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.

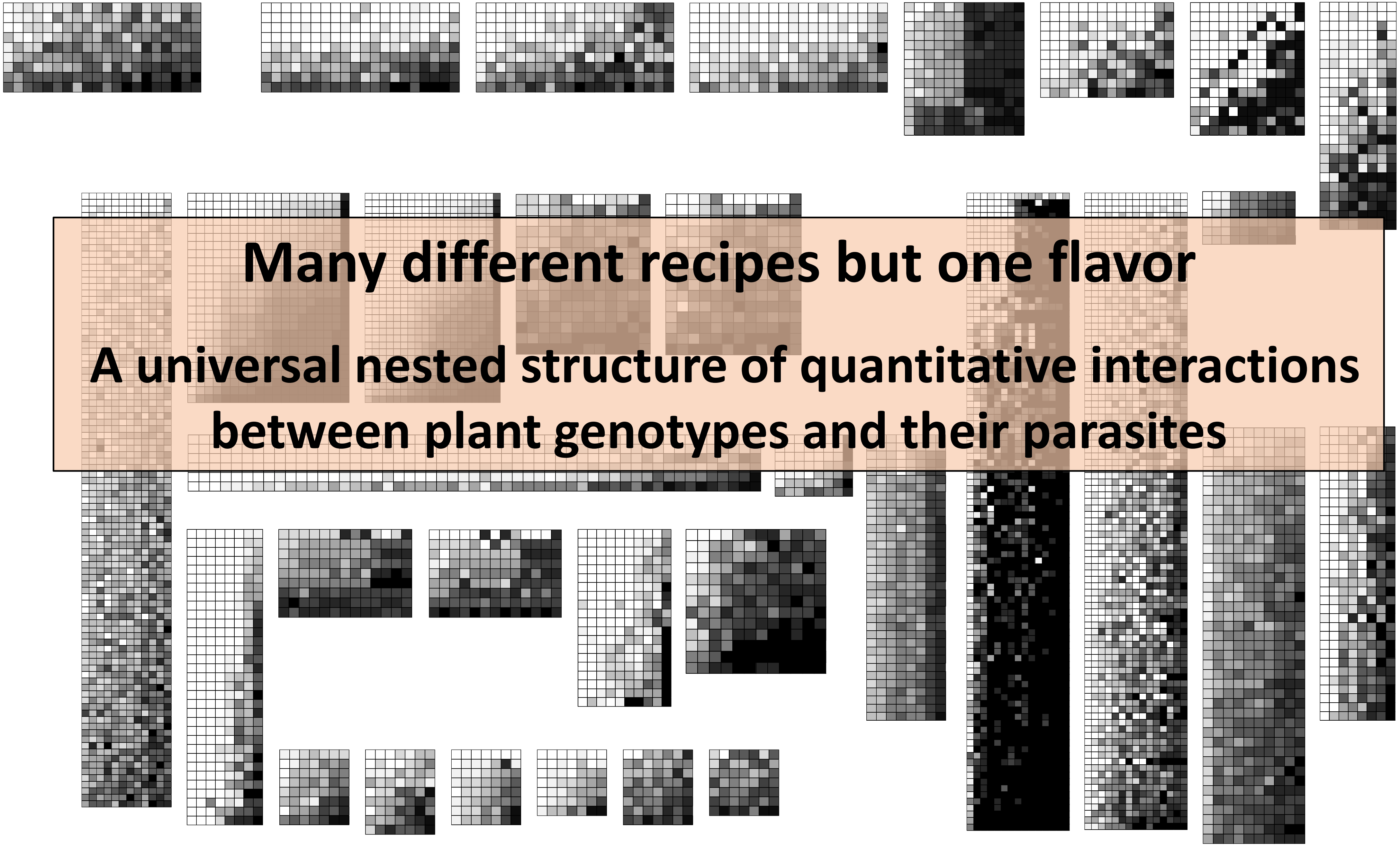
To cite this version:

Benoît Moury, Jean-Marc Audergon, Sylvie Baudracco-Arnas, Safa Ben Krima, François Bertrand, et al.. Une structure emboîtée universelle pour les interactions quantitatives entre les plantes et leurs parasites ?. Réunion annuelle du réseau E3GP3, Dec 2021, Visioconférence, France. hal-03553078

HAL Id: hal-03553078
https://hal.inrae.fr/hal-03553078
Submitted on 3 Feb 2022

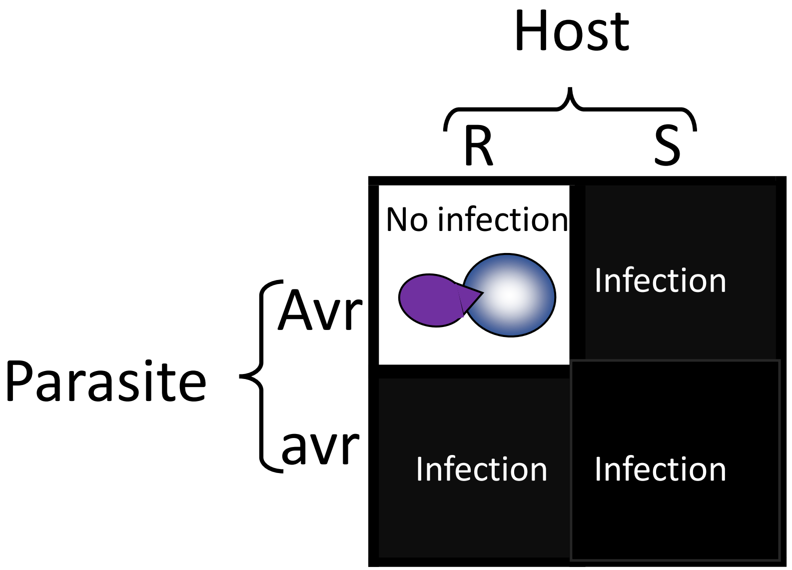
Many different recipes but one flavor

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



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

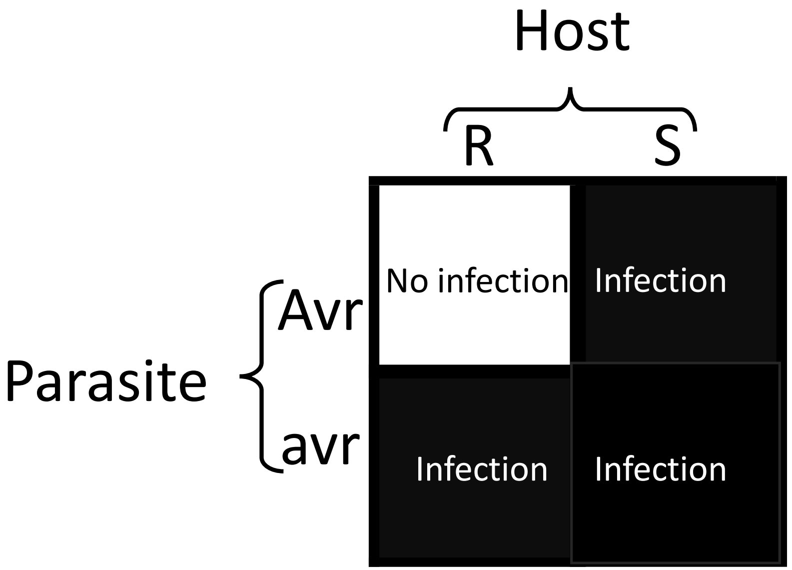
Qualitative plant immunity: two main genetic and evolutionary models



		Host	
		R	S
Parasite	Avr	No infection	Infection
	avr	Infection	Infection

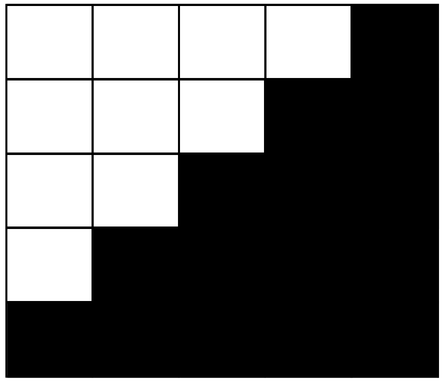
Gene-for-gene

Qualitative plant immunity: two main genetic and evolutionary models



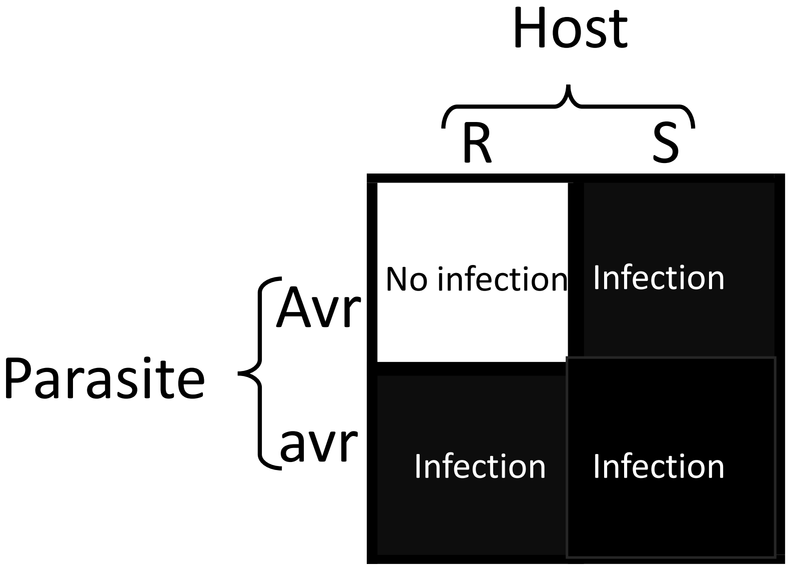
Parasite \ Host	R	S
Avr	No infection	Infection
avr	Infection	Infection

Gene-for-gene



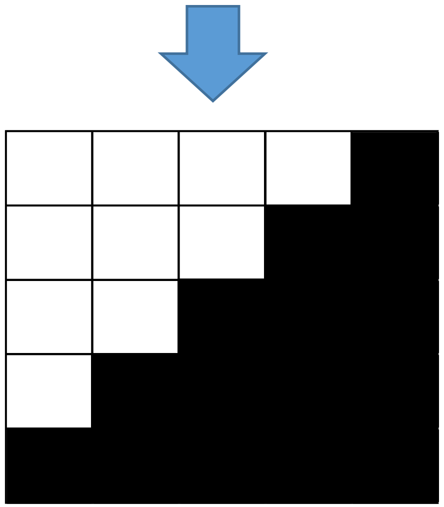
Nested structure

Qualitative plant immunity: two main genetic and evolutionary models

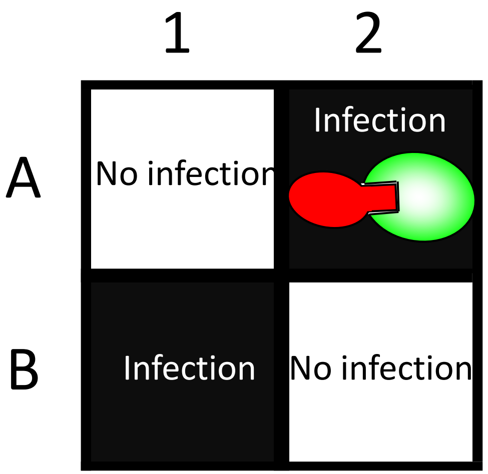


		Host: R	Host: S
Parasite	Avr	No infection	Infection
	avr	Infection	Infection

Gene-for-gene

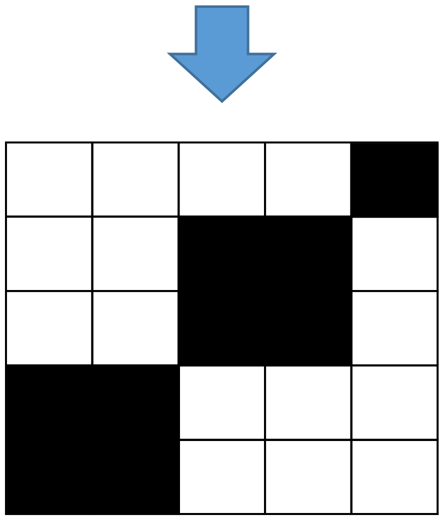


Nested structure



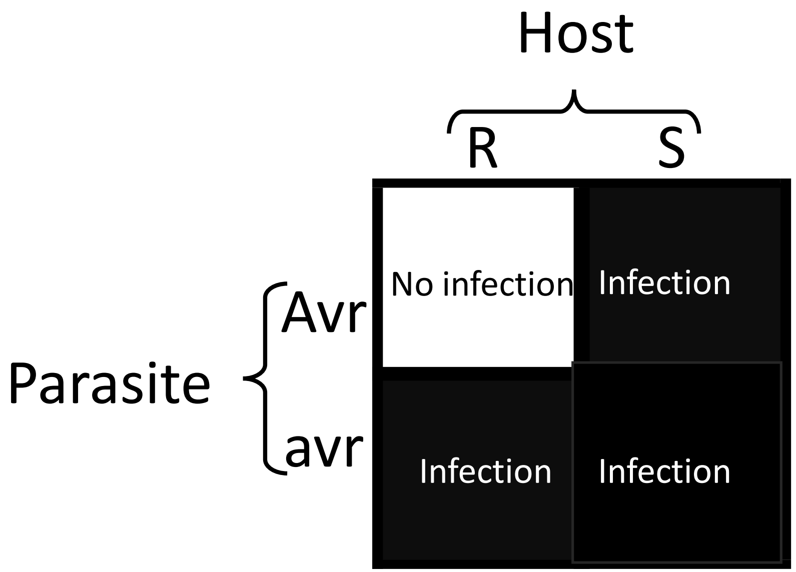
	1	2
A	No infection	Infection
B	Infection	No infection

Matching allele



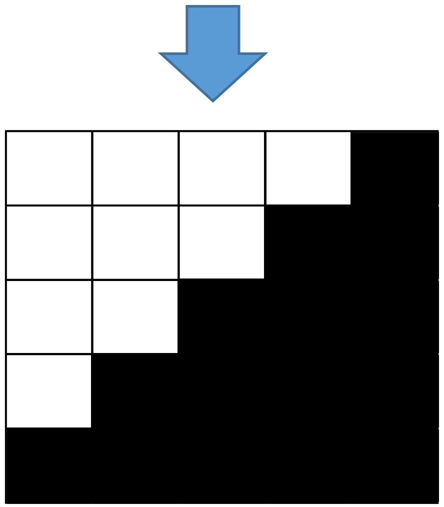
Modular structure

Qualitative plant immunity: two main genetic and evolutionary models

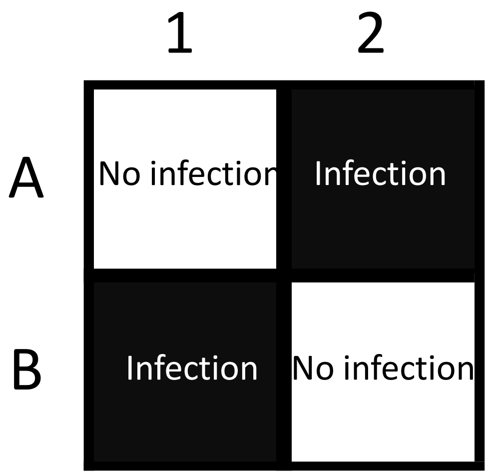


		Host: R	Host: S
Parasite	Avr	No infection	Infection
	avr	Infection	Infection

Gene-for-gene



Nested structure



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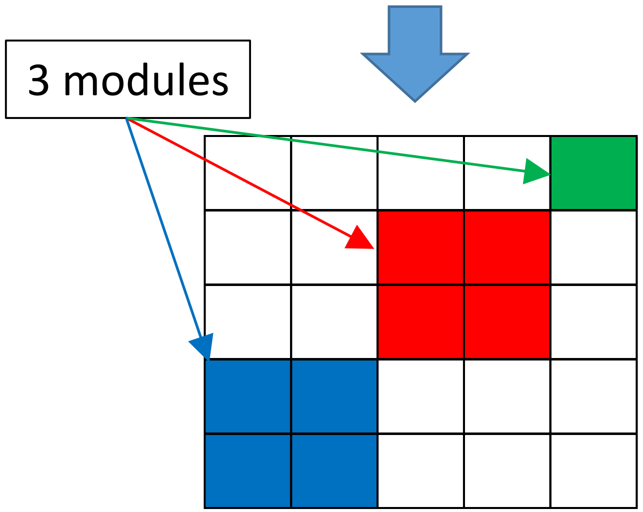
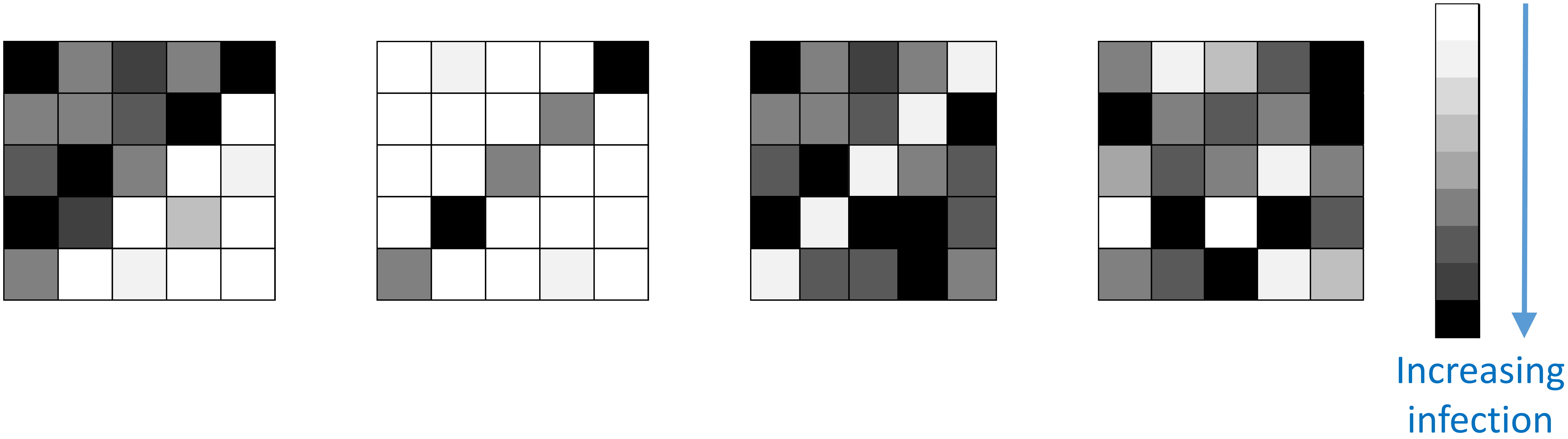
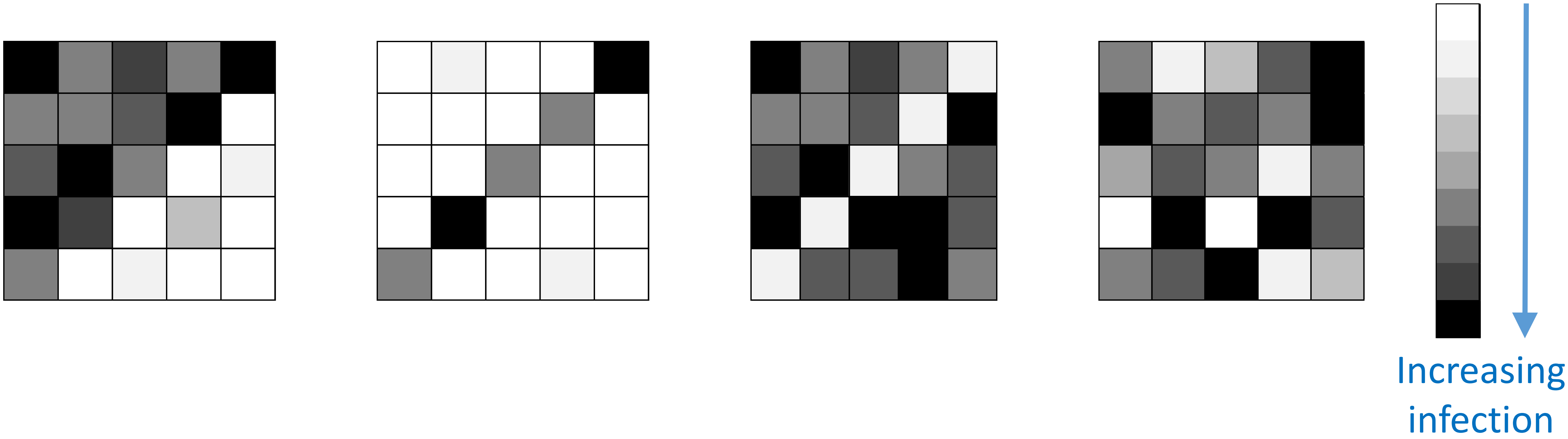


Modular structure

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



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



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

Estimating the degrees of nestedness/modularity and testing their significance

Infection trait values

0,27	0,69	0,36	0,47	0,15
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0	1,26	2,51	0,84	0,09
0,78	1	1,77	0,99	1,03

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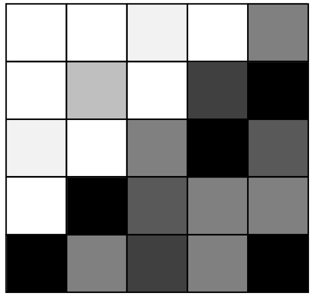
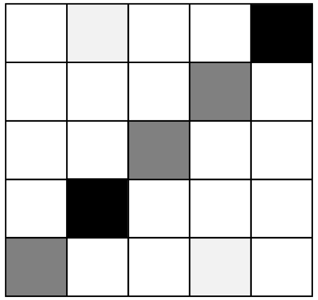
Nestedness/modularity value (*X*)
of the experimental matrix

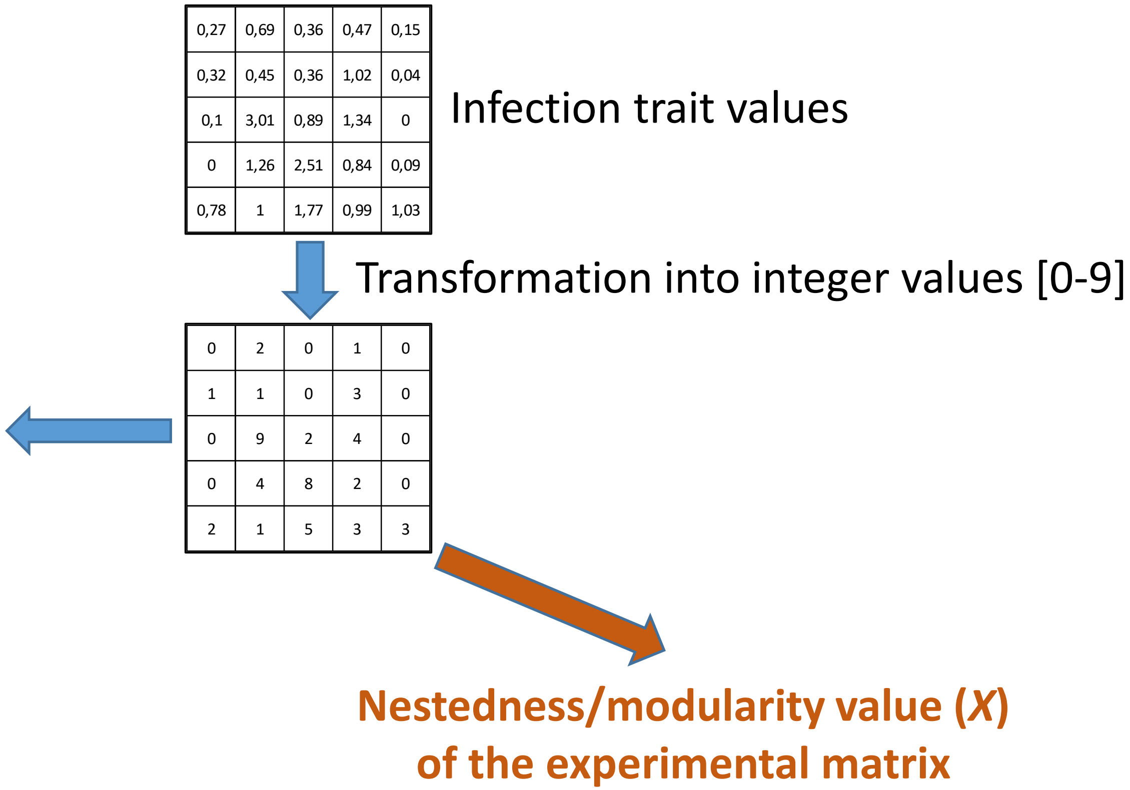


High nestedness



High modularity

Estimating the degrees of nestedness/modularity and testing their significance



0,27	0,69	0,36	0,47	0,15
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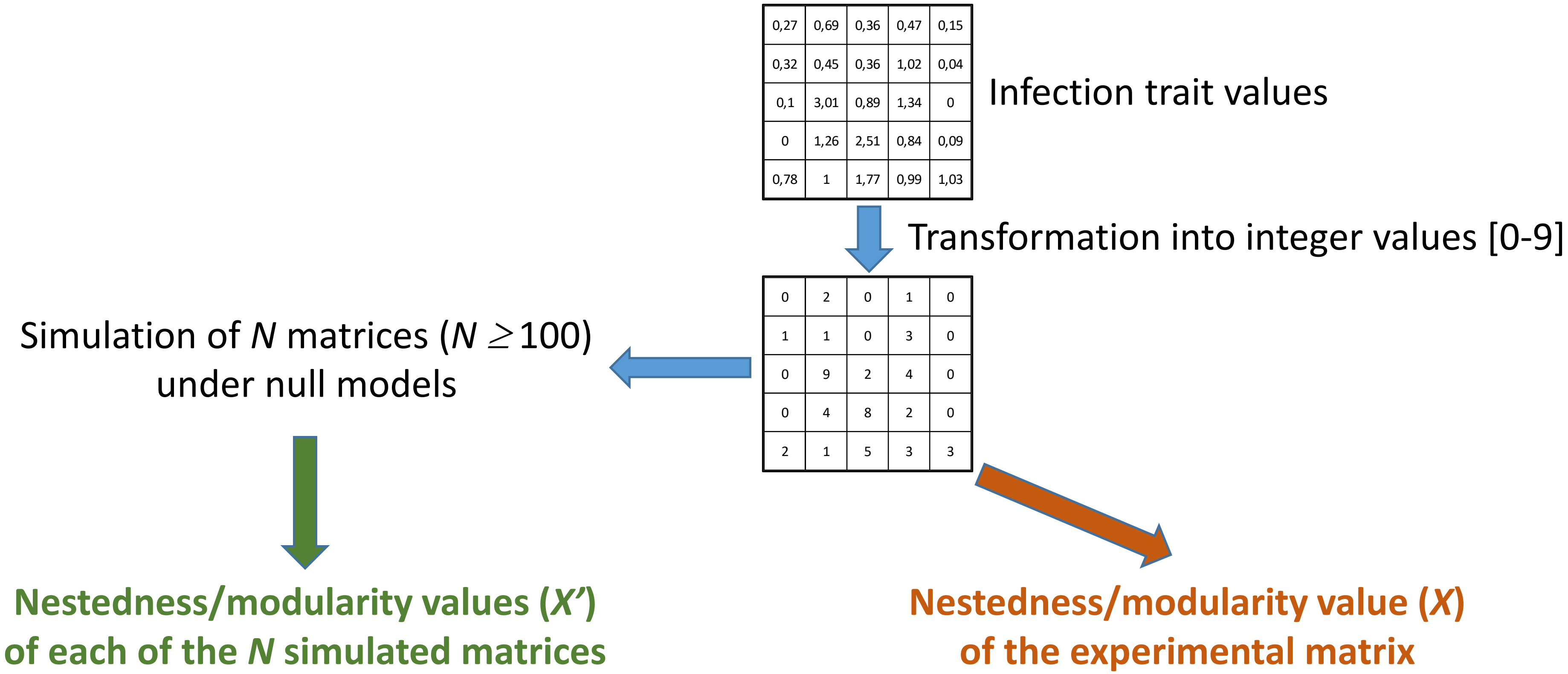
2	1	5	3	3

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

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

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
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Infection trait values

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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**

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
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Infection trait values

Transformation into integer values [0-9]

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0	9	2	4	0
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Simulation of *N* matrices ($N \geq 100$)
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**Nestedness/modularity values (*X'*)
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**Nestedness/modularity value (*X*)
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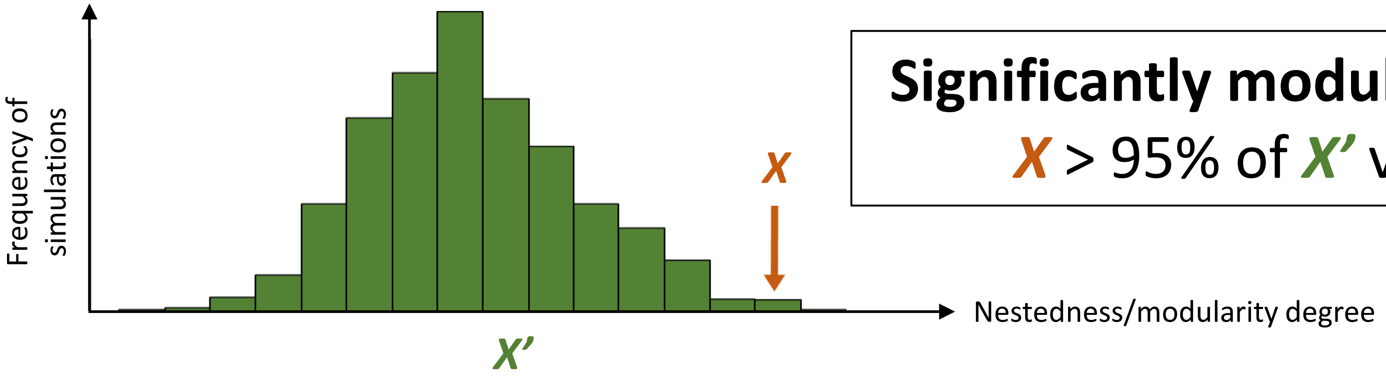
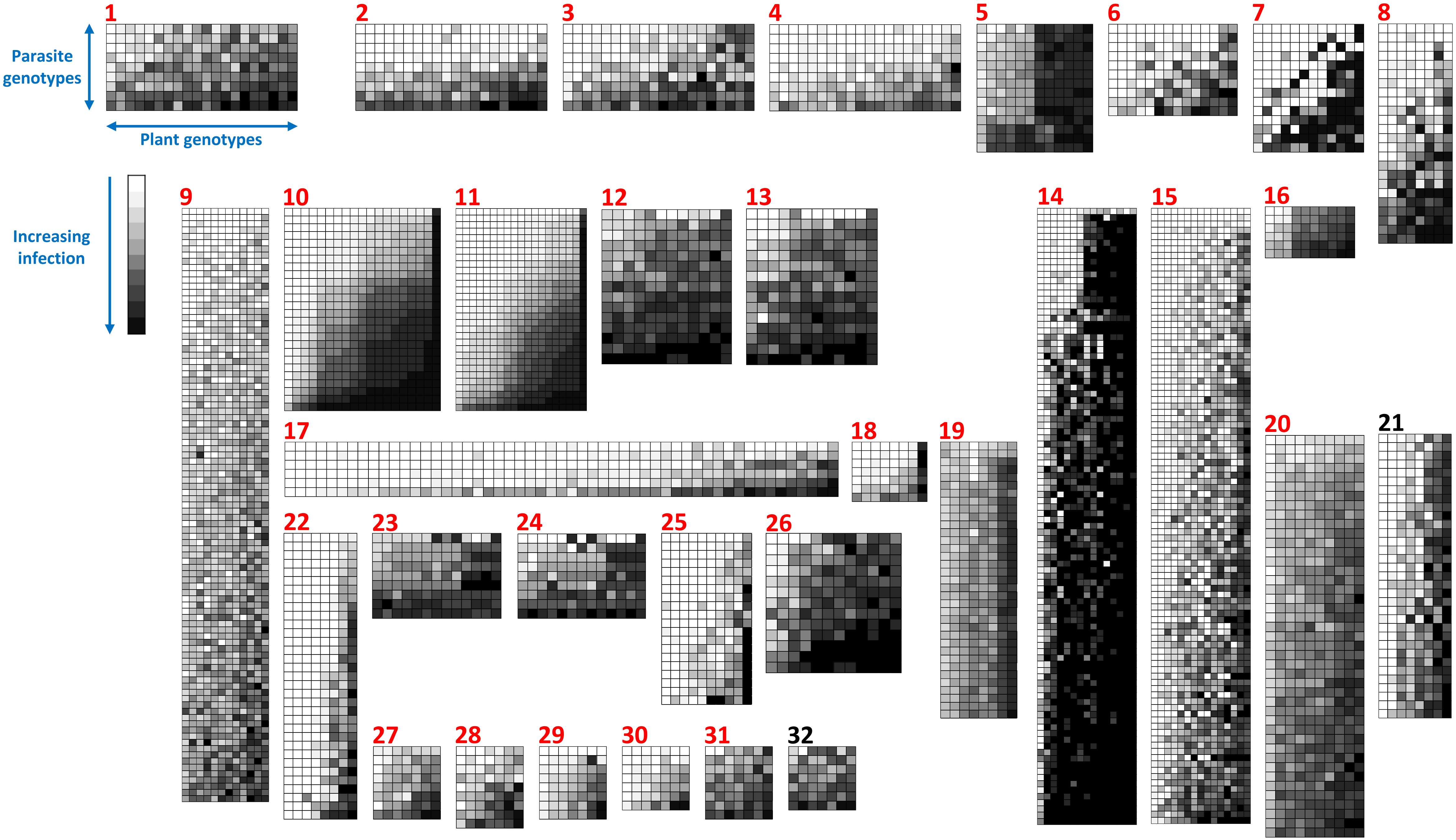


Significantly modular matrix:
X > 95% of *X'* values

Nestedness results


Parasite genotypes
Plant genotypes
Increasing infection
1
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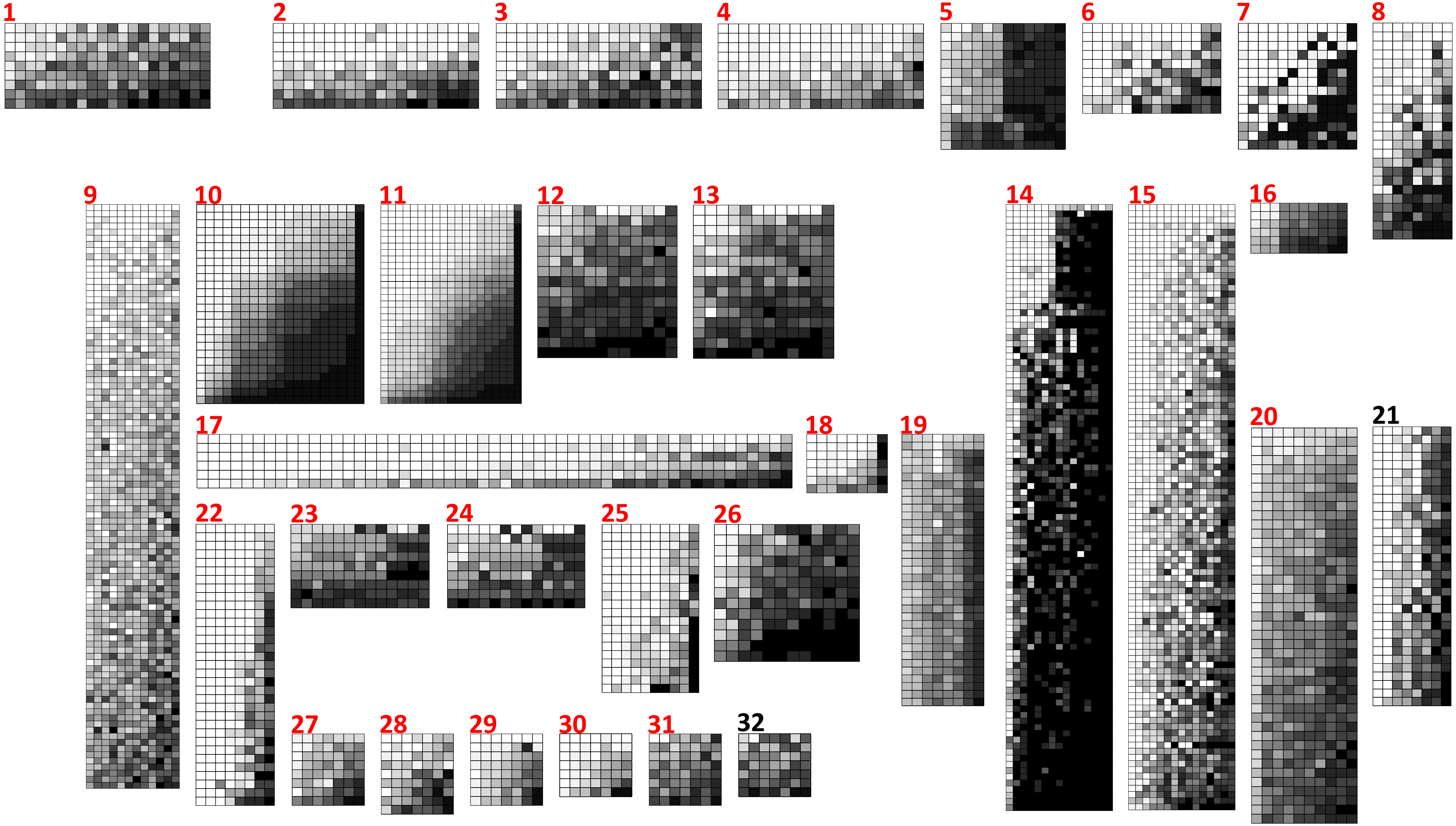
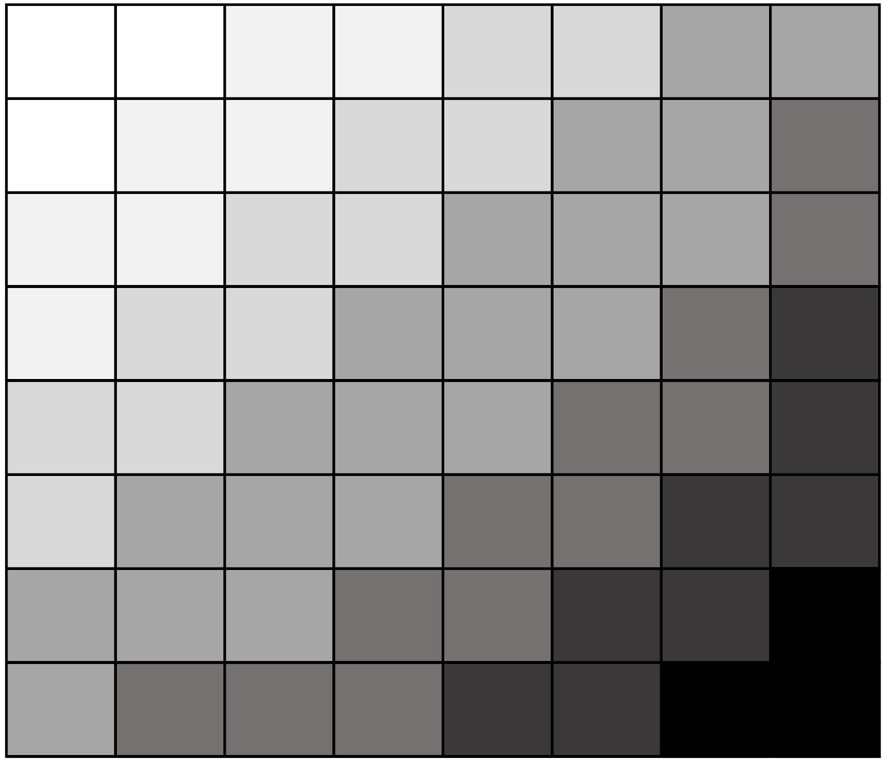
32

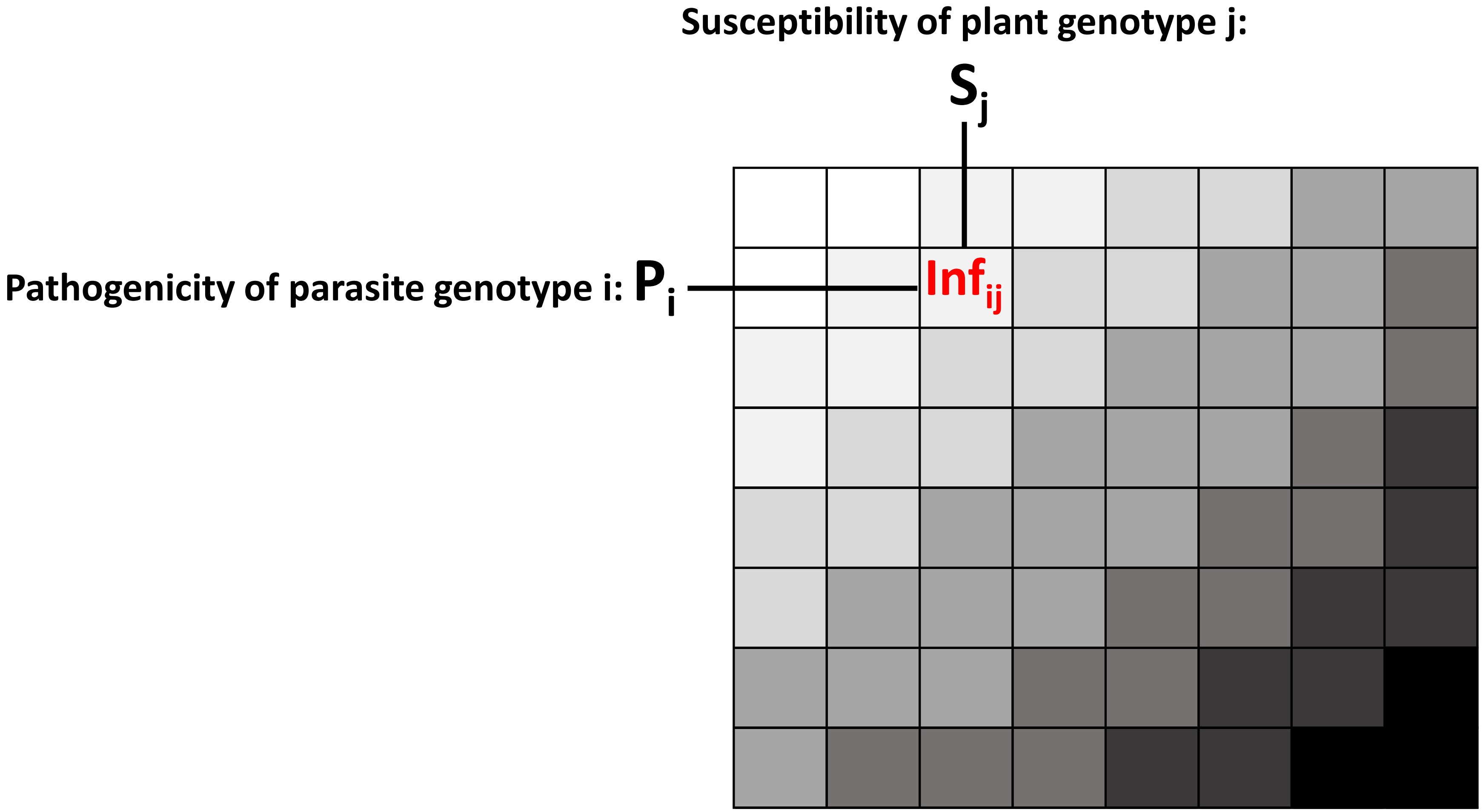


All matrices but two (n°21 and 32) are strongly and significantly nested

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

  → Interaction not significant for 5 matrices

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

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

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

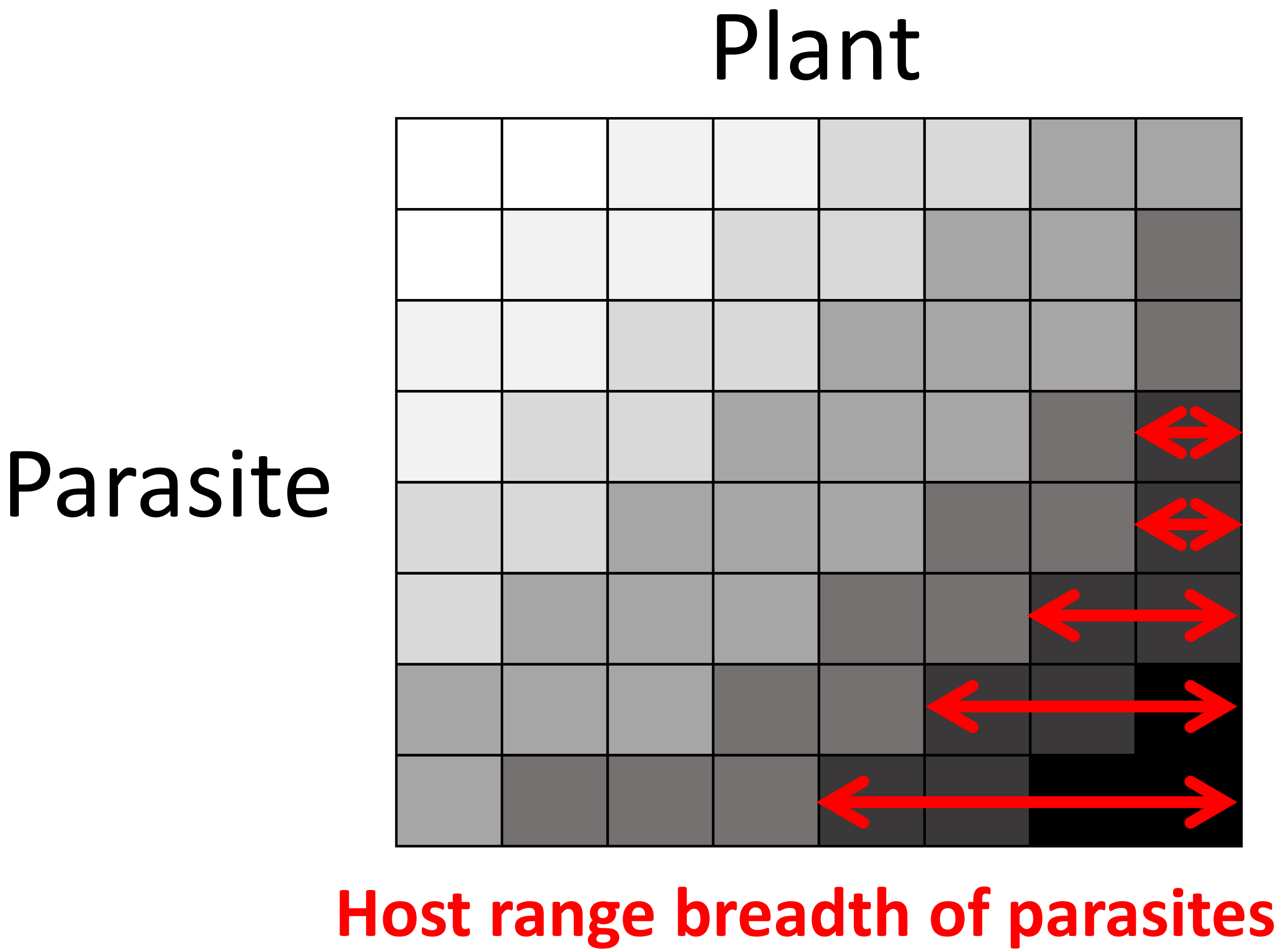
Biological interpretation of nestedness: trade-offs

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

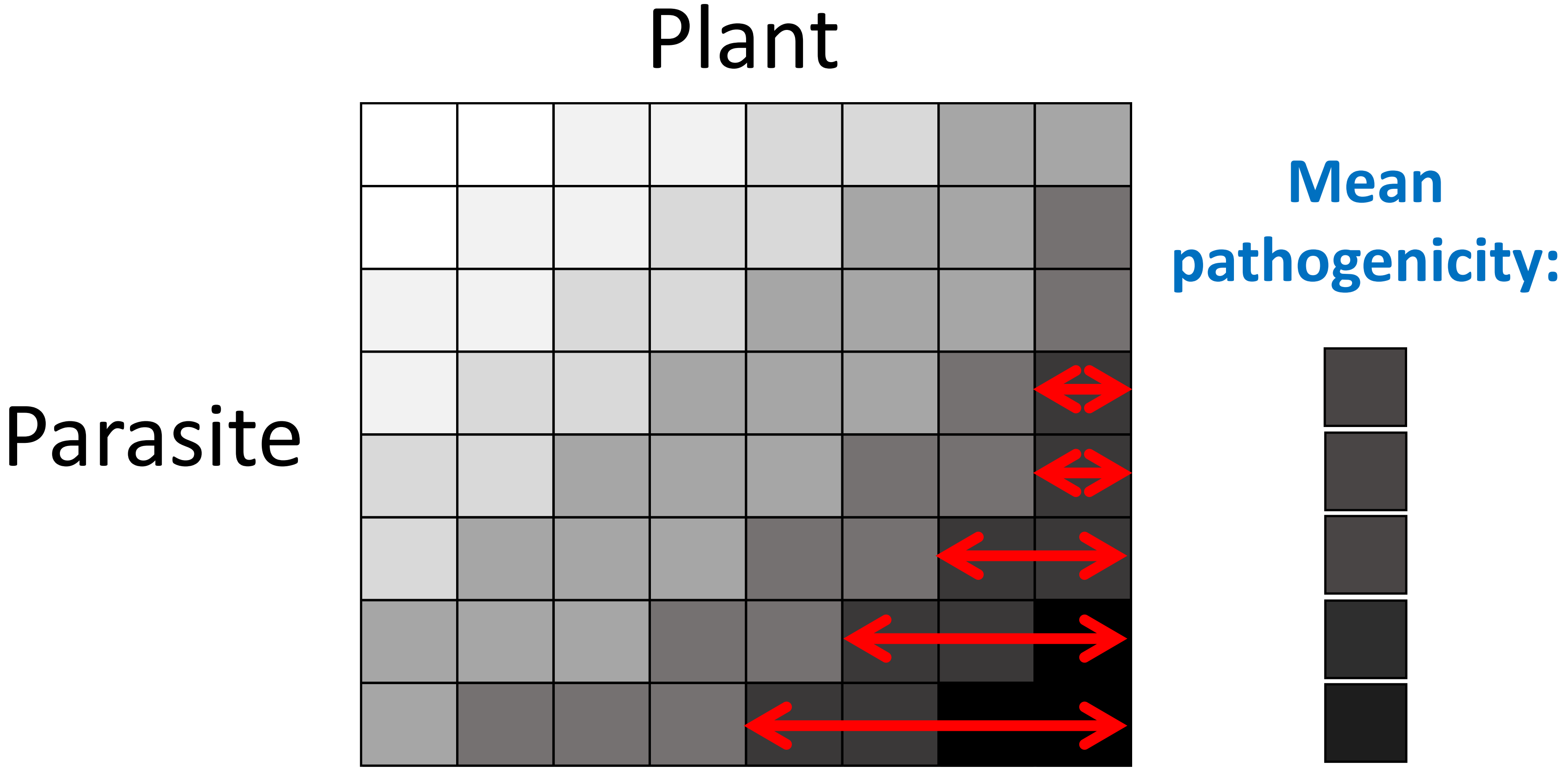
- spectrum and efficiency of resistance among plant genotypes
- host range breadth and pathogenicity among parasite genotypes

… but nestedness suggests the opposite

Biological interpretation of nestedness: trade-offs



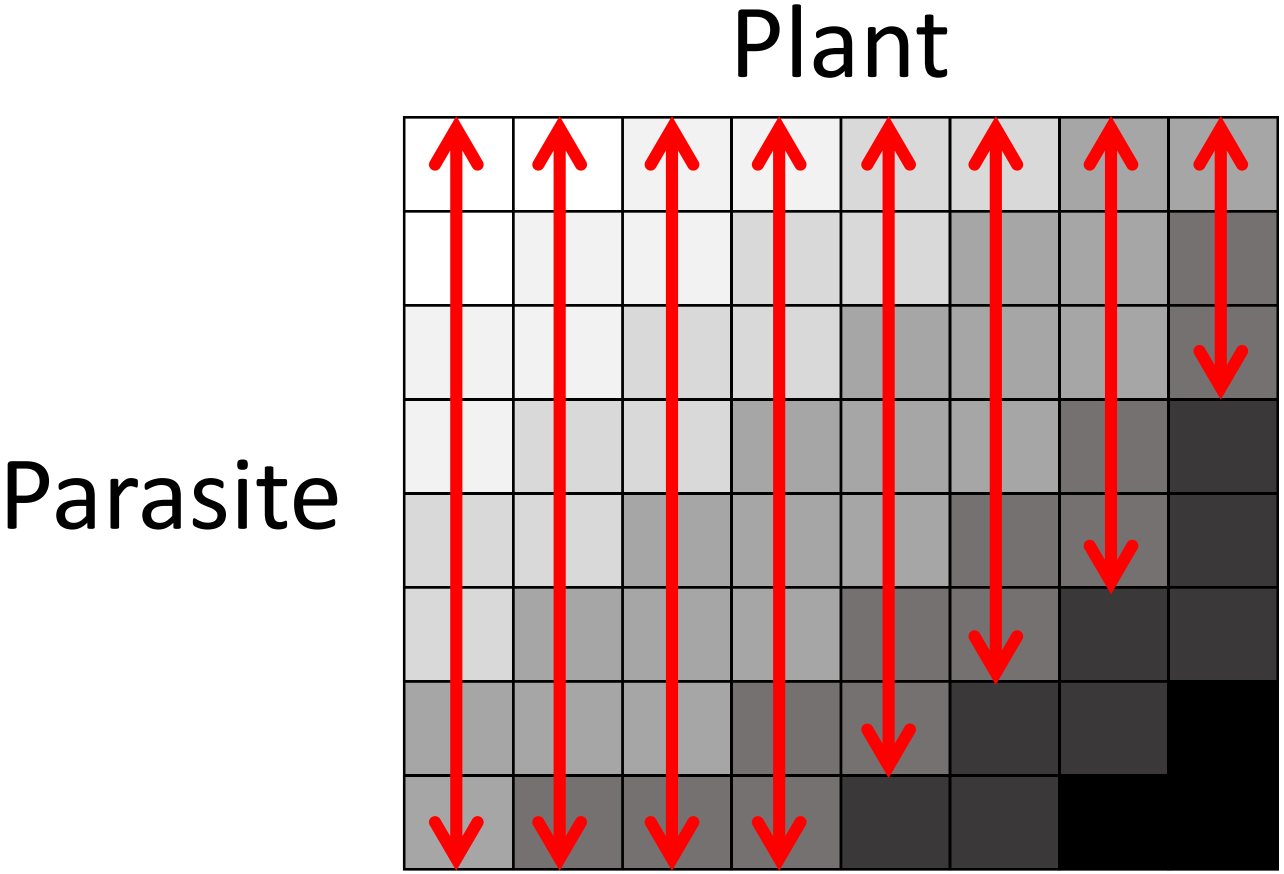
Biological interpretation of nestedness: trade-offs



Host range breadth of parasites

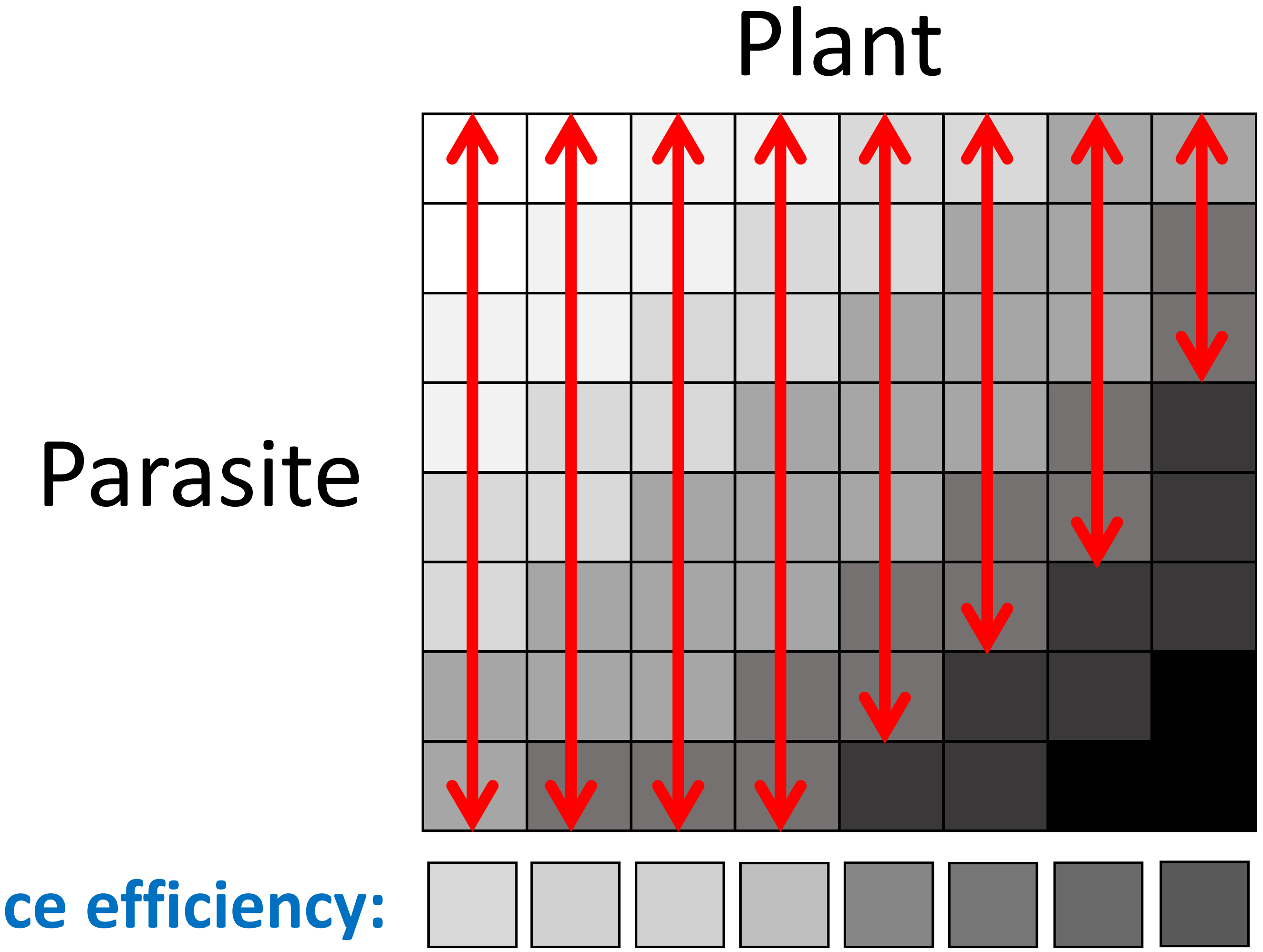
is positively correlated to the mean pathogenicity (in hosts)

Biological interpretation of nestedness: trade-offs



Spectrum of action of plant resistance

Biological interpretation of nestedness: trade-offs



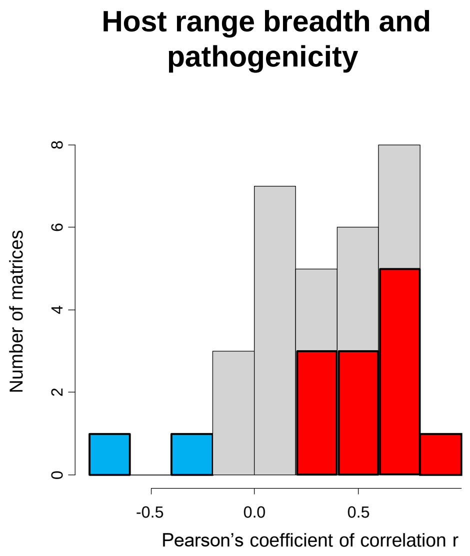
Mean resistance efficiency:

Spectrum of action of plant resistance

is positively correlated to the mean resistance efficiency

Occurrence of trade-offs in plant or parasite genotypes?

Among parasites



Threshold = 30% of maximal infection value

🟥 Significantly positive r

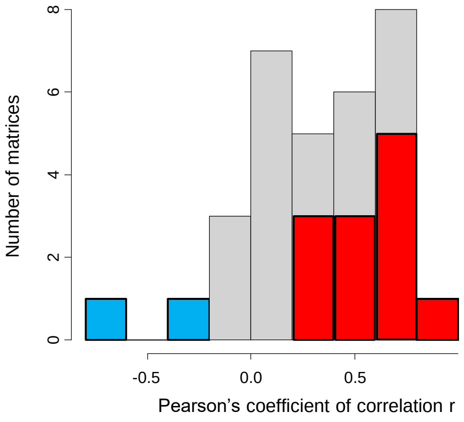
🟦 Significantly negative r

Occurrence of trade-offs in plant or parasite genotypes?

Threshold = 30% of maximal infection value

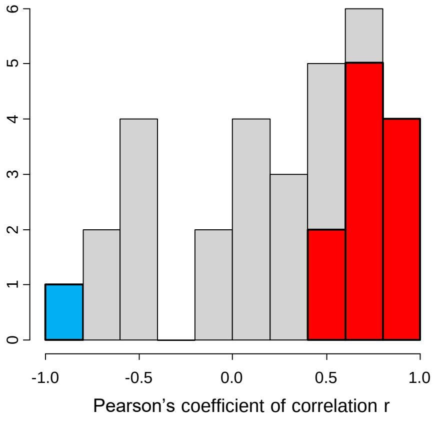
Among parasites

Host range breadth and pathogenicity



Among plants

Spectrum and efficiency of resistance

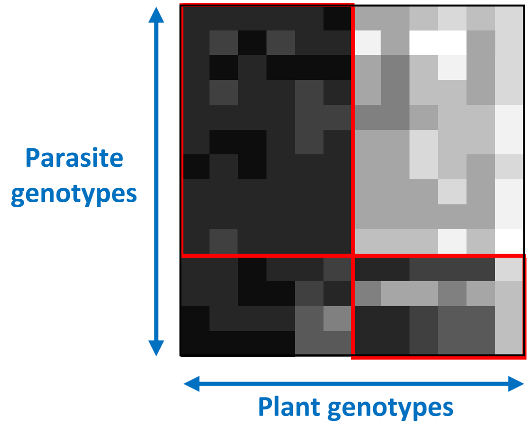


🟥 Significantly positive r

🟦 Significantly negative r

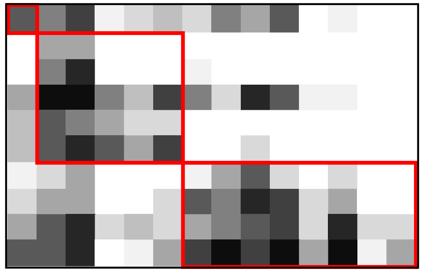
Modularity results

5



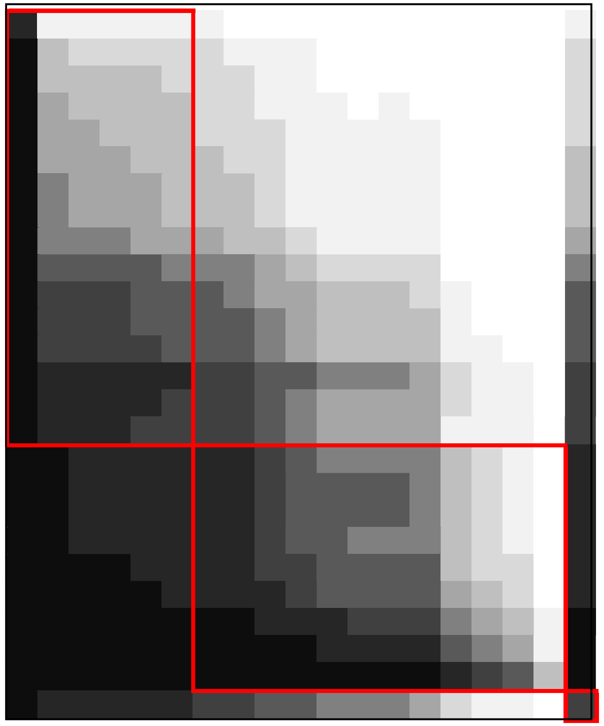
Barley - *Puccinia hordei*

6



Apple - *Venturia inaequalis*

10



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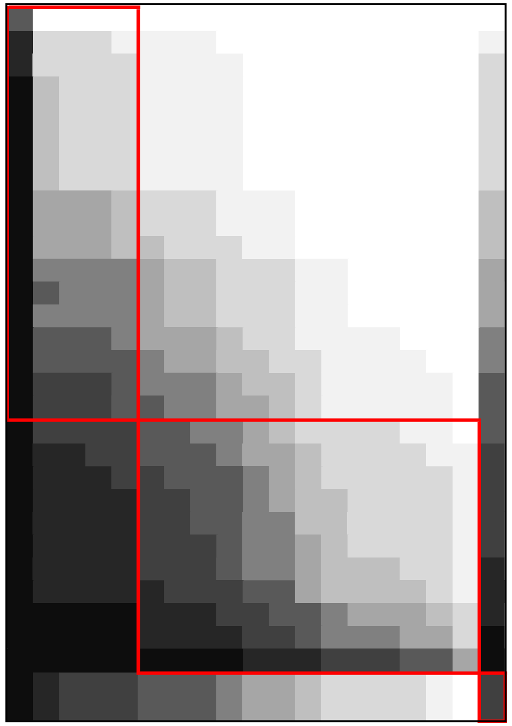
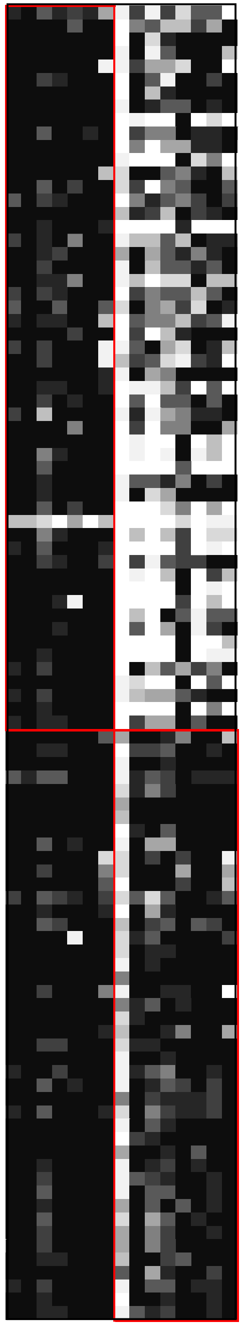
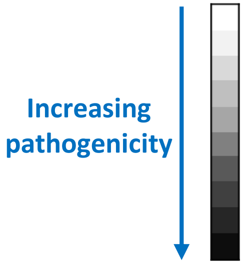


Melon - *Podosphaera xanthii*

14



Wheat - *Zymoseptoria tritici*

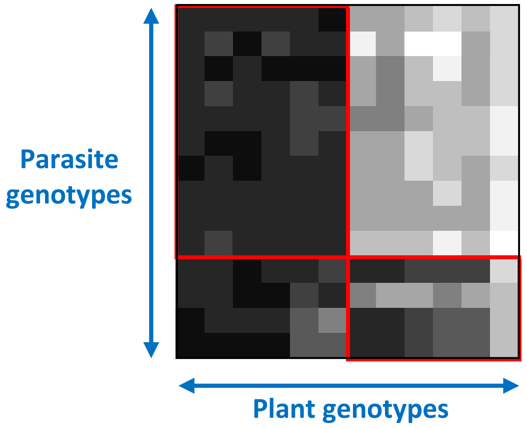


17b

Pepper - *Phytophthora capsici*

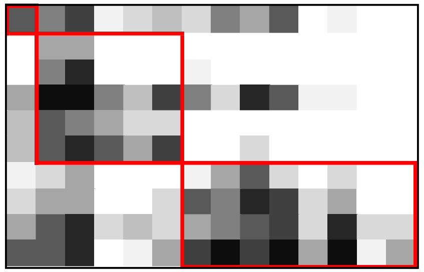
- Six matrices show weak but significant modularity (2 or 3 modules)

5



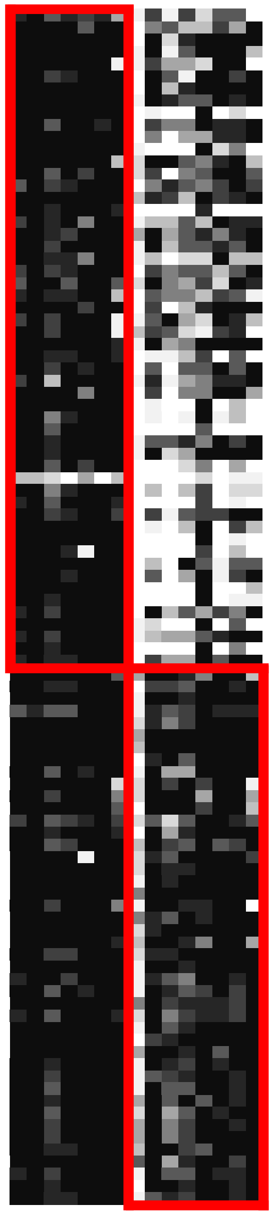
Barley - *Puccinia hordei*

6



Apple tree -
Venturia inaequalis

14



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)

  → Reject the "matching allele" model

  → 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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