

Genetic diversity and functional polymorphism of avirulent genes of *Phytophthora infestans* in China

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Outline

I. Research substructure

II. Current interests

III. Further work



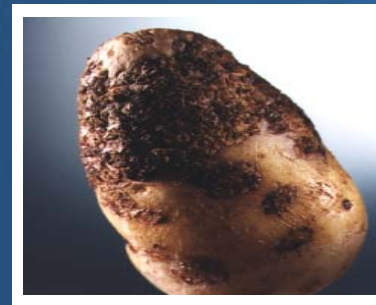
I. Research substructure

- Under Biotechnology Group, IVF-CAAS
- Supported by National network of *P.infestans* and International collaborations
- Research materials and methods:
 - 100 isolate collection from main potato areas
 - Storage: rye medium plate, nitrogen



II. Current interests

- Background:
 - R-gene stacking breeding in China
 - Chinese *P.infestans* population previously used
 - lack of population genetics research in China





Current interests

1. Genetic diversity and functional polymorphism of avirulent genes
2. Mathematical simulation of R-AVR interaction in the field



II. Current interests - avirulent genes

INF1, Avr3a, Avrblb1, Avrblb2

Isolates from Heilongjiang, Inner Mongolia, Fujian

Avr3a:

1. Chinese isolates: virulent gene, very conserved;

2. 99018 & 428-2: unique SNP, but...

3. 82001: heterozygous, race

Avr3a

		83	239	310	363	370	416
DNA	AVR3a	C	A	T	T	C	A
	avr3a	C	G	G	T	C	C
	Chinese	T	G	G	T	C	C
	99018	T	A/G	T/G	T/C	C/G	C
	428-2	T	G	G	T/C	C/G	C
	82001	T	A/G	T/G	T	C	C
Protein	AVR3a	L	K	I	L	R	L
	avr3a	L	E	M	L	R	M
	Chinese	L	E	M	L	R	M
	99018	L	K/E	I/M	L	R/G	M
	428-2	L	E	M	L	R/G	M
	82001 ?	L	K/E	I/M	L	R	M



II. Current interests - avirulent genes

AVRblb1 (RB)

ipiO1 & 2: linked

Unique SNPs

	0	0	0	0	1	1	1	1	1	1	1	1	2	2	2	2
	1	2	3	7	0	4	7	7	8	9	9	9	0	0	1	1
	8	9	4	7	2	2	4	9	4	3	7	9	1	6	0	3
ipiO1	C	T	T	A	A	T	G	C	C	A	T	C	T	G	C	A
ipiO2	A	T	T	A	A	T	G	C	C	A	T	C	T	G	C	A
Chinese	C	T	T	A	A	T	G	C	C	A	T	C	T	G	C	A
H30P04	C	TG	T	AG	AG	TG	G	C	C	A	T	GT	T	GC	C	A
avrblb1	/	G	G	A	G	G	C	T	A	T	G	T	G	C	A	G

	2	2	2	2	2	2	2	2	2	2	2	3	3	3	3	3
	1	1	1	2	2	7	7	7	8	9	9	0	0	0	4	7
	4	8	9	5	8	7	8	9	3	0	1	4	5	6	2	0
ipiO1	C	G	A	T	T	G	C	T	T	C	C	A	G	A	C	A
ipiO2	C	G	A	T	T	G	C	C	T	T	A	A	T	A	G	C
Chinese	C	G	A	T	T	G	C	TG	T	GT	GA	A	GT	A	CG	AC
H30P04	GA	G	A	T	T	G	C	TG	T	GT	GA	A	GT	A	CG	AC
avrblb1	A	C	T	C	A	T	A	T	C	C	C	G	C	T	C	C



H30P04

	0	1	1
	7	0	4
	2	2	2

A6 G G G

B5 A A T

B6 A A T

G1 A A T

	0	0	0	0	1	1	1	1	1	1	1	1	2	2	2	2
	1	2	3	7	0	4	7	7	8	9	9	9	0	0	1	1
	8	9	4	7	2	2	4	9	4	3	7	9	1	6	0	3
ipi01	C	T	T	A	A	T	G	C	C	A	T	C	T	G	C	A
ipi02	A	T	T	A	A	T	G	C	C	A	T	C	T	G	C	A
Chinese	C	T	T	A	A	T	G	C	C	A	T	C	T	G	C	A
H30P04	C	TG	T	AG	AG	TG	G	C	C	A	T	GT	T	GC	C	A
avrblb1	/	G	G	A	G	G	C	T	A	T	G	T	G	C	A	G
	2	2	2	2	2	2	2	2	2	2	2	3	3	3	3	3
	1	1	1	2	2	7	7	7	8	9	9	0	0	0	4	7
	4	8	9	5	8	7	8	9	3	0	1	4	5	6	2	0
ipi01	C	G	A	T	T	G	C	T	T	C	C	A	G	A	C	A
ipi02	C	G	A	T	T	G	C	C	T	T	A	A	T	A	G	C
Chinese	C	G	A	T	T	G	C	TG	T	GT	GA	A	GT	A	CG	AC
H30P04	GA	G	A	T	T	G	C	TG	T	GT	GA	A	GT	A	CG	AC
avrblb1	A	C	T	C	A	T	A	T	C	C	C	G	C	T	C	C



II. Current interests - avirulent genes

AVRblb2 (R gene: blb2):

1. All Chinese isolates have Avrblb2-like amplicons;
2. Polymorphic, but one unique nucleotide at 123bp;
3. Functional complement

	0	0	0	0	1	1	1	1	1	1	1	1	2	2	2
	2	5	6	7	2	4	4	4	4	6	7	8	0	2	2
	0	6	1	6	3	1	2	3	4	3	0	7	0	0	1
Avrblb2.1 /2.2	T	T	C	G/A	A/T	A	G	T/C	C	G	A/G	G/A	A/C	G	C
Chinese	T/A	T/G	C/A	G/A	T	A/T	G/T	T/C	C/T	G/A	A/G	G/A	A/C	G/A	C/A
Avrblb2.1 /2.2	V	V	P	V/I	G	V	V/A	V	K/R	G/S	E/A	A			
Chinese	V/E	V/G	P/T	V/I	G	V	?	V/I	K/R	G/S	E/A	?			



Simulation model - general aspects

1. MATLAB model, Monte Carlo simulation
2. Based on "gene-for-gene" - R-AVR interactions
3. Multi-gene interactions in potato field
4. Simulation of co-evolution of R-AVR genes
5. Reference to further release GMOs



II. Current interests - Model

Some basic examples:

To assume

1. Genotypes of Zoospore

a b c ab cb ac abc

2. Genotypes of potato

A B C AB CB AC ABC

3. R-AVR: A-a, B-b, C-c

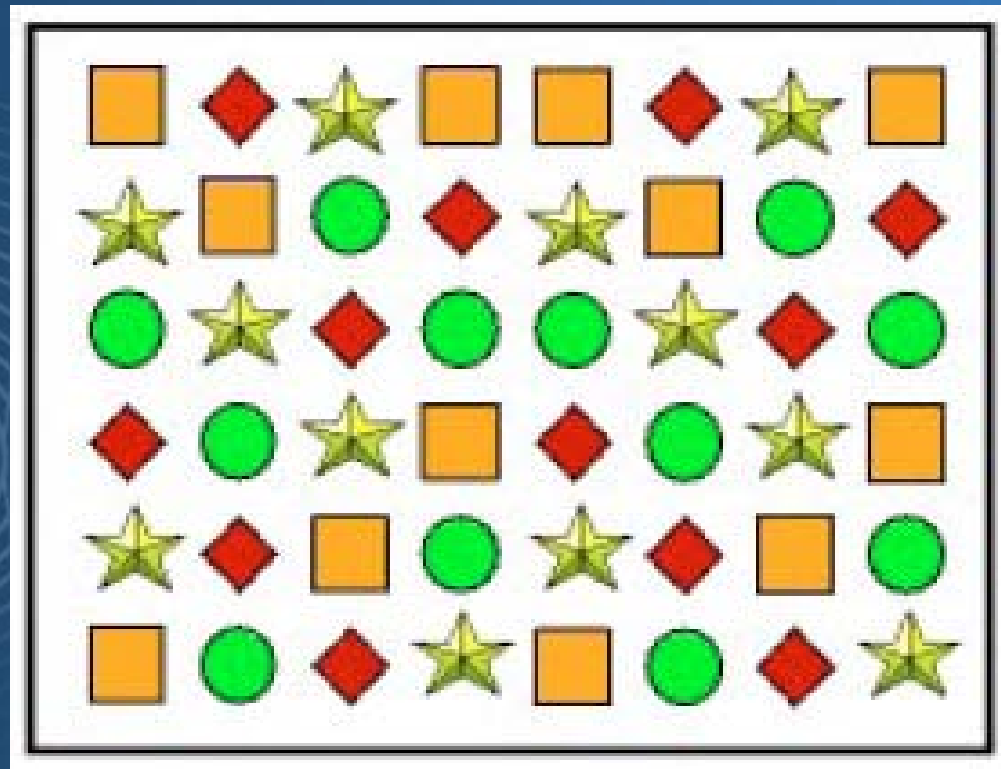
4. Potato growth: No mutation !!

5. Pathogen reproduction: No mutation!!



6. Potato seedling: random

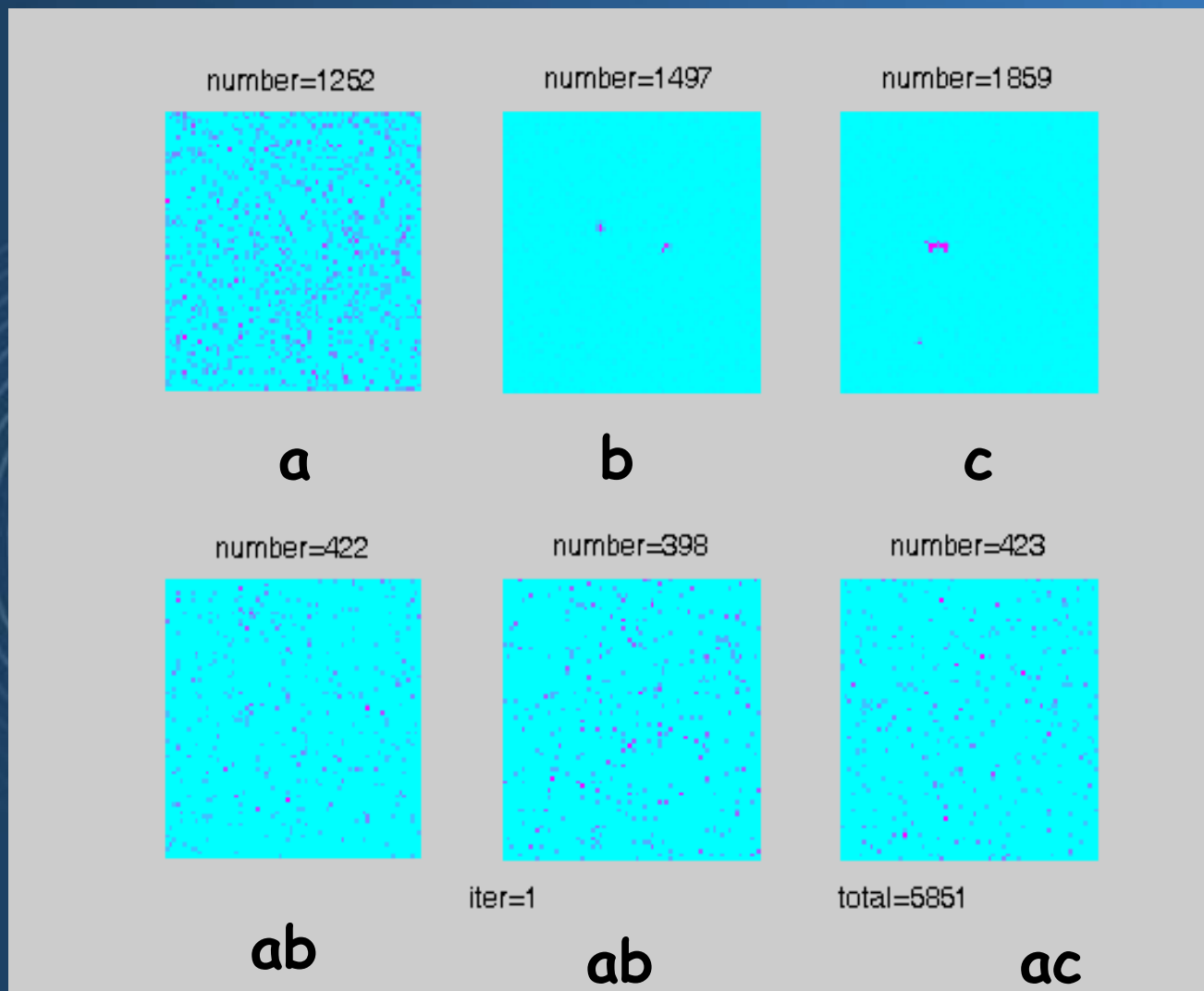
- 70x70 plants
- Per iter = a cycle from one dispersal to next dispersal
- Total iter= 100 cycles



7. Genotypes
of zoospore:
random

8. Dispersal
of zoospore:
random

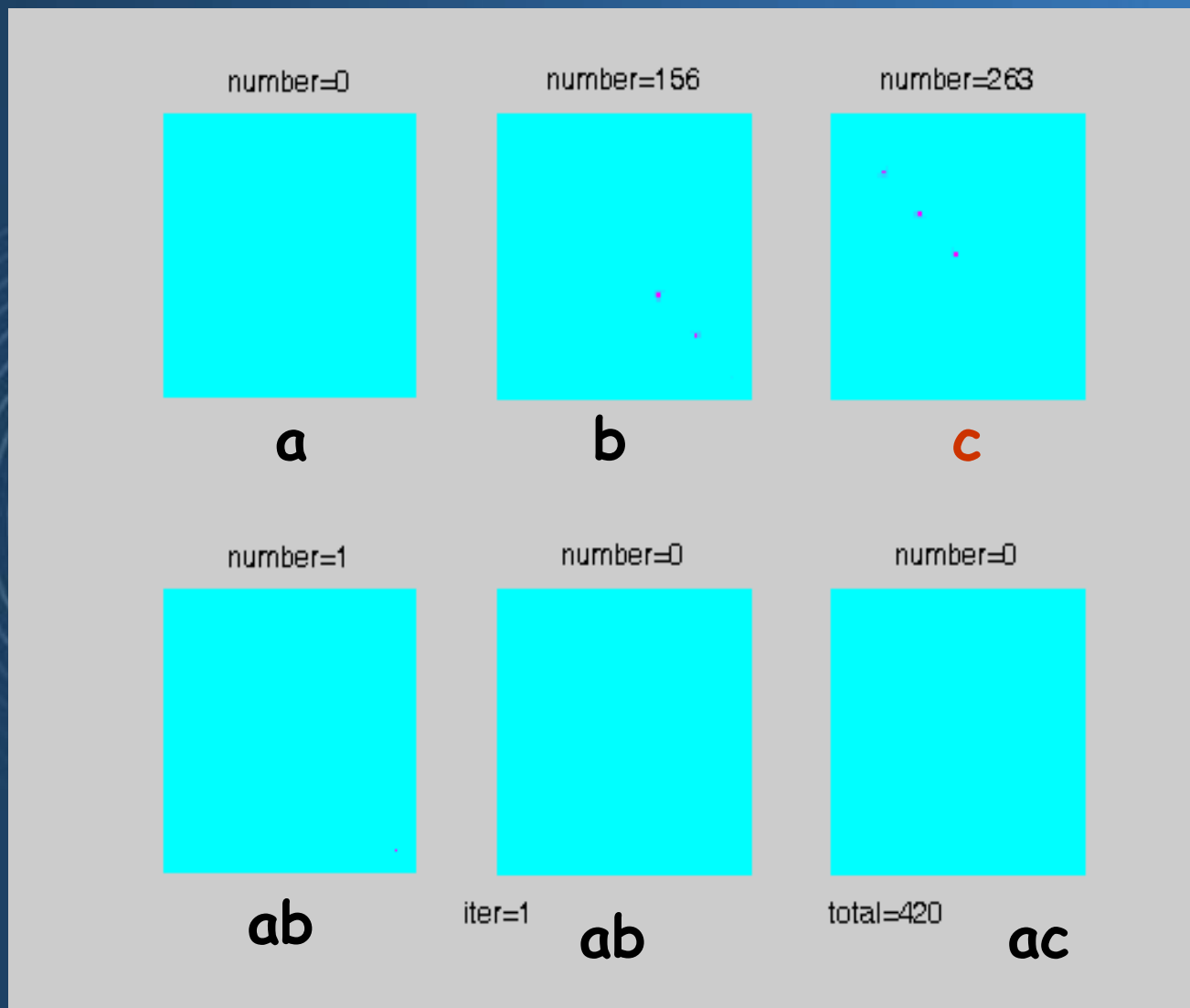
Initial
zoospore:
20,000



7. Genotypes
of zoospore
Gaussian
distribution

8. Dispersal
of zoospore:
limit points

Initial
zoospore:
200



6. Potato seedling: blocked

- 70x70 plants
- Per iter = a cycle from one dispersal to next dispersal
- Total iter=100 cycles

Line: 70

A
B
C
AB
BC
AC
ABC

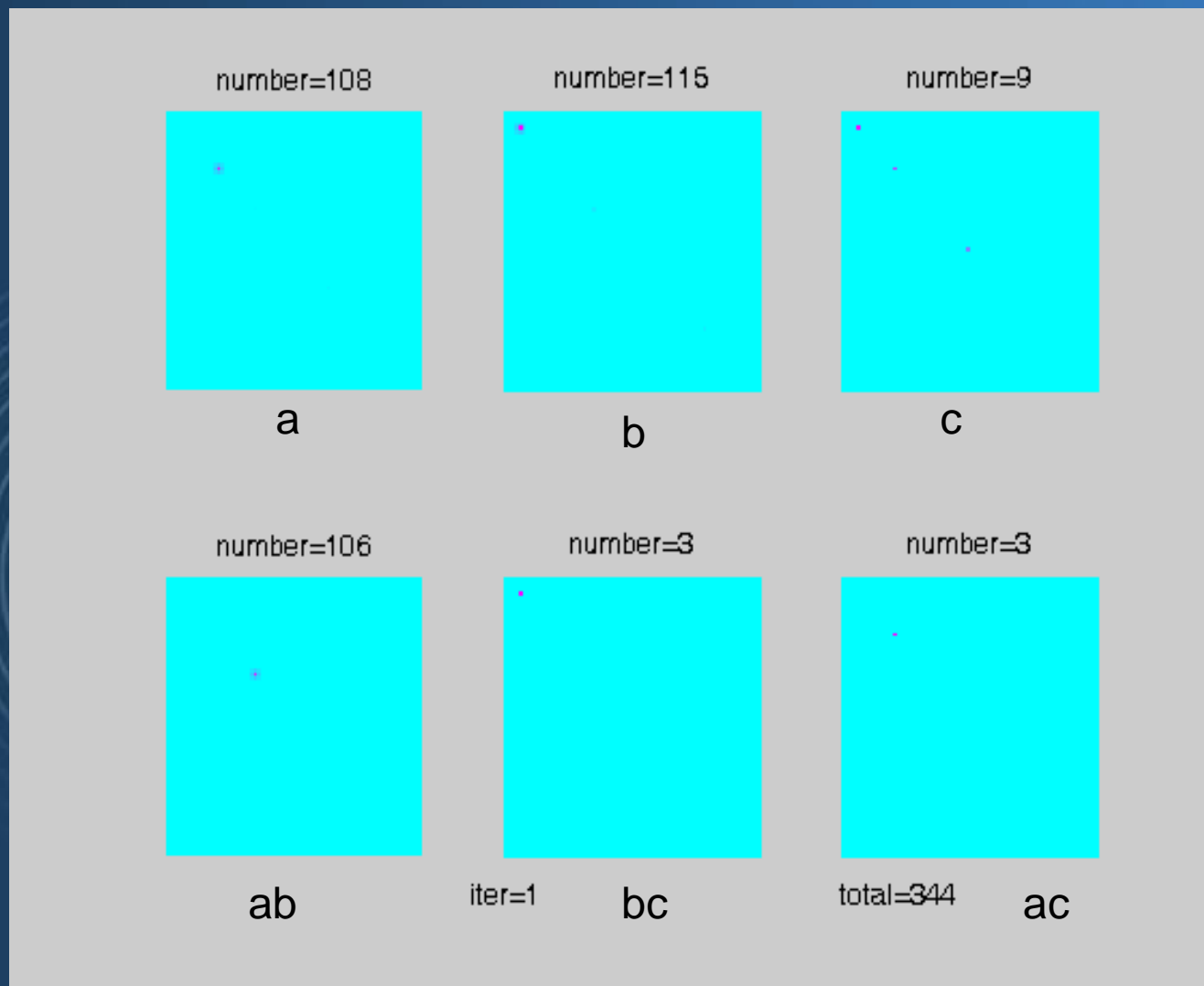
Row:10



7. Genotypes
of zoospore
random

8. Dispersal
of zoospore:
limit points

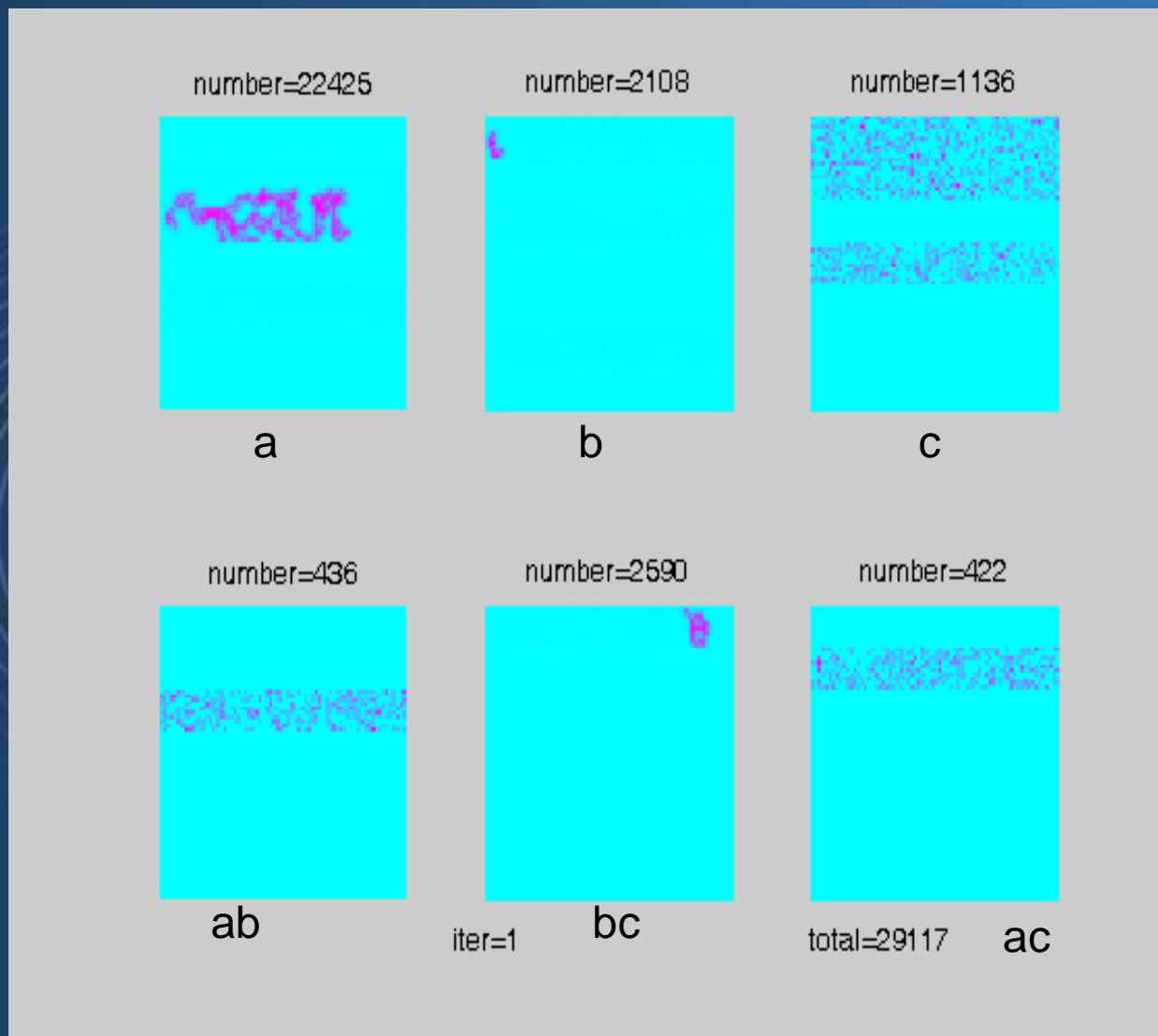
Initial
zoospore:
200





7. Genotypes
of zoospore
random

8. Dispersal
of zoospore:
random

Initial
zoospore:
20,000



-  To use more AVR genes to learn genetic diversity of *P.infestans* in China
 - ← High throughput screening technology to detect the different allelic variants of the main AVR genes
-  To learn co-evolution process
 - Fitness, penalty



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