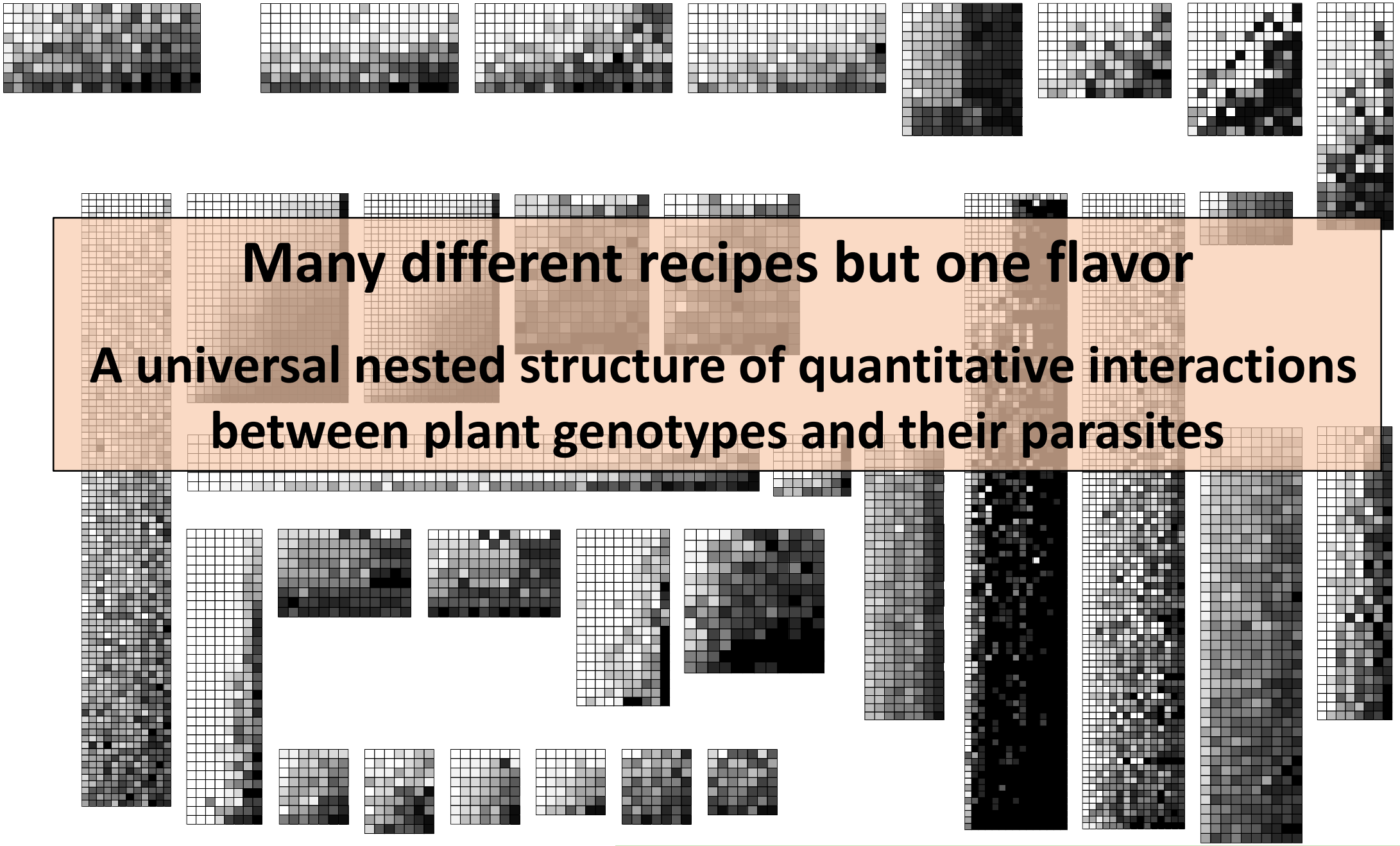
Une structure emboîtée universelle pour les interactions quantitatives entre les plantes et leurs parasites ?

Benoît Moury, Jean-Marc Audergon, Sylvie Baudracco-Arnas, Safa Ben Krima, François Bertrand, Nathalie Boissot, Mireille Buisson, Valérie Caffier, Melissa Cantet, Sylvia Chanéac, et al.

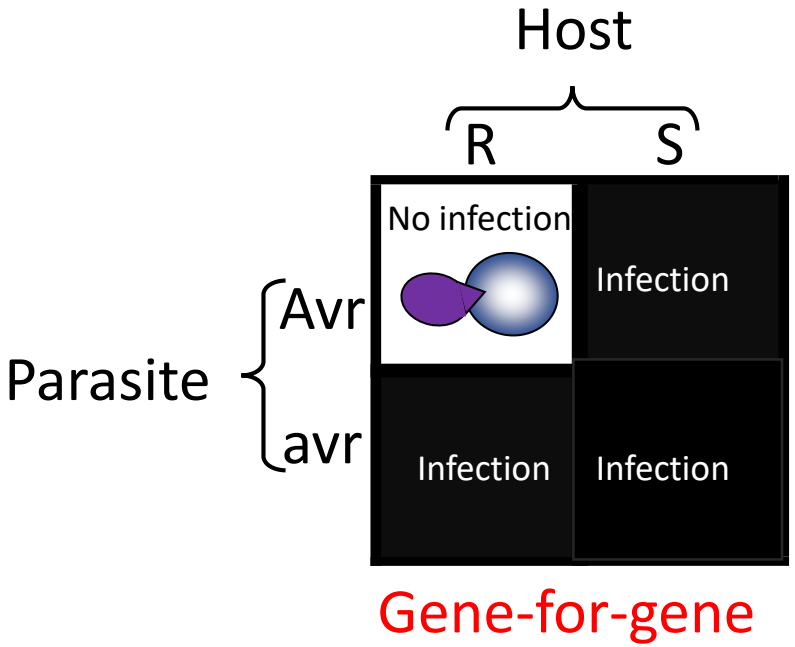


Many different recipes but one flavor

A universal nested structure of quantitative interactions between plant genotypes and their parasites

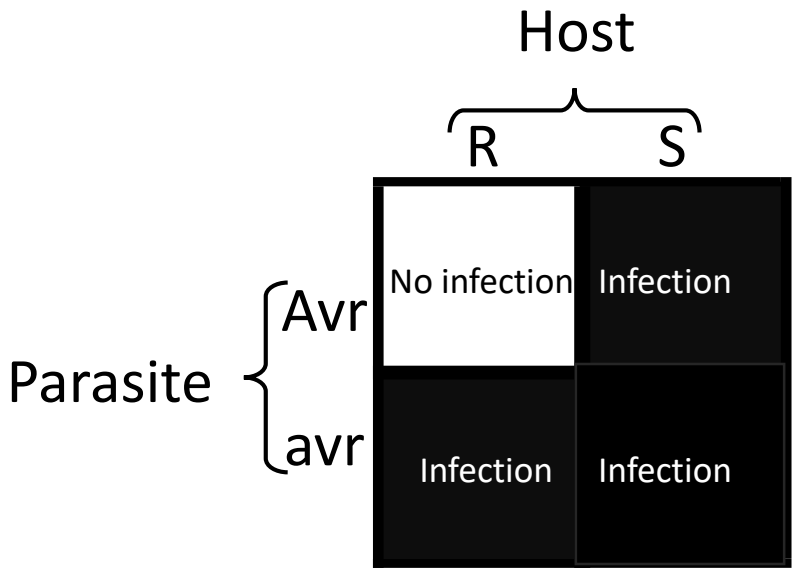
Benoît Moury – Réseau e3gp3 – Paris (enfin presque) – 6-7/12/2021

Qualitative plant immunity: two main genetic and evolutionary models



Gene-for-gene

Qualitative plant immunity: two main genetic and evolutionary models



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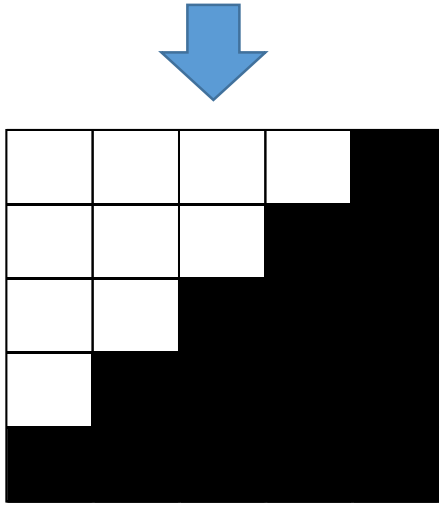
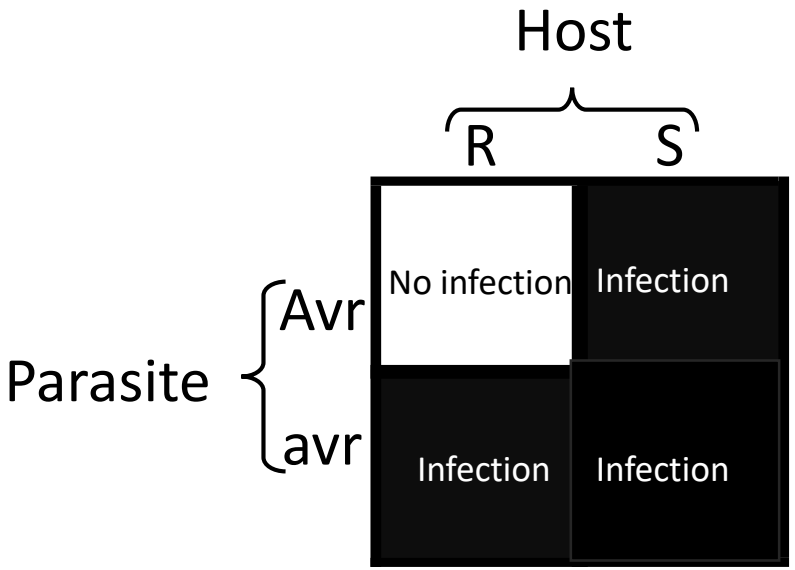
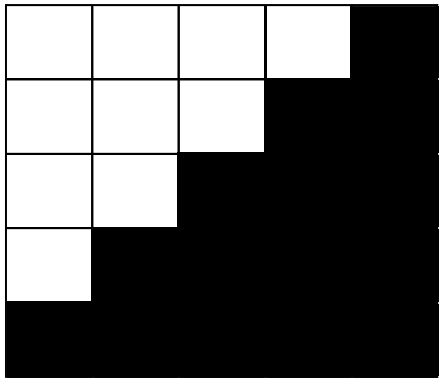


Nested structure

Qualitative plant immunity: two main genetic and evolutionary models



Gene-for-gene



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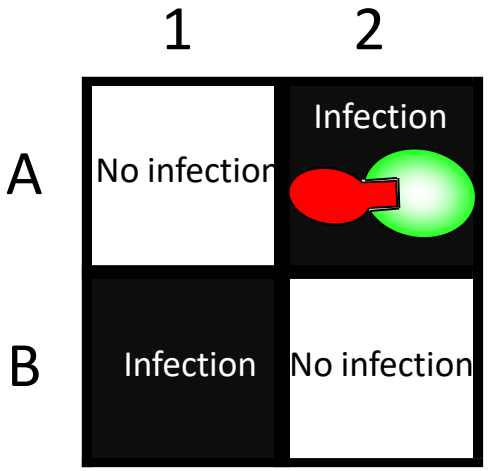
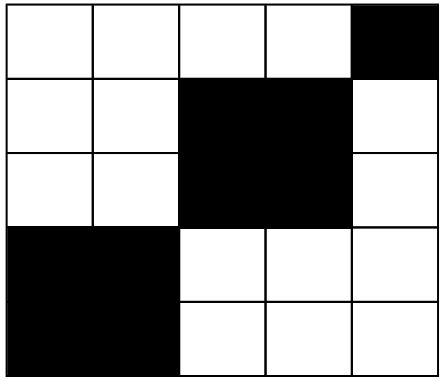
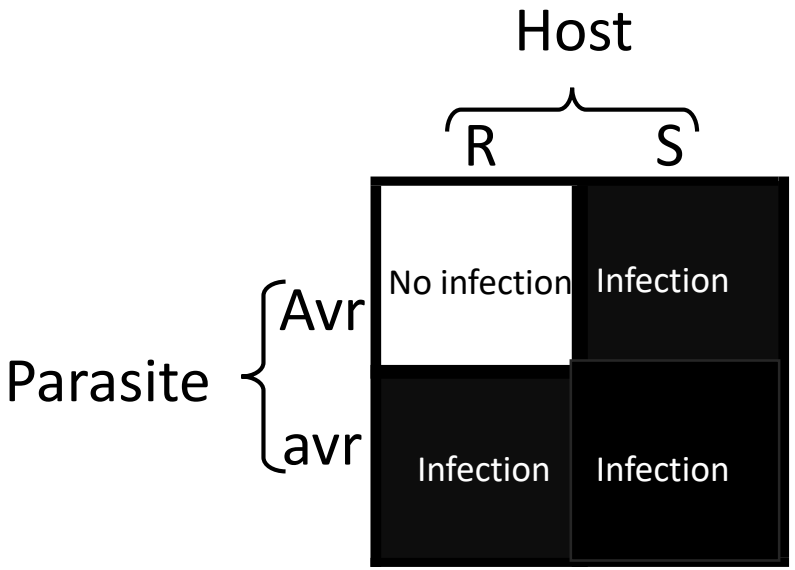


Matching allele

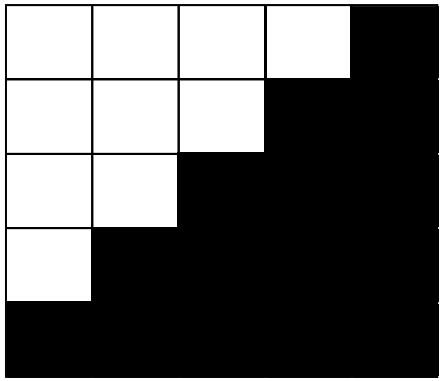


Modular structure

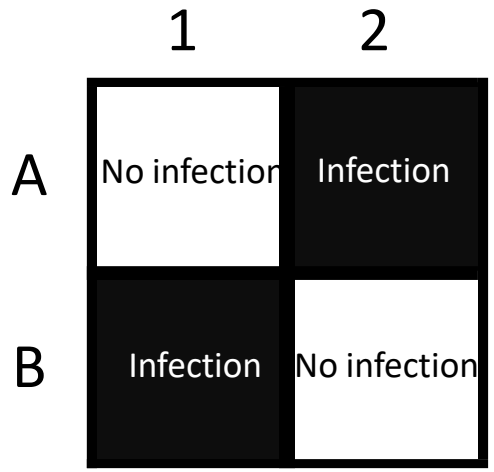
Qualitative plant immunity: two main genetic and evolutionary models



Gene-for-gene



Nested structure



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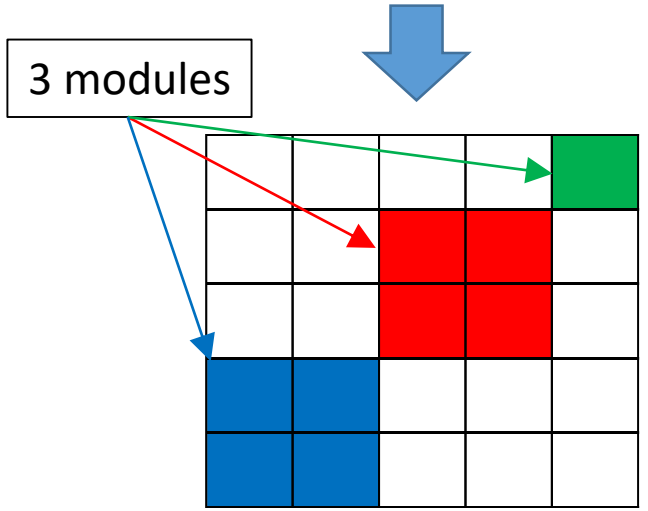
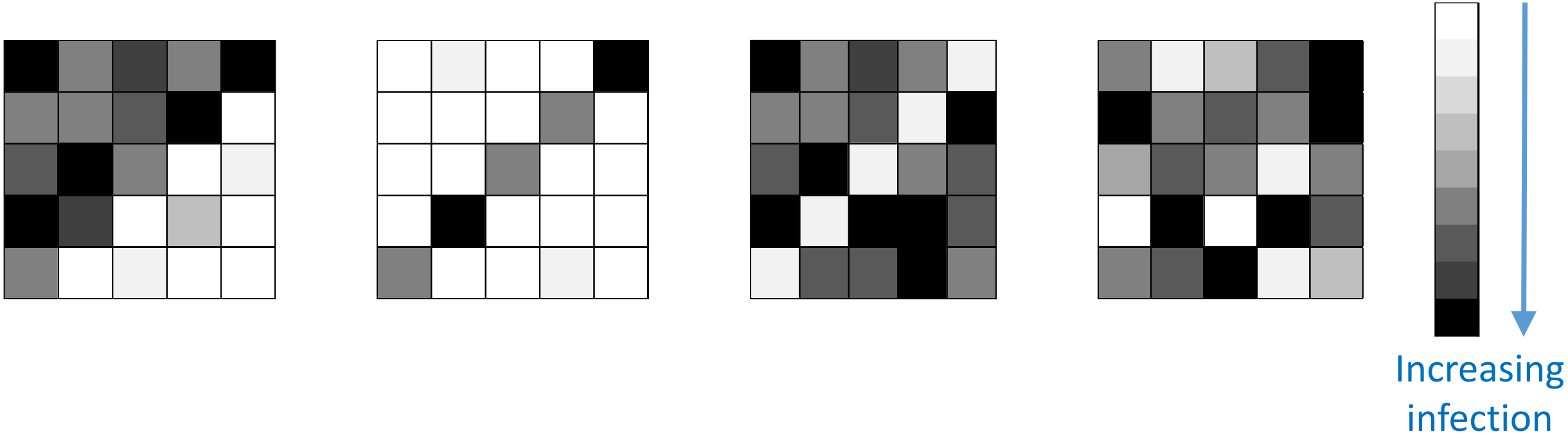


Modular structure

Is there analogous structures (and genetic models) in the case of quantitative infection matrices?



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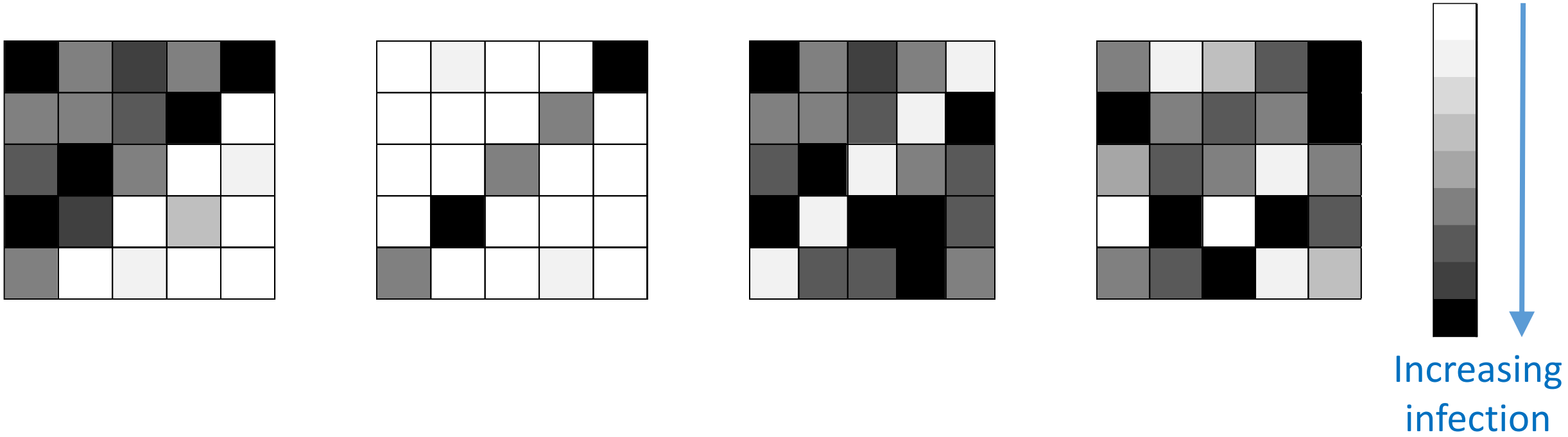

What can these structures tell us about evolution and genetic bases of quantitative plant – parasite interactions?

Analysis of 32 quantitative matrices

Plant	Parasite	
Apricot	*Pseudomonas syringae*	Bacteria
Barley	*Puccinia hordei*	Fungi/oomycetes
Apple tree	*Venturia inaequalis*	
Tomato	*Botrytis cinerea*	
Melon	*Podosphaera xanthii*	
Wheat	*Zymoseptoria tritici*	
Pepper	*Phytophthora capsici*	
Tomato and other *Solanum* spp.	*Phytophthora infestans*	
Fabaceae	*Aphanomyces euteiches*	
Pea	*Aphanomyces euteiches*	
Grapevine	*Plasmopara viticola*	
Melon	*Aphis gossypii*	Insects
Potato	*Globodera pallida*	Nematodes
Potato and other *Solanum* spp.	*Globodera pallida*	
Pepper	*Potato virus Y*	Viruses

Analysis of 32 quantitative matrices

- Resulting from cross-inoculations under controlled conditions
- Dimensions: at least 6 × 6
- Without missing data
- Quantitative traits: parasite load, parasite-induced damages, latency period, dissemination capacity

Estimating the degrees of nestedness/modularity and testing their significance

0,27	0,69	0,36	0,47	0,15
0,32	0,45	0,36	1,02	0,04
0,1	3,01	0,89	1,34	0
0	1,26	2,51	0,84	0,09
0,78	1	1,77	0,99	1,03

Infection trait values

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Infection trait values

Transformation into integer values [0-9]

0	2	0	1	0
1	1	0	3	0
0	9	2	4	0
0	4	8	2	0
2	1	5	3	3

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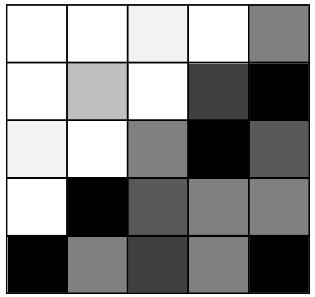
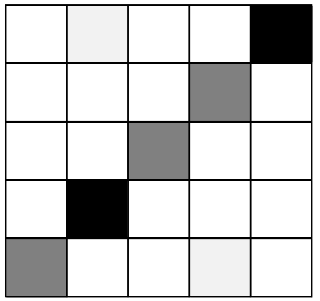
Nestedness/modularity value (*X*) of the experimental matrix

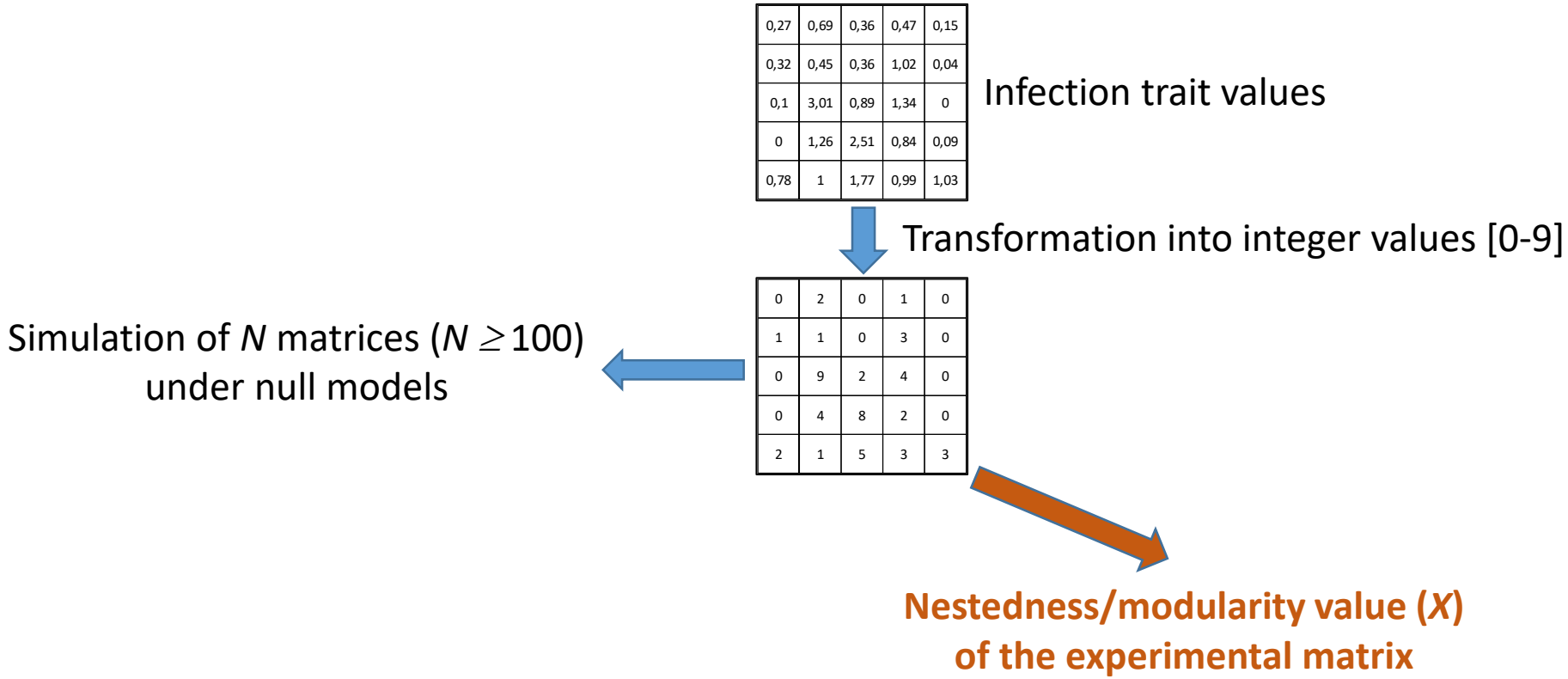


High nestedness

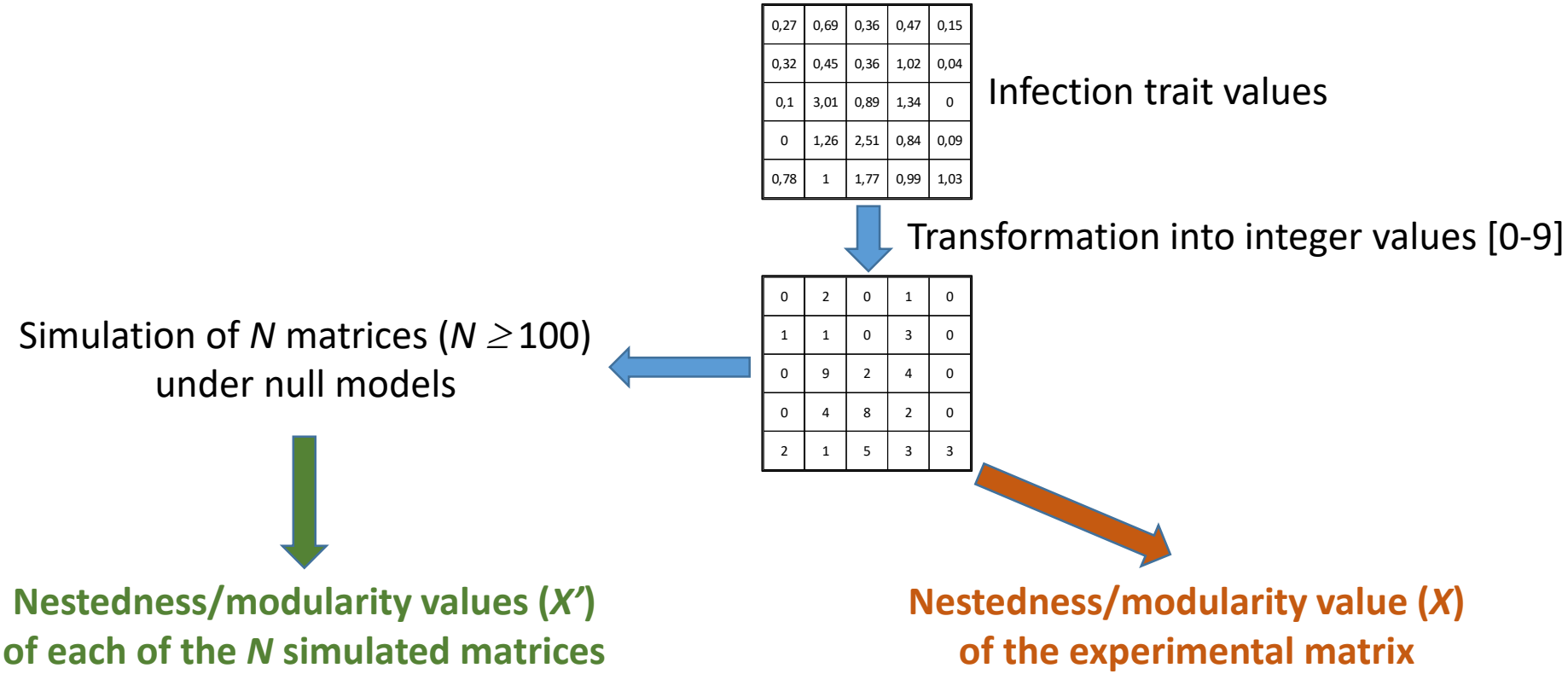


High modularity

Estimating the degrees of nestedness/modularity and testing their significance



Estimating the degrees of nestedness/modularity and testing their significance



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0	2	0	1	0
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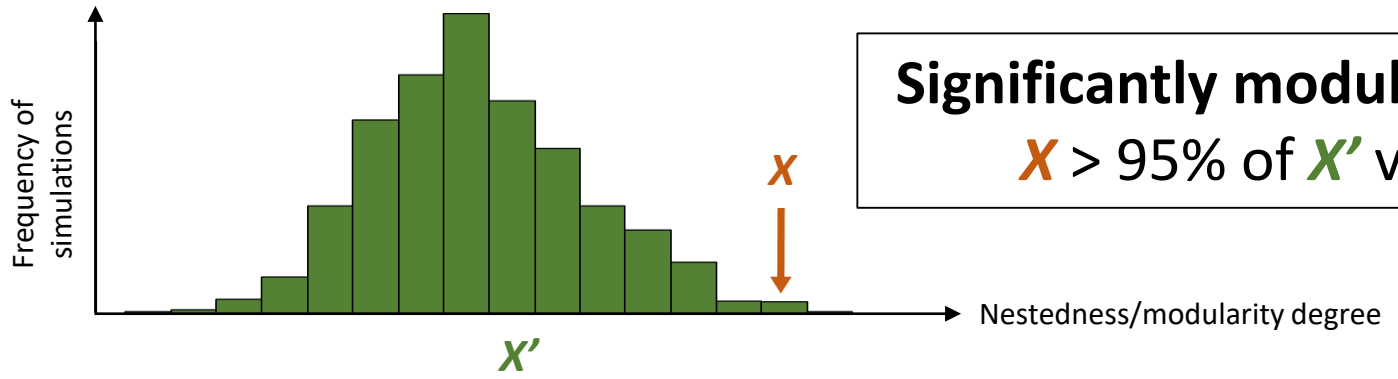
2	1	5	3	3

Simulation of *N* matrices ($N \geq 100$) under null models

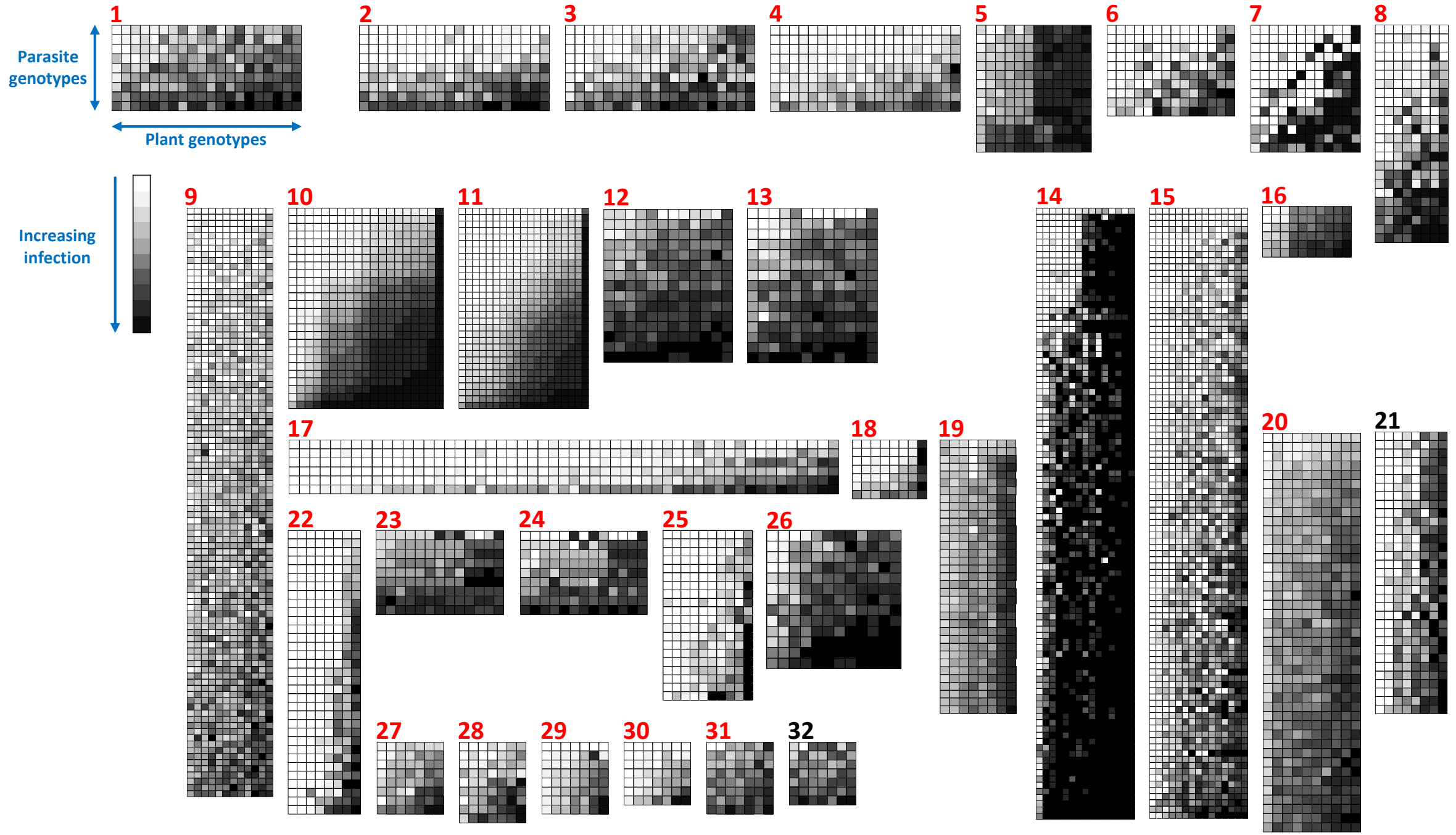
Nestedness/modularity values (*X'*) of each of the *N* simulated matrices

Nestedness/modularity value (*X*) of the experimental matrix



Significantly modular matrix:
X > 95% of ***X'*** values

Nestedness results


Parasite genotypes
Plant genotypes
Increasing infection
1
2
3
4
5
6
7
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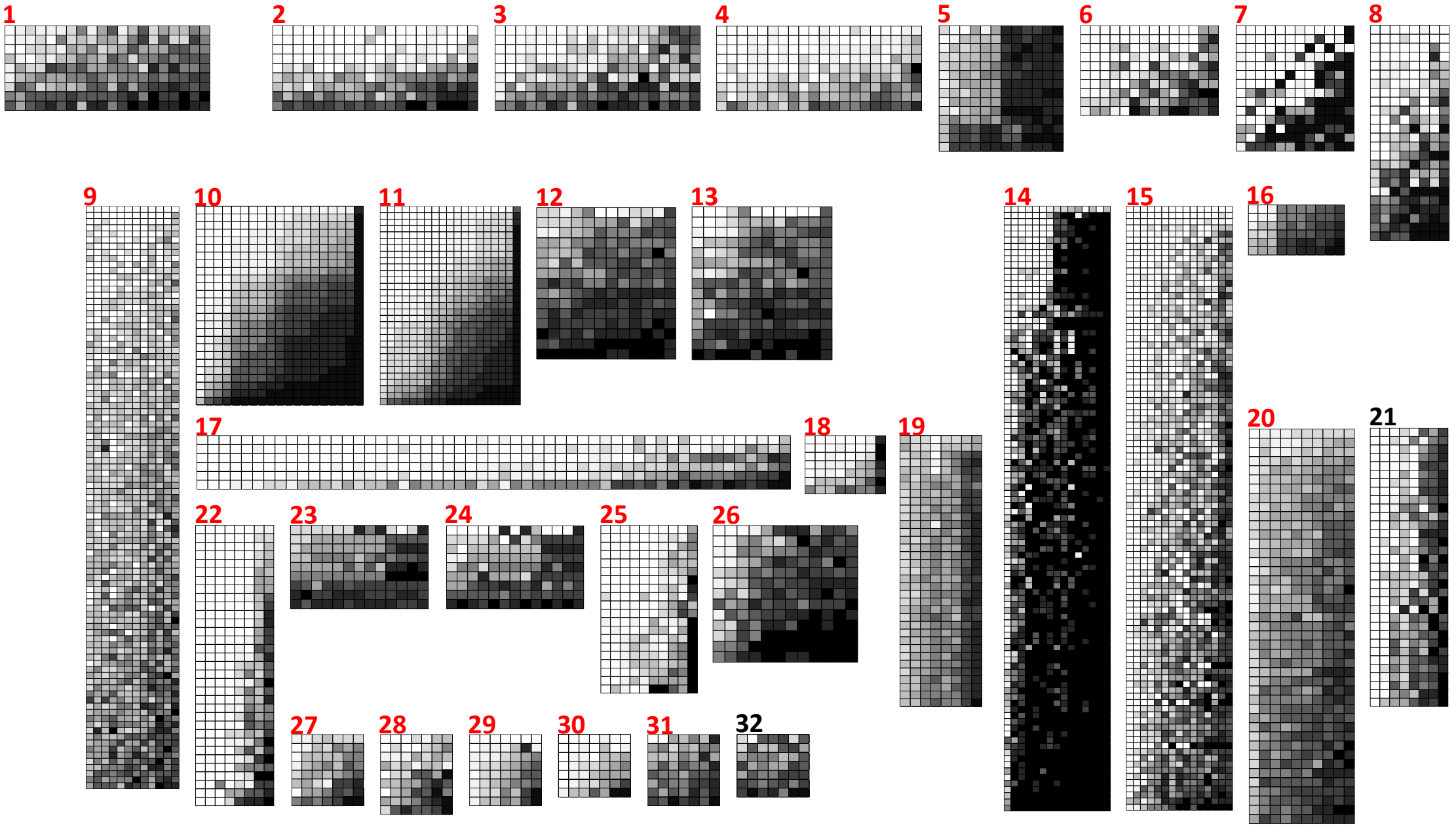
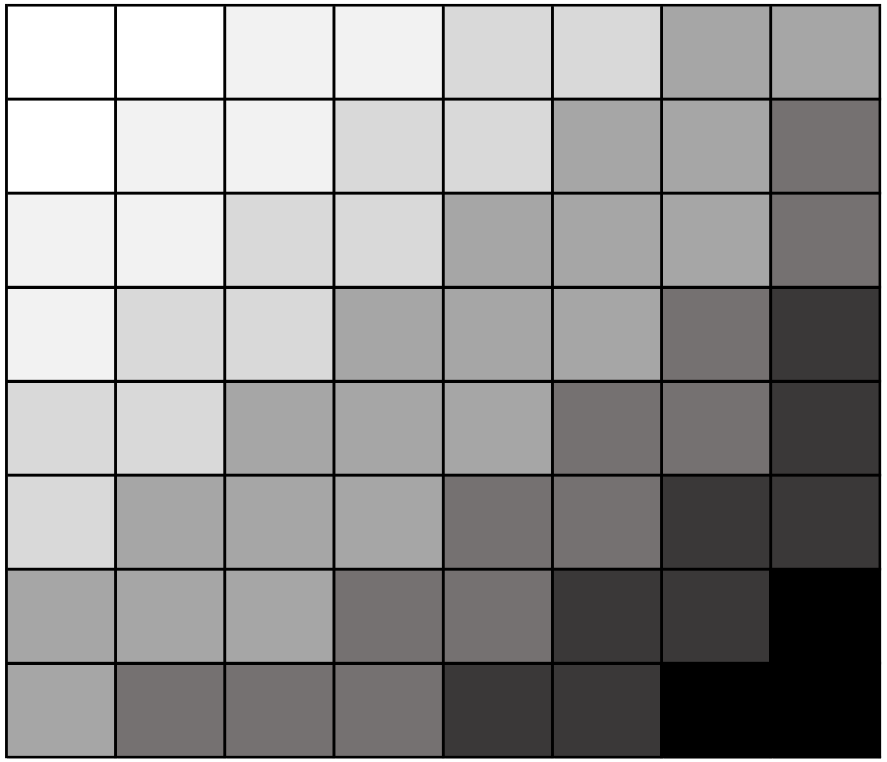
32

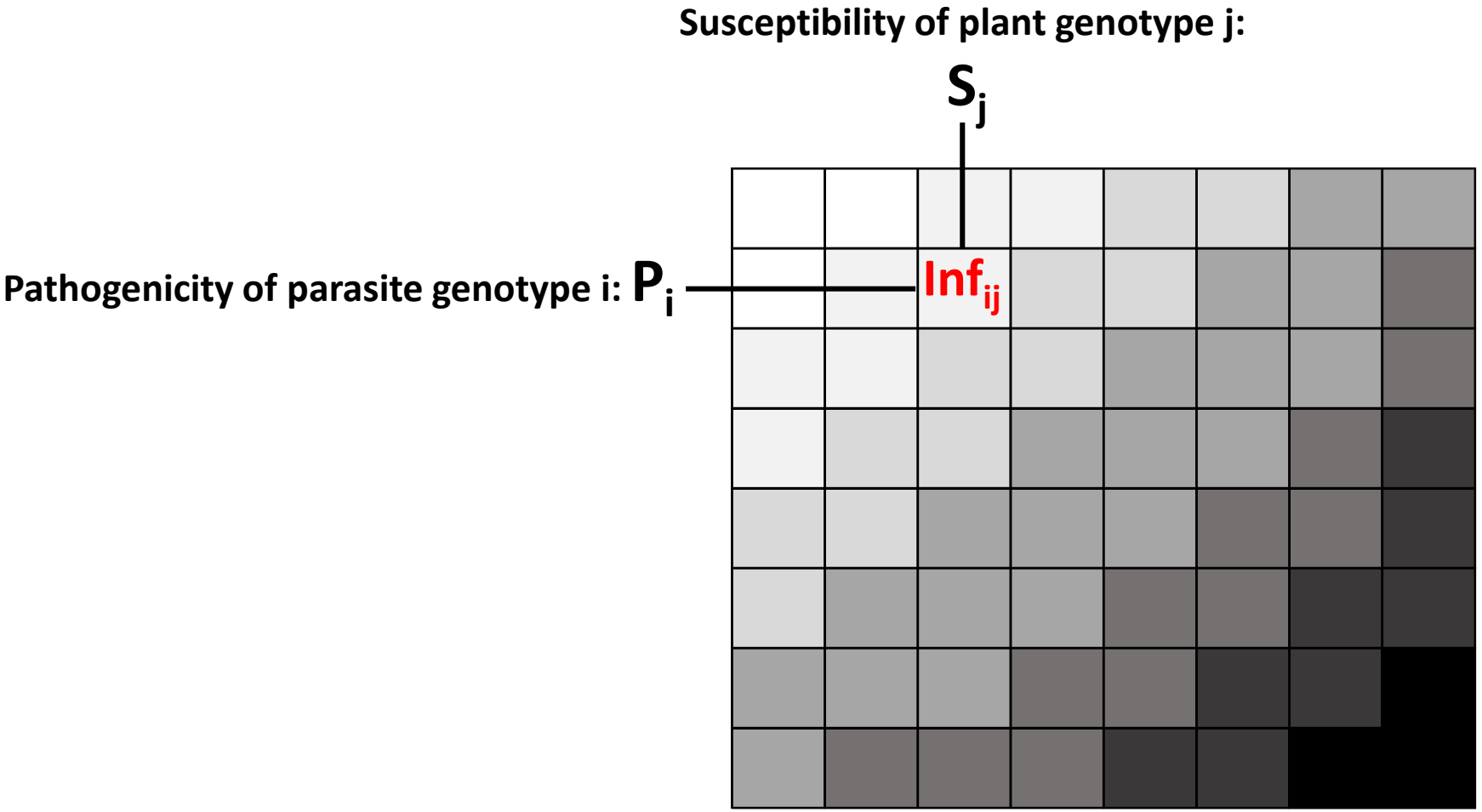


All matrices but two (n°21 and 32) are strongly and significantly nested

Biological interpretation of nestedness: genetics



Biological interpretation of nestedness: genetics



→ Suitability of an « additive » model: Inf_{ij} (infection level) = $P_i \times S_j$

Biological interpretation of nestedness: genetics

Suitability of the additive model

- Model 1 (27 matrices) : Infection ~ parasite **+** plant **+** parasite ***** plant

  $\rightarrow$ Interaction not significant for 5 matrices

  $\rightarrow$ Part of variance explained by interaction ω^2 = 0 to 0.28 (mean 0.11)

- Model 2 (all 32 matrices) : Infection ~ parasite **+** plant

  $\rightarrow$ part of variance explained by model ω^2 = 0.40 to 0.98 (mean 0.69)

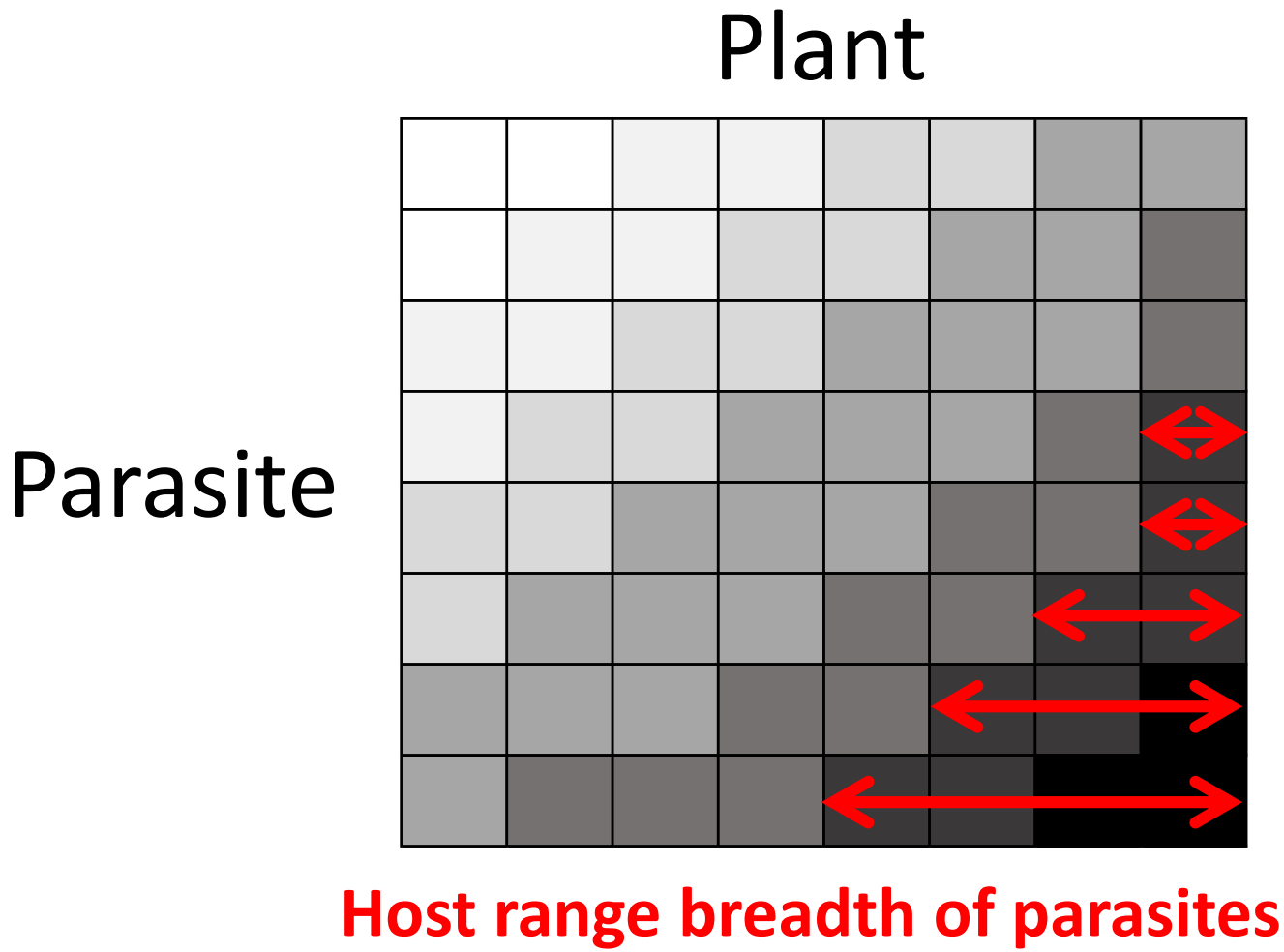
Biological interpretation of nestedness: trade-offs

One could have imagined **trade-offs** between:

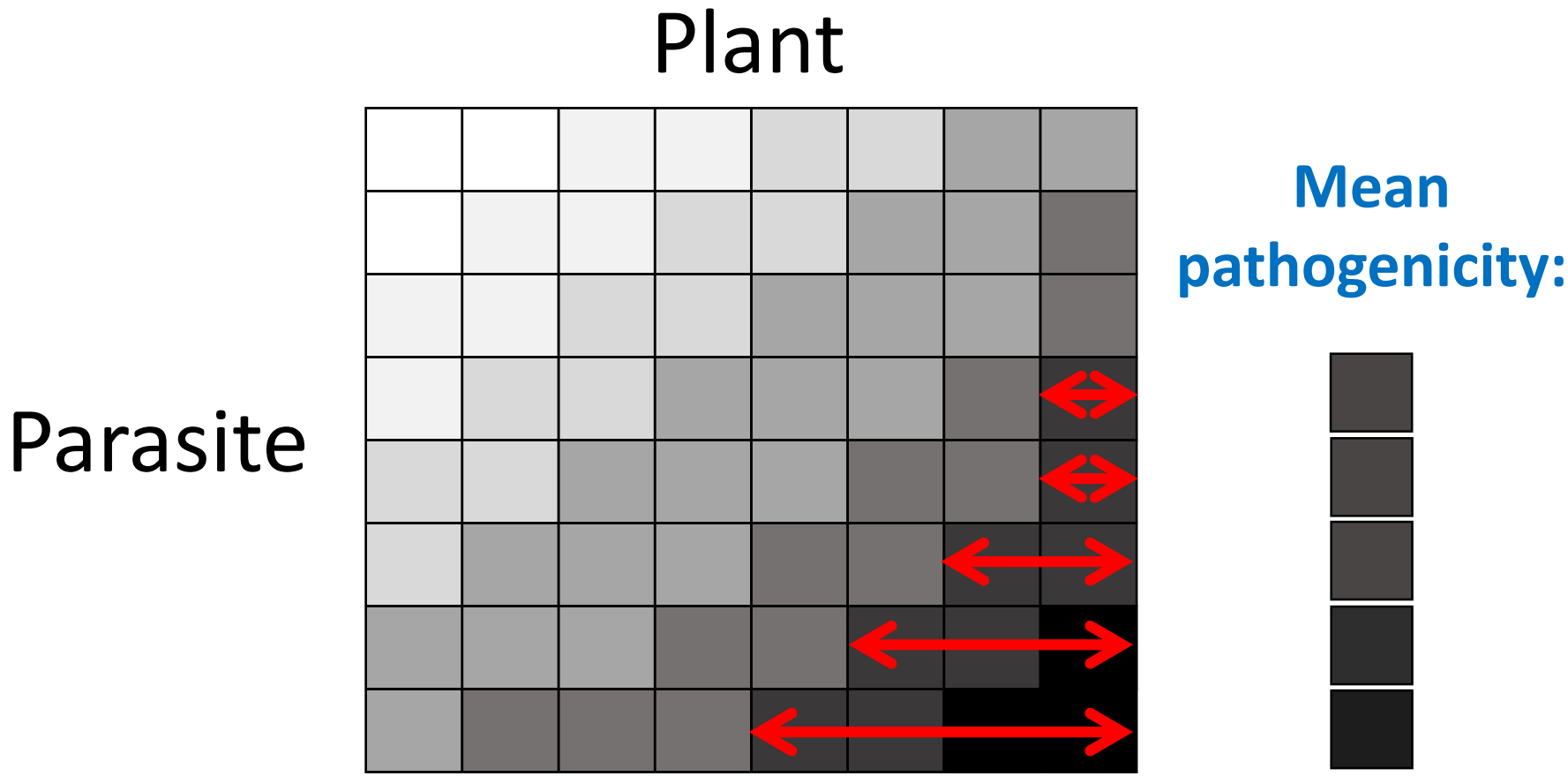
- spectrum and efficiency of resistance among plant genotypes
- host range breadth and pathogenicity among parasite genotypes

… but nestedness suggests the opposite

Biological interpretation of nestedness: trade-offs



Biological interpretation of nestedness: trade-offs



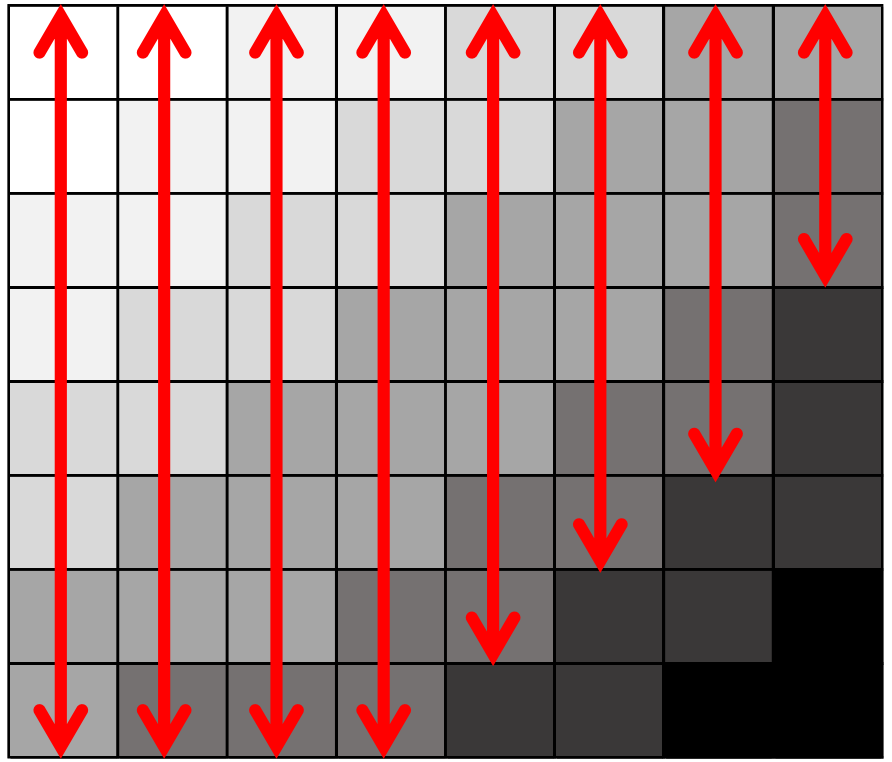
Host range breadth of parasites

is positively correlated to the mean pathogenicity (in hosts)

Biological interpretation of nestedness: trade-offs

Plant

Parasite

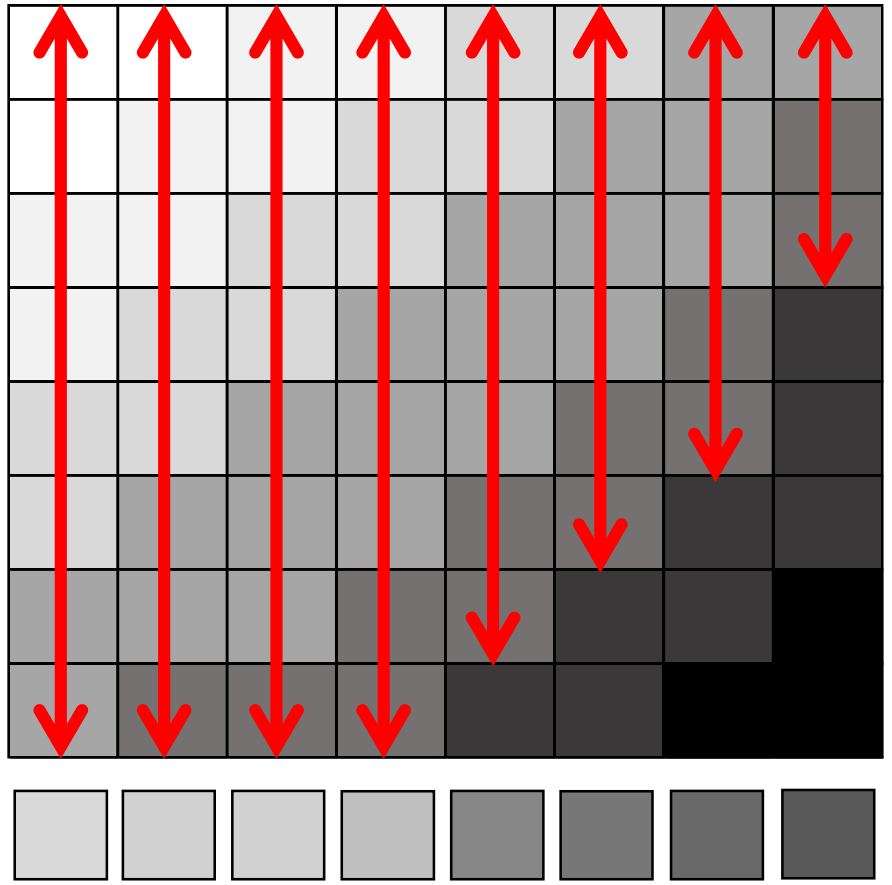


Spectrum of action of plant resistance

Biological interpretation of nestedness: trade-offs

Plant

Parasite



Mean resistance efficiency:

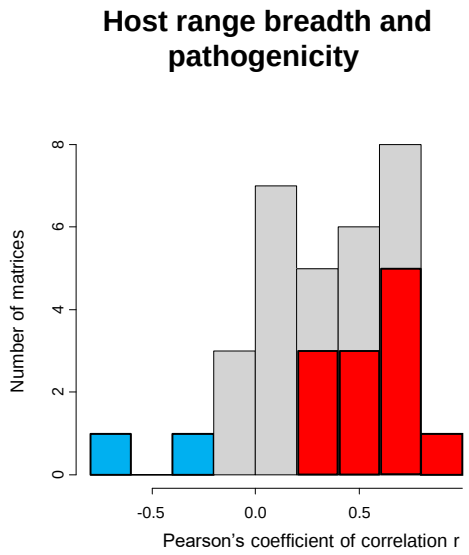
Spectrum of action of plant resistance

is positively correlated to the mean resistance efficiency

Occurrence of trade-offs in plant or parasite genotypes?

Threshold = 30% of maximal infection value

Among parasites



Significantly positive r

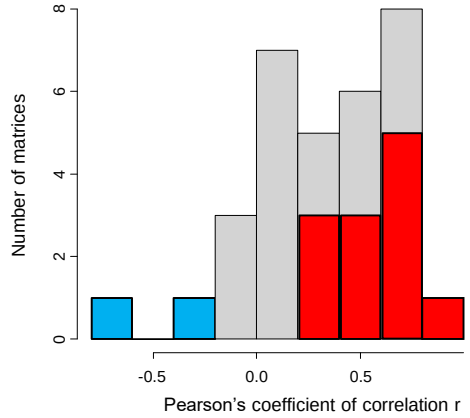
Significantly negative r

Occurrence of trade-offs in plant or parasite genotypes?

Threshold = 30% of maximal infection value

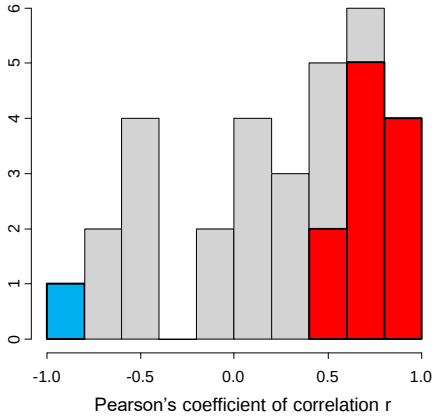
Among parasites

Host range breadth and pathogenicity



Among plants

Spectrum and efficiency of resistance

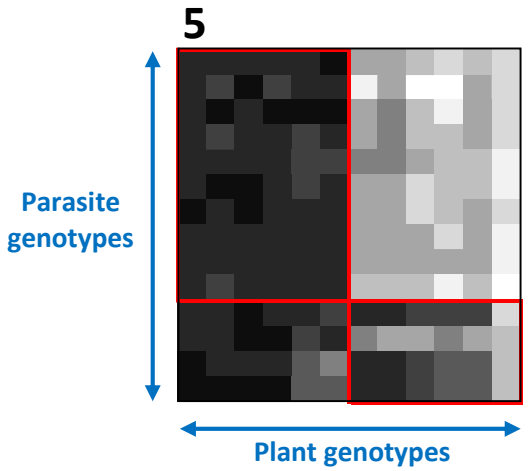


Significantly positive r

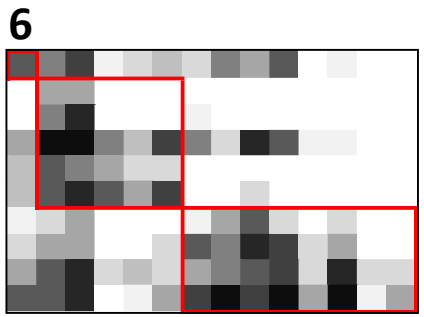
Significantly negative r

Modularity results

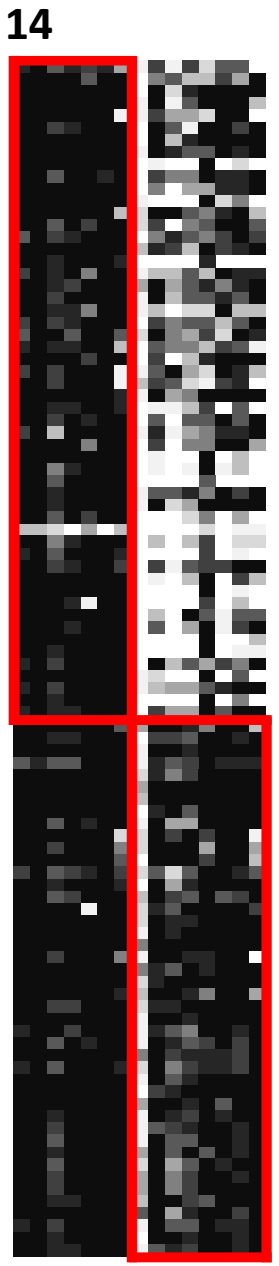
- Six matrices show weak but significant modularity (2 or 3 modules)



Barley - *Puccinia hordei*



Apple tree - *Venturia inaequalis*



Wheat- *Zymoseptoria tritici*

- Modules linked to the presence of resistance genes / QTLs

(3 of 6 matrices)

Messages à rapporter à la maison

- Strong nestedness for almost all matrices (30/32) / weak and rare modularity (6/32)

  $\rightarrow$ Reject the "matching allele" model

  $\rightarrow$ Possible models: additive model; variations on the "gene for gene" model

Messages à rapporter à la maison

- Strong nestedness for almost all matrices (30/32) / weak and rare modularity (6/32)

  → Reject the "matching allele"

  → Possible models: additive model; variations on the "gene for gene" model

- Rare trade-off between the level of resistance and its spectrum of action (plant)

- Rare trade-off between the level of pathogenicity and host range breadth (parasite)

  → Consequences in terms of management of quantitative resistance

Contributors

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