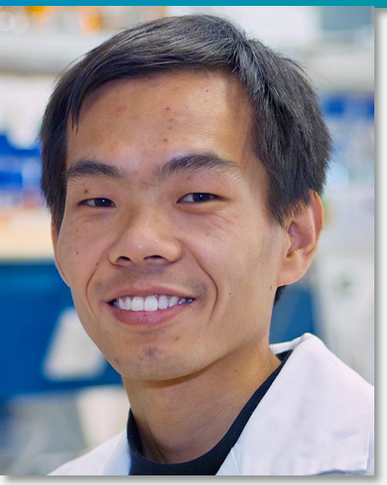
Parent 1 F_1 Parent 2



*RPW8/HR homologs of MLKL & HELL/HeLo domain proteins; share CC_R domain with an NLR subclass

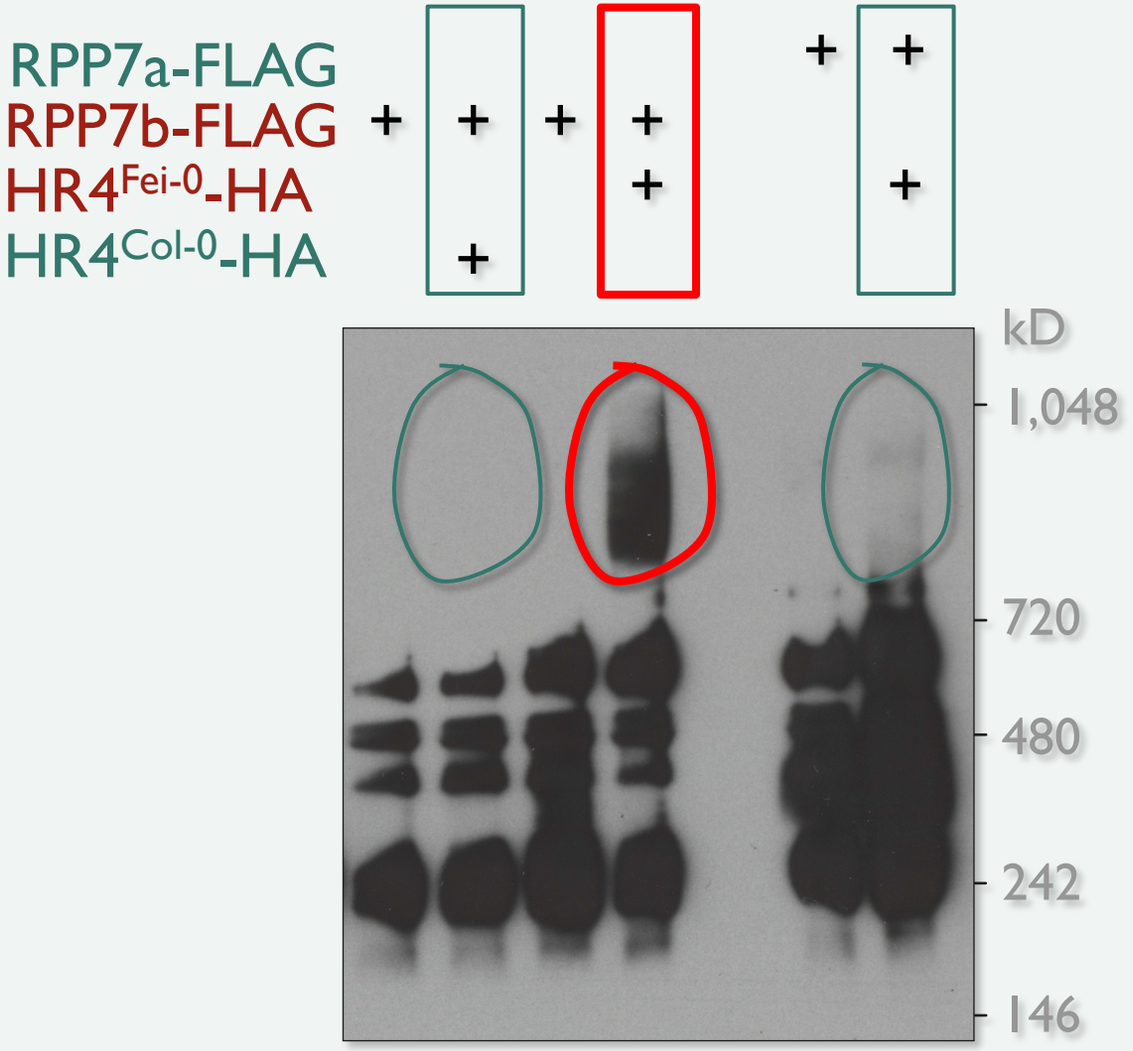
bioRxiv 559864

Specific Interactions between RPP7 and RPW8/HR Proteins



Lei Li

Only between proteins encoded by causal alleles of *RPP7* and *RPW8/HR*

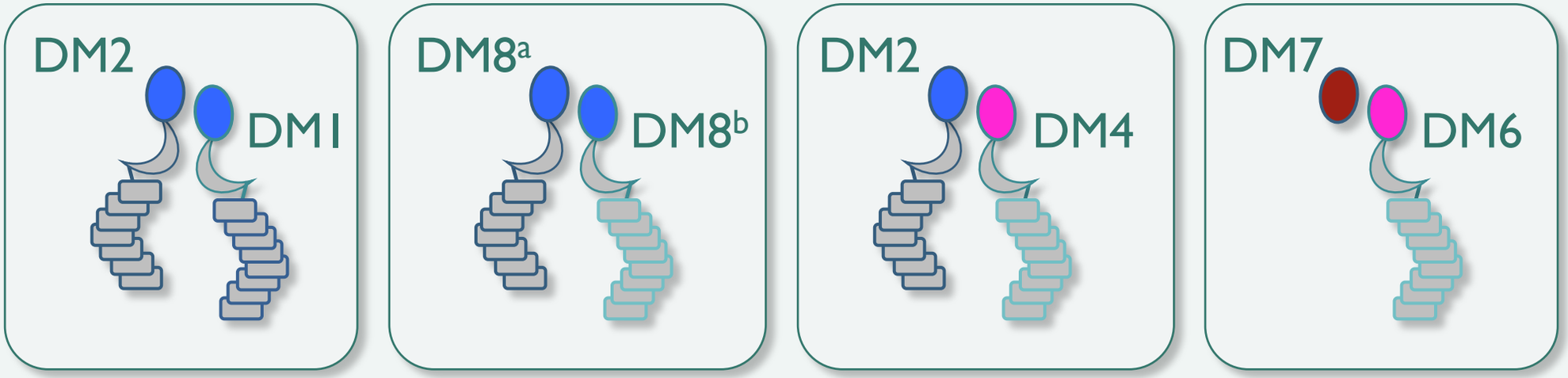


3-12% native PAGE

A Wide Range of (Direct?) NLR Interactions

Hypothesis:

Potentially promiscuous NLR interactions limit possible immune receptor combinations in single genotype

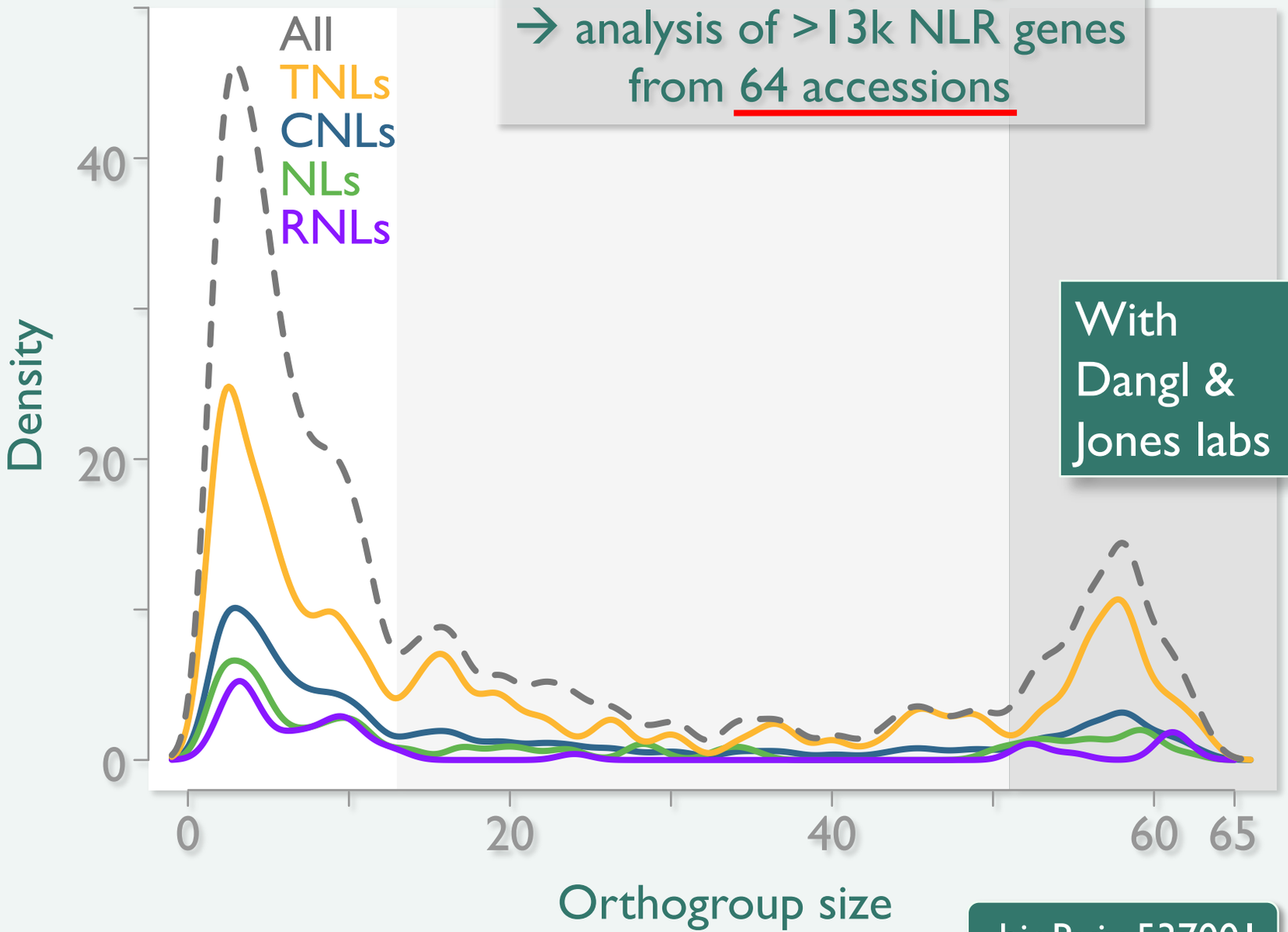


(Too Much) NLR Immune Receptor Diversity …

Anna-Lena Van de Weyer (now LaboKlin)

Felix Bemm (now KWS)

NLR sequence enrichment & PacBio sequencing
→ analysis of >13k NLR genes from 64 accessions



With Dangl & Jones labs

bioRxiv 537001

What causes and limits immune system diversification in the wild?

Question #1:
Who is there and how many of them?

Microbiome Analyses: Amplicon Data Are Compositional

Metagenome Shotgun Sequencing

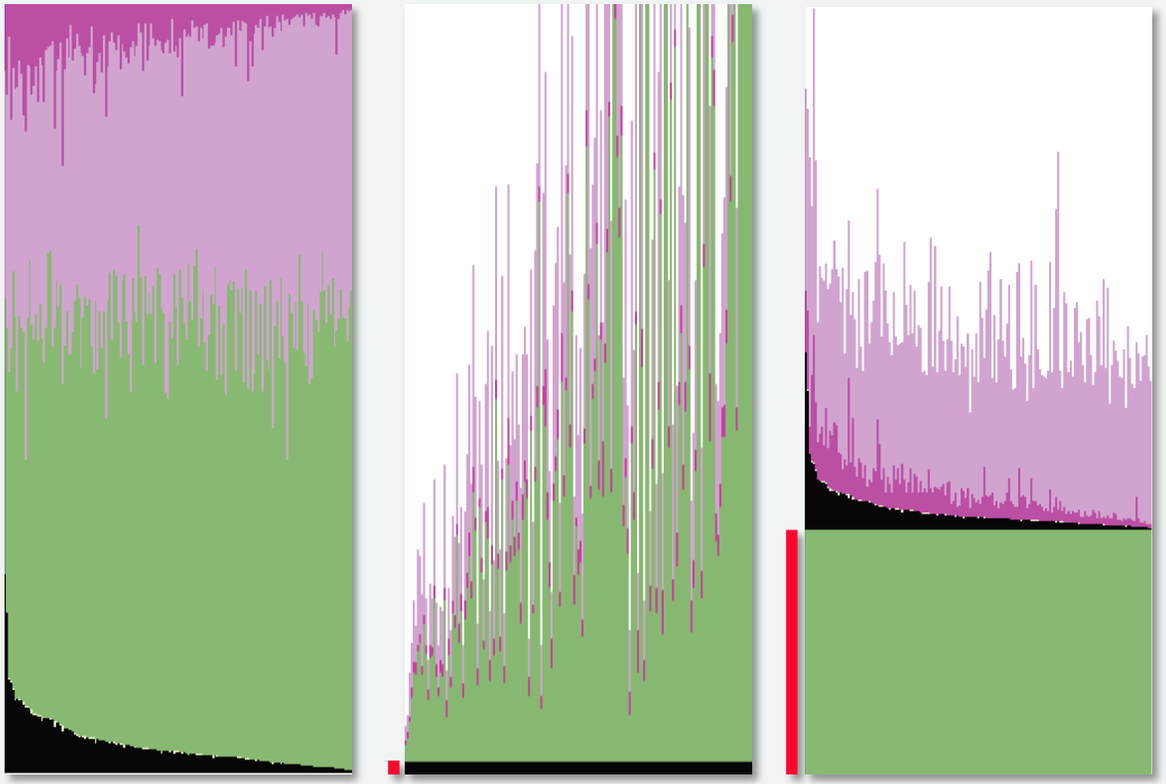
Julian Regalado

Derek Lundberg

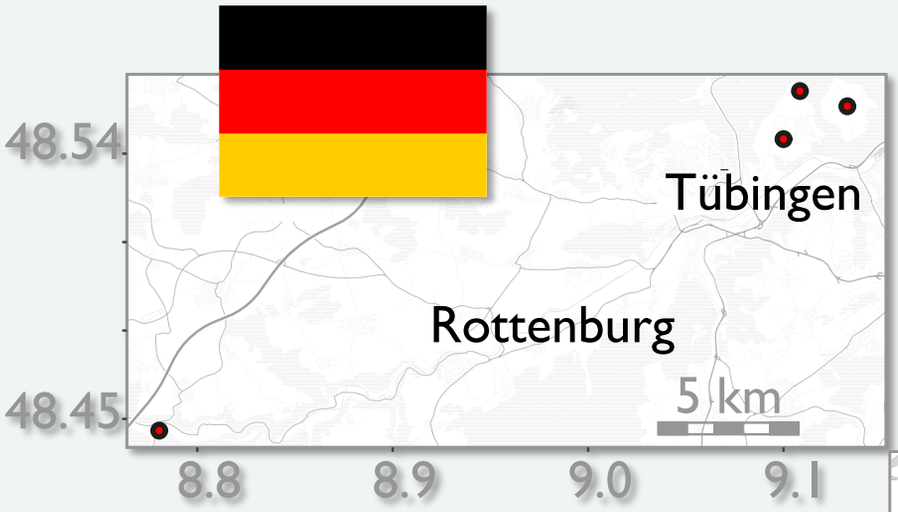
Total reads equal = raw data

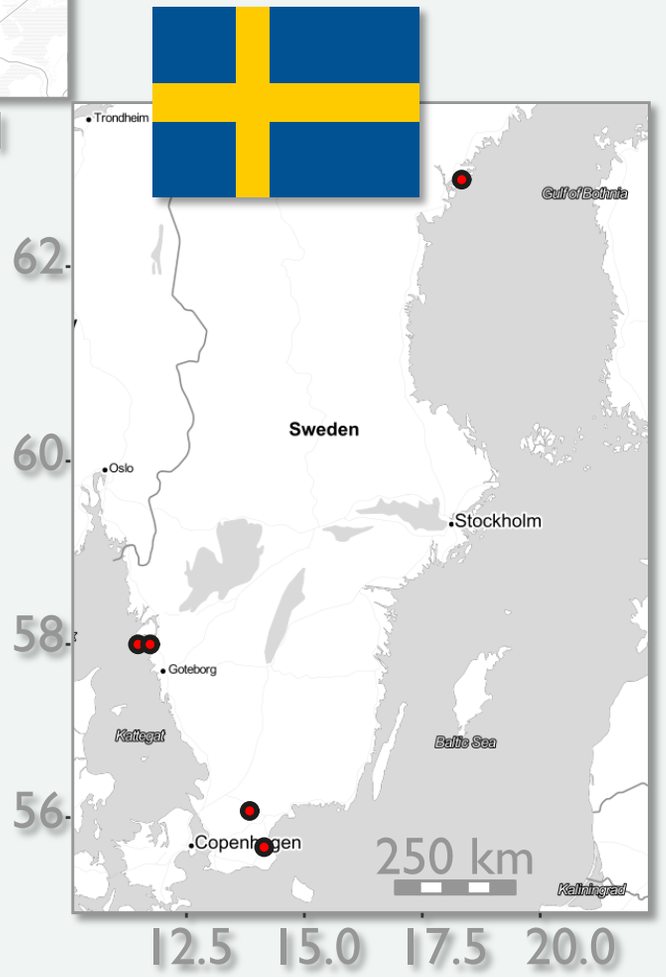
Microbial reads equal = amplicons

Plant nuclear reads equal



Pilot: Sampling Germany and Sweden





SW Germany
176 plants
4 populations
2 seasons

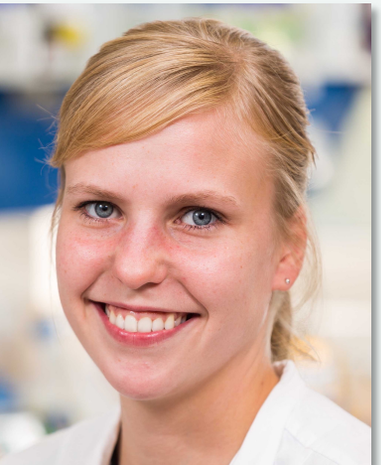
S Sweden
50 plants
5 populations
1 season

With Bergelson lab

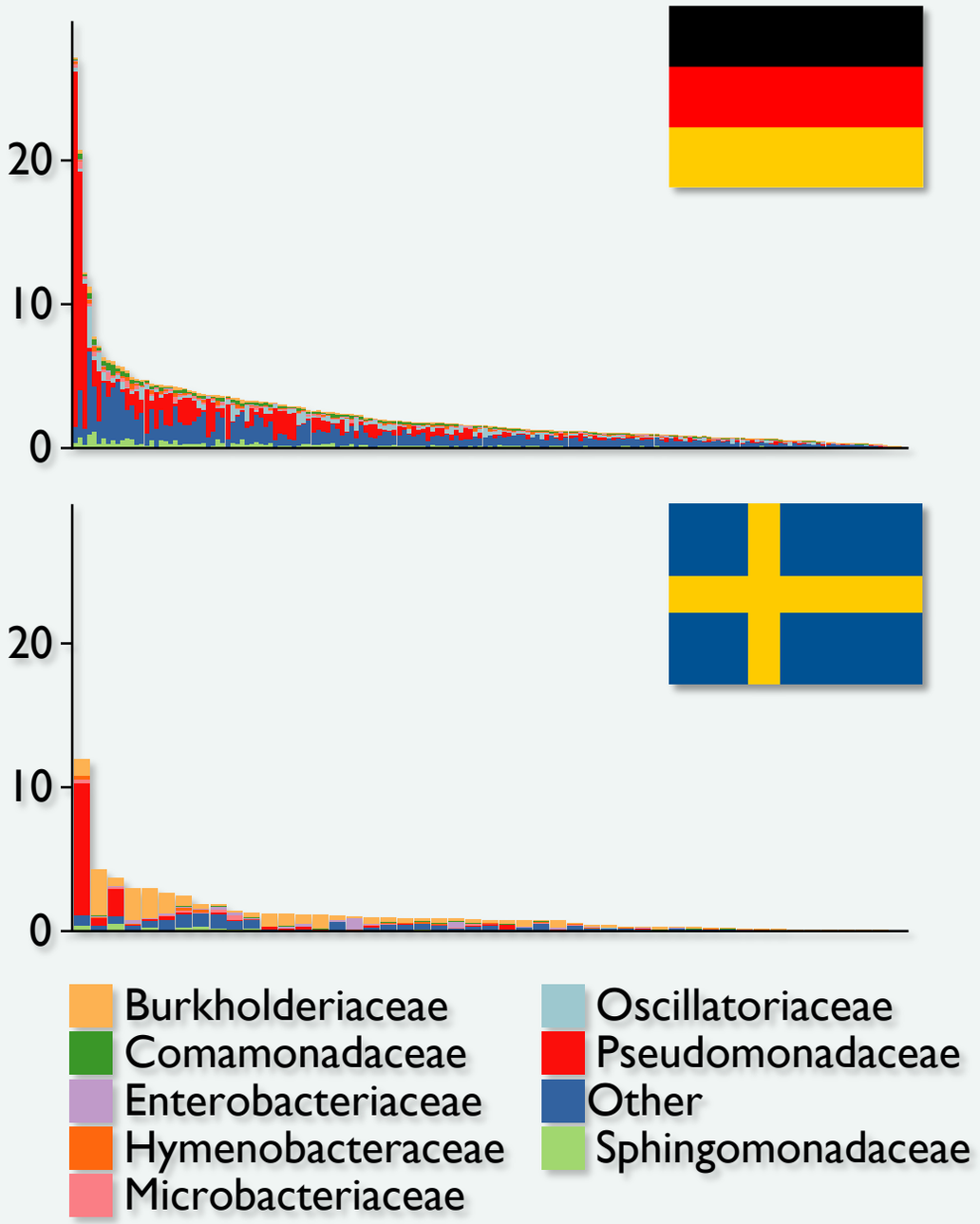
Within-region Similarity / Between-region Difference

Talia Karasov

Manuela Neumann



Bacteria



Within-region Similarity / Between-region Difference

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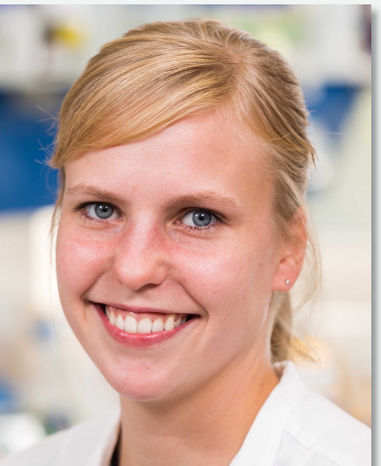
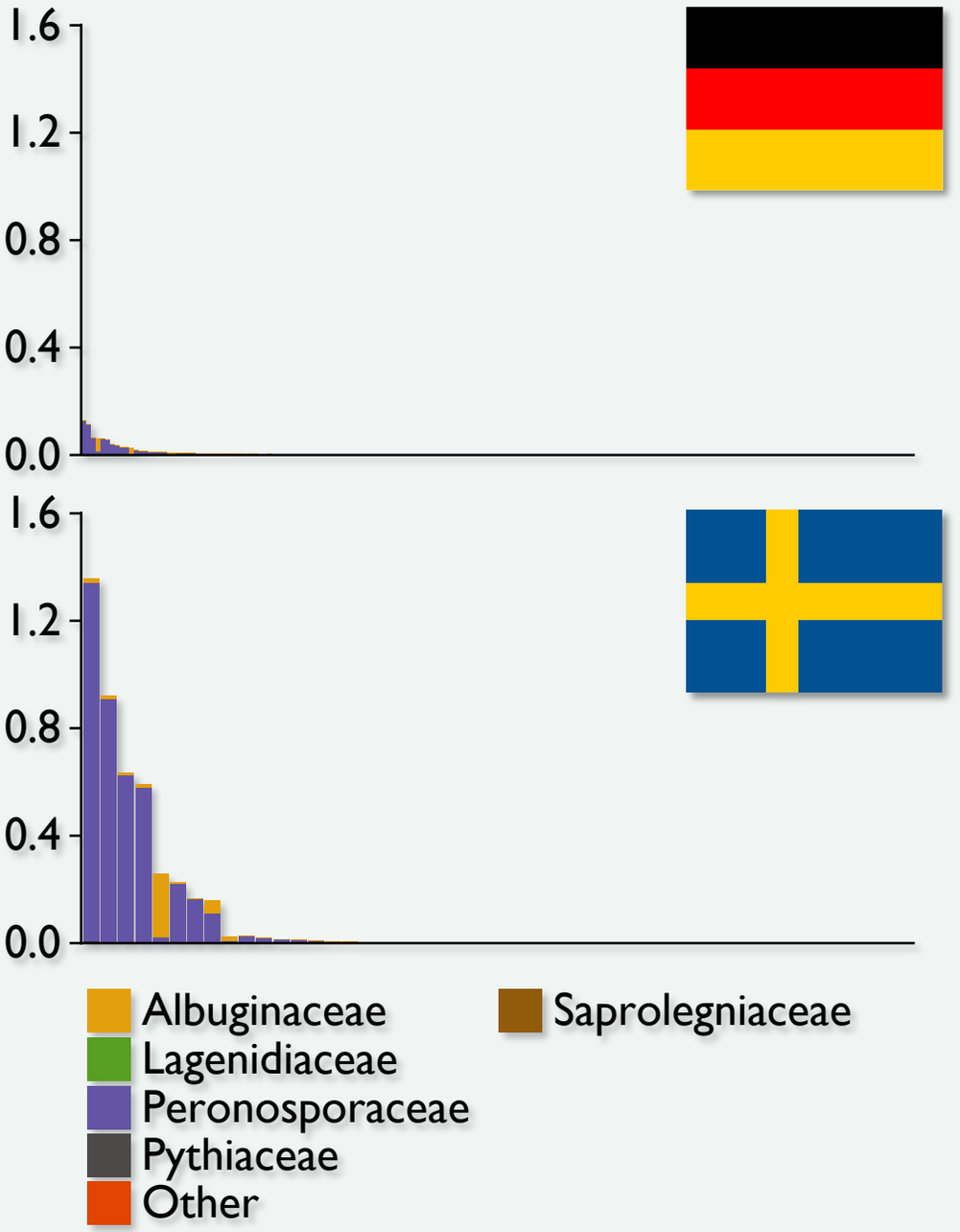
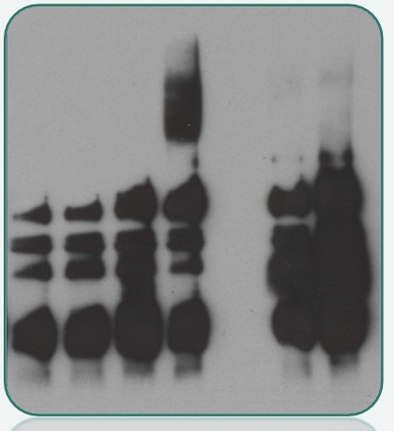


Oomycetes

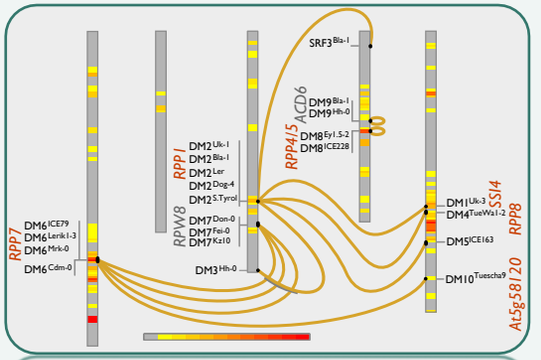


Lessons

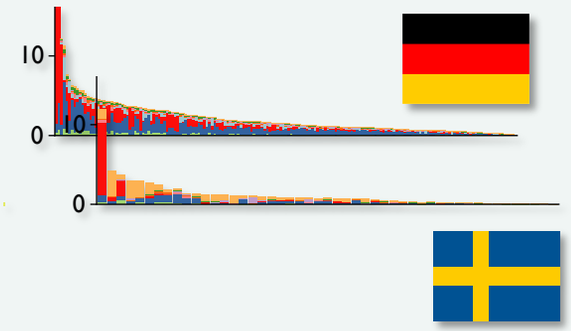
- Epistatic interactions in immune system are common



- Too much diversity at NLR and other immune loci can backfire



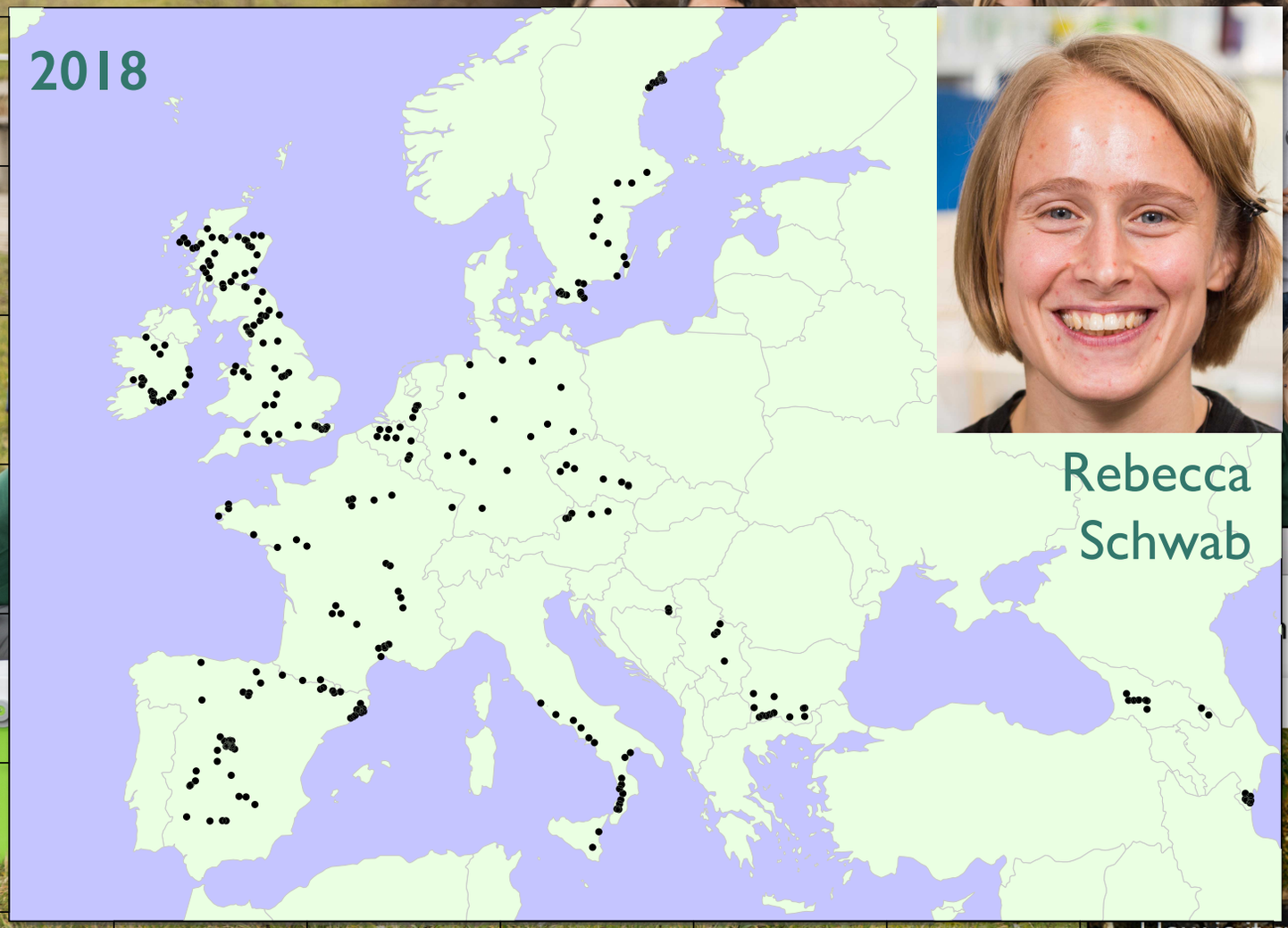
- Extreme geographic diversity in *A. thaliana* phyllosphere microbiome



Project Pathodopsis

Patho(gens on Arabi)*dopsis*

>650 plants
- Metagenome
- Bacterial 16S rDNA
- Eukaryotic ITS
- Environmental variables



Rebecca Schwab