

Durability of resistance to late blight associated with stacking of R-genes

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Lay-out

- Introduction
- DuRPh
- Bait fields
 - *P. infestans* monitoring
- Sensor technique
- Durability of resistance
- Conclusions



Introduction

- Resistance breeding
- Adaptation of *P. infestans*
- Monogenic resistance overcome
- Stacking R-genes: Durable resistance?
- DuRPh funded by the Ministry of Economic Affairs, Agriculture & Innovation



DuRPh

- Durable blight management
 - High resistance
 - Low fungicide input
- Combining resistance & agronomical value
 - Conventional breeding
 - Genetic modification: cis – genesis
- Which & how many R-genes



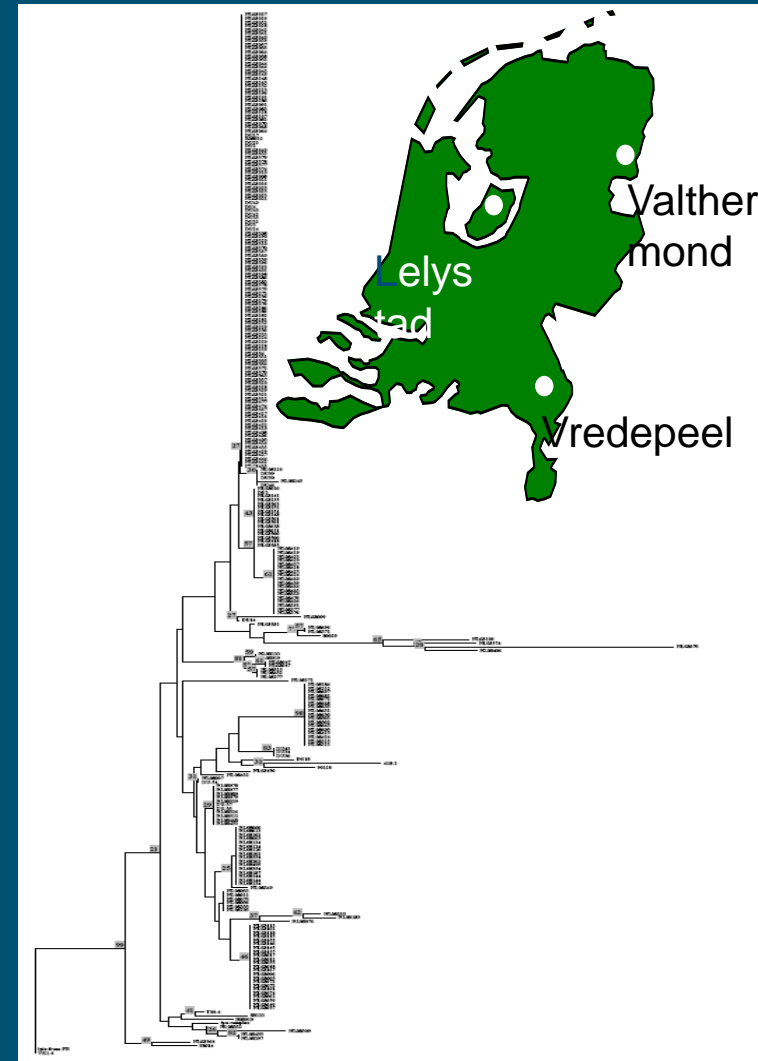
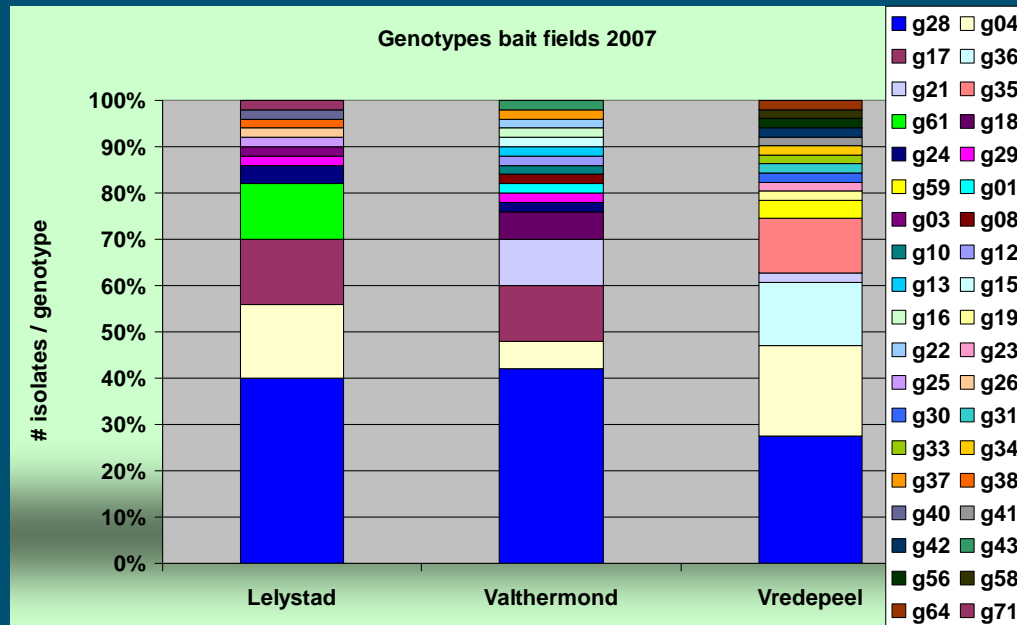
Bait fields: Monitoring of *P. infestans* 2006-2010

P. infestans is extremely adaptive:

Host plant resistance

Fungicide resistance

Increased aggressiveness



Bait fields

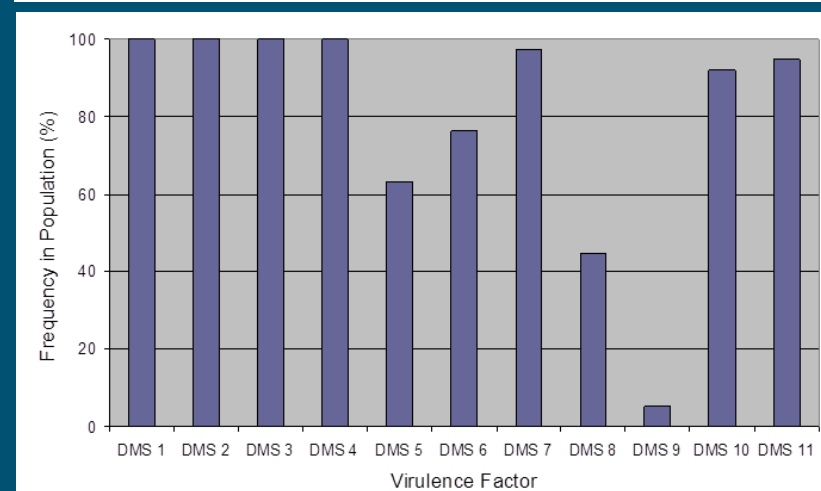
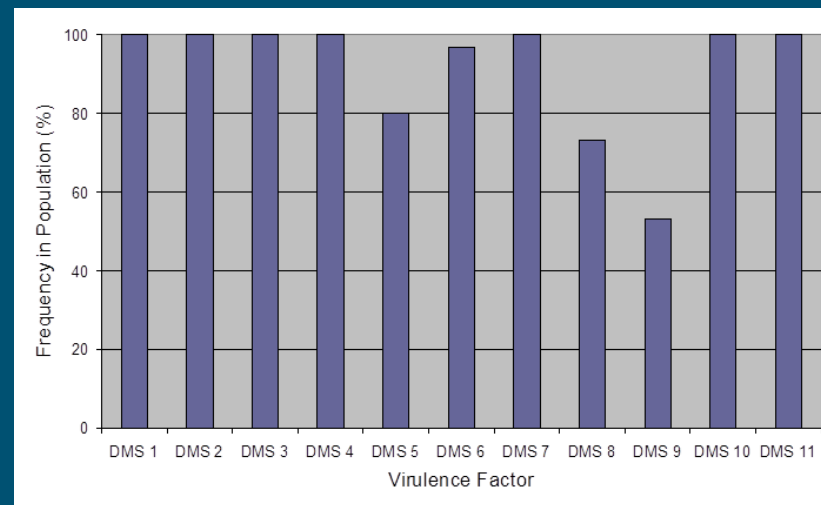
- Bait field ~100 genotypes; among which 34 varieties / genitors of breeders and 66 wild spp DuRPh
 - KP: 42 % (2009)
 - LS: 39 % (2009)
 - VP: 38 % (2009)
- First day of infection
- 33 varieties / genitors / accessions not blighted at all on 3 locations
- Some blighted on 1 or 2 locations



R-genes

- R-genes derived from *S. demissum* R1 – R11
- *P. infestans* highly virulent
- DMS 5, 8 & 9 maybe of interest
- New interesting R-genes blb, chc, pta, vnt

2006



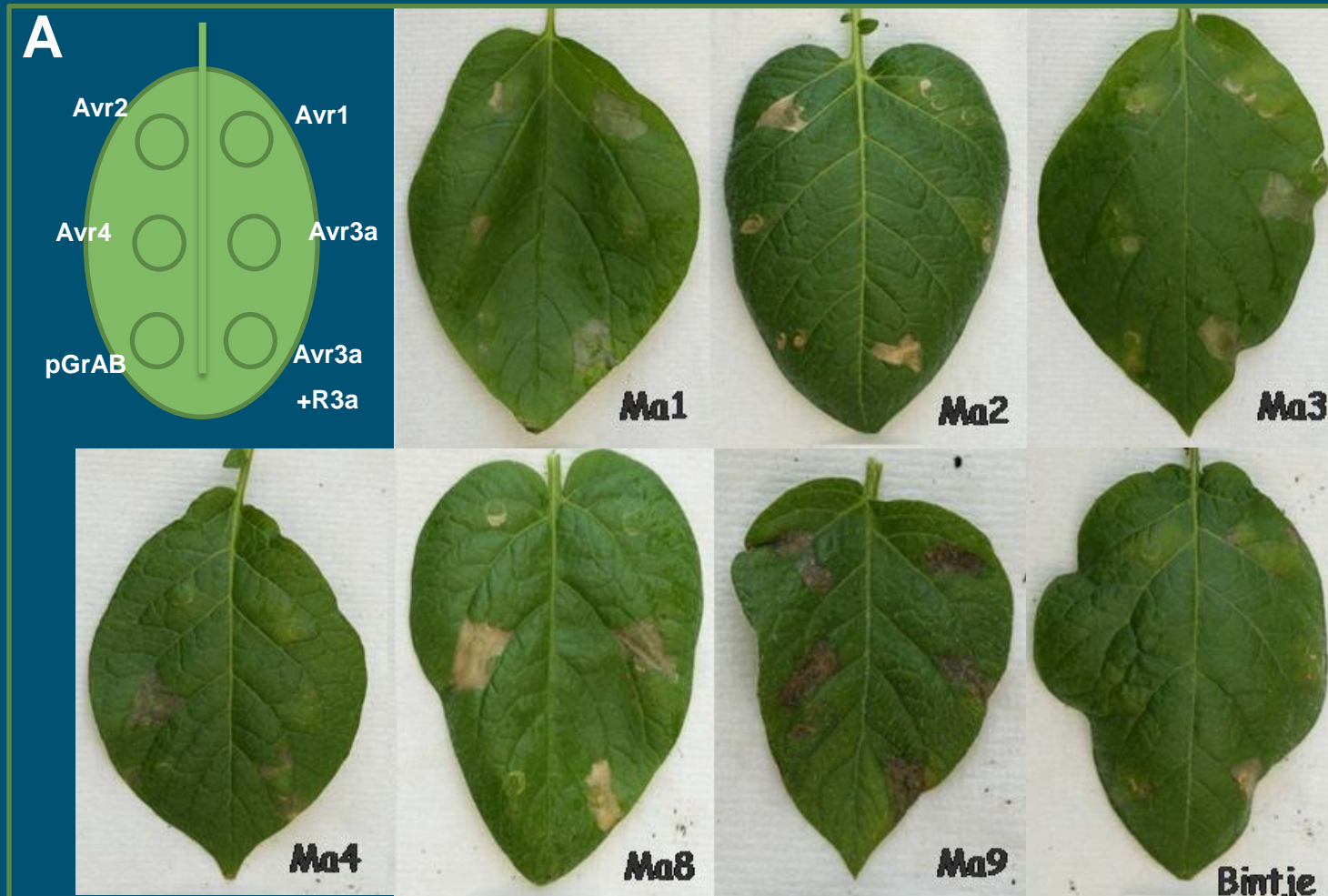
2007

R8 and R9, F1 offspring in trap fields

Year	Genotype	R gene content
2010	Bintje	-
	R8-18	R8
	MaR8	R3a,R3b,R4,R8
	Sarpo mira	R3a,R3b,R4,smira1,2
	R9-53	R3a,R3b,R4,R8,R9



Avirulence



Censor

- Establish the first day of infection in the field
 - Most susceptible variety
 - Usually R_0
- Establish first day of infection target variety
 - Establish delay for each year & location
- Censor technique
 - Replace MV; fit curve
- Calculate delay (variety)

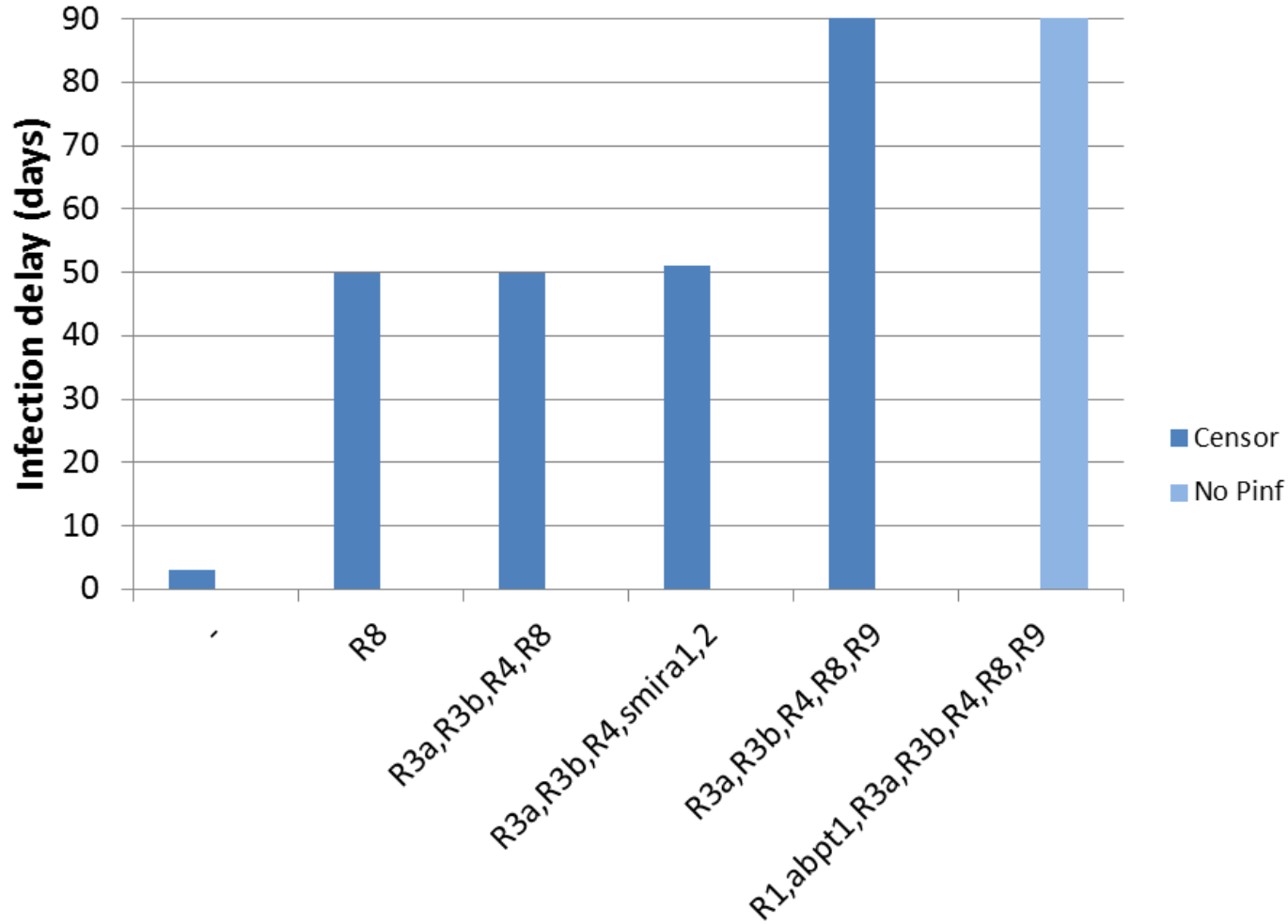


S. demissum R genes in bait fields

Year	Genotype	Calculated delay in <i>Pi</i> symptoms (days)	Relative delay in <i>Pi</i> symptoms*	
2006	Bintje	4	a . .	
	MaR1	4	a . .	
	MaR2	8	a b .	
	MaR3	4	a . .	
	MaR4	7	a b .	
	MaR8	37	. b .	
	MaR9	66	. . c	
	2007	Bintje	1	a . . .
		MaR1	2	a b . .
MaR2		2	a b . .	
MaR3		2	a b . .	
MaR4		1	a . . .	
MaR8		13	. . c d	
MaR9		No lesions**	. . . d	
2008		Bintje	3	a b . .
		MaR1	1	a . . .
	MaR2	3	a b . .	
	MaR3	2	a b . .	
	MaR4	2	a b . .	
	MaR8	24	. . c d	
	MaR9	15	. . c .	
	2009	Bintje	1	a . .
MaR8		113	. b .	
MaR9		No lesions**	. . c	
Sarpo mira		No lesions**	. . c	
2010	Bintje	3	a . . .	
	MaR8	50	. b . .	
	MaR9	No lesions**	. . . d	
	Sarpo mira	51	. b . .	



Delay 2010



2011 bait fields

GMO regulations

- 4 locations
- GMO at 2
- Basis cv Desire
 - 1 – 3 resistance genes
- Delay
 - Additional PLB severity

Quite a hurdle



Rpi-chc1



Rpi-pta1



Rpi-vnt1



Rpi-blb1



Rpi-sto1



R3a



R3b



Rpi-blb3



Desiree



vnt1:chc1



sto1:blb3



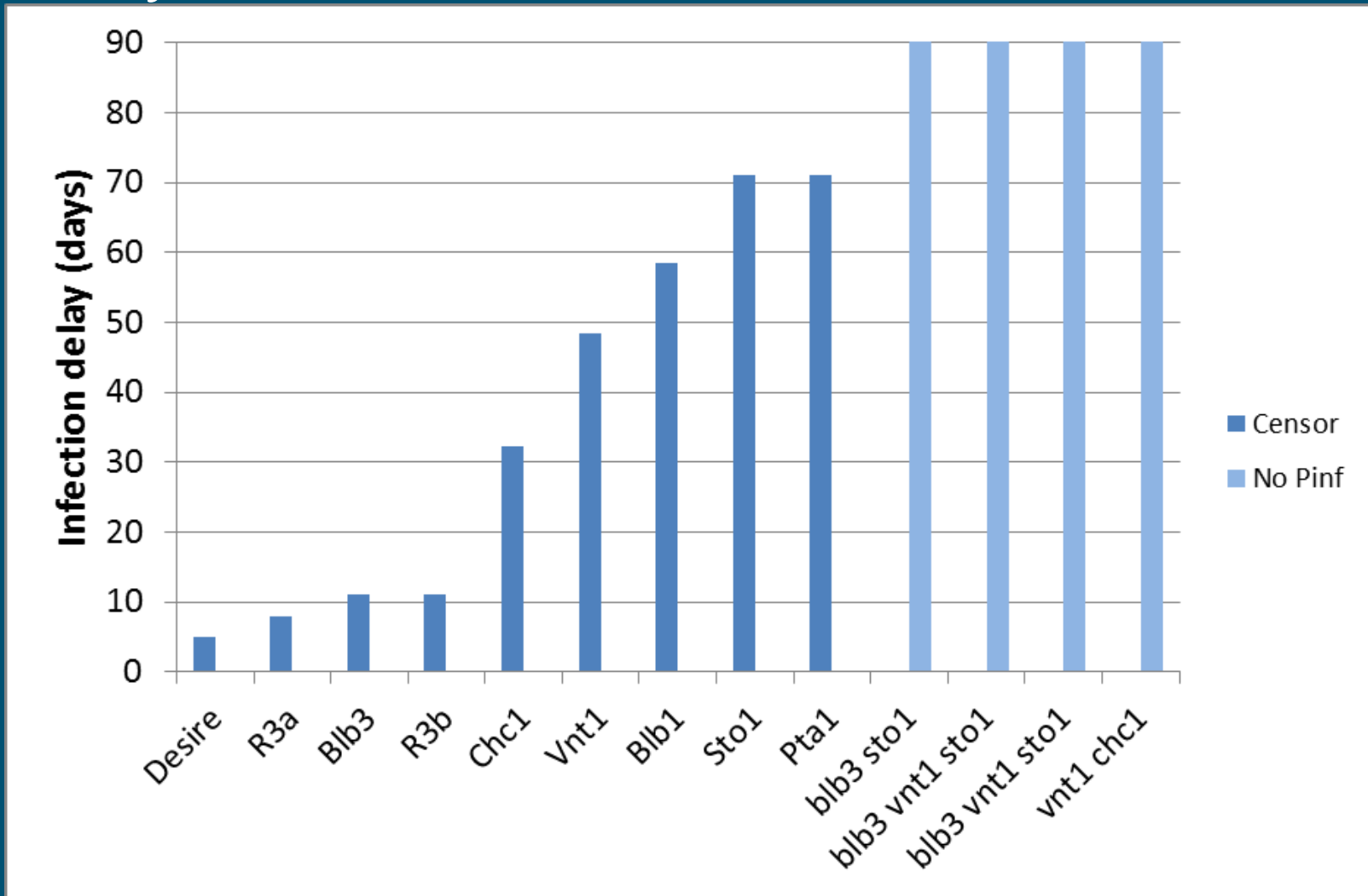
sto1:vnt1:blb3



vnt1:sto1



Delay 2011



Conclusion

- *R* gene stacking contributes to isolate resistance spectrum
- On site virulence monitoring is an excellent tool to predict the potential durability of *R* gene stacks
- But what if grown on 20.000 ha?



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Thank for your attention

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