Co-evolution of virulence and resistance in heterogeneous wheat populations

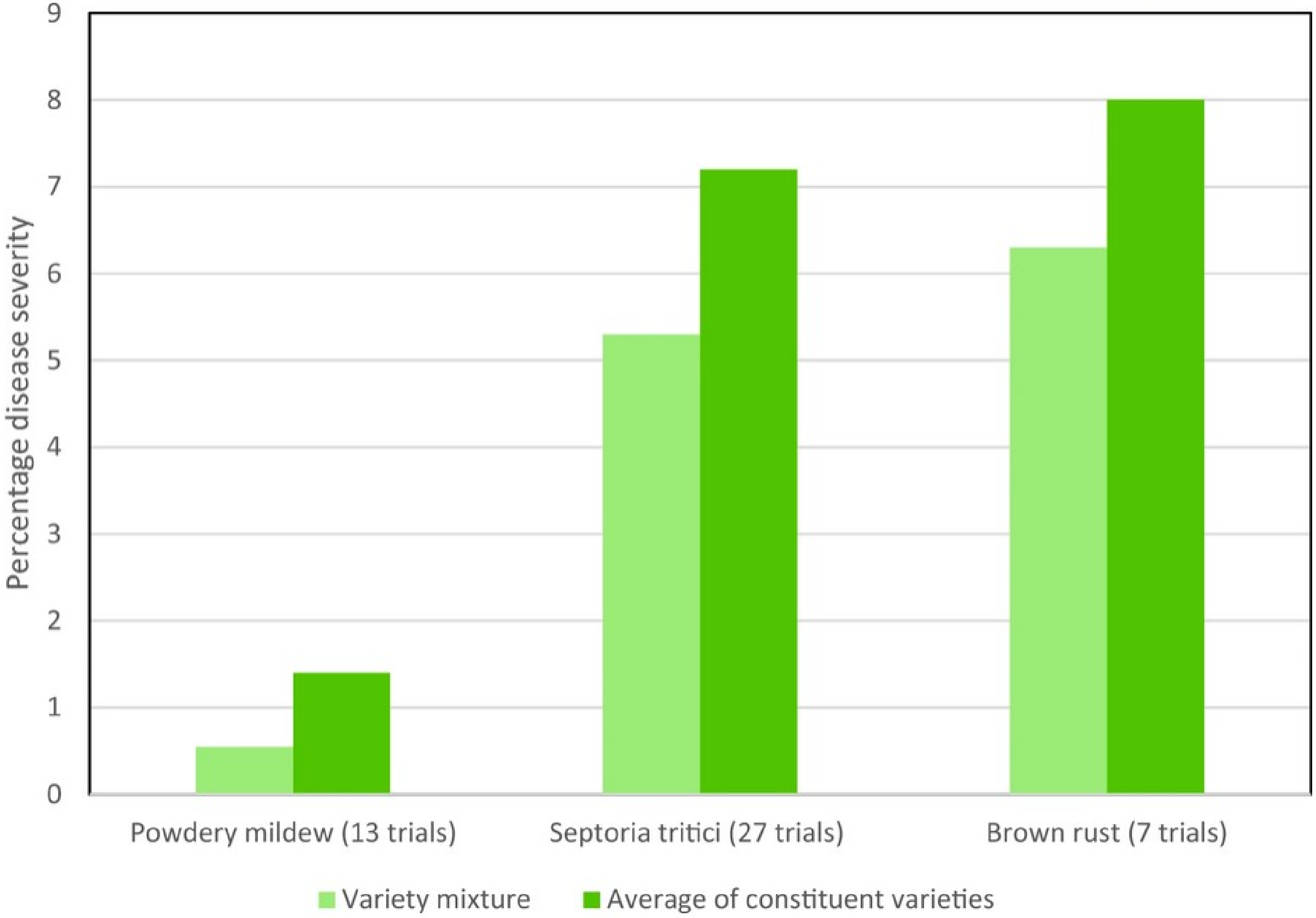
XXIII International Workshop on Bunt and Smut Diseases

Uppsala, Sweden, 1st-2nd June 2025

Anders Borgen and Dennis Kjær Christensen,

Project funding by
DIVERSILIENCE (CoreOrganic)

From: Variety mixtures of winter wheat: a general status and national case study



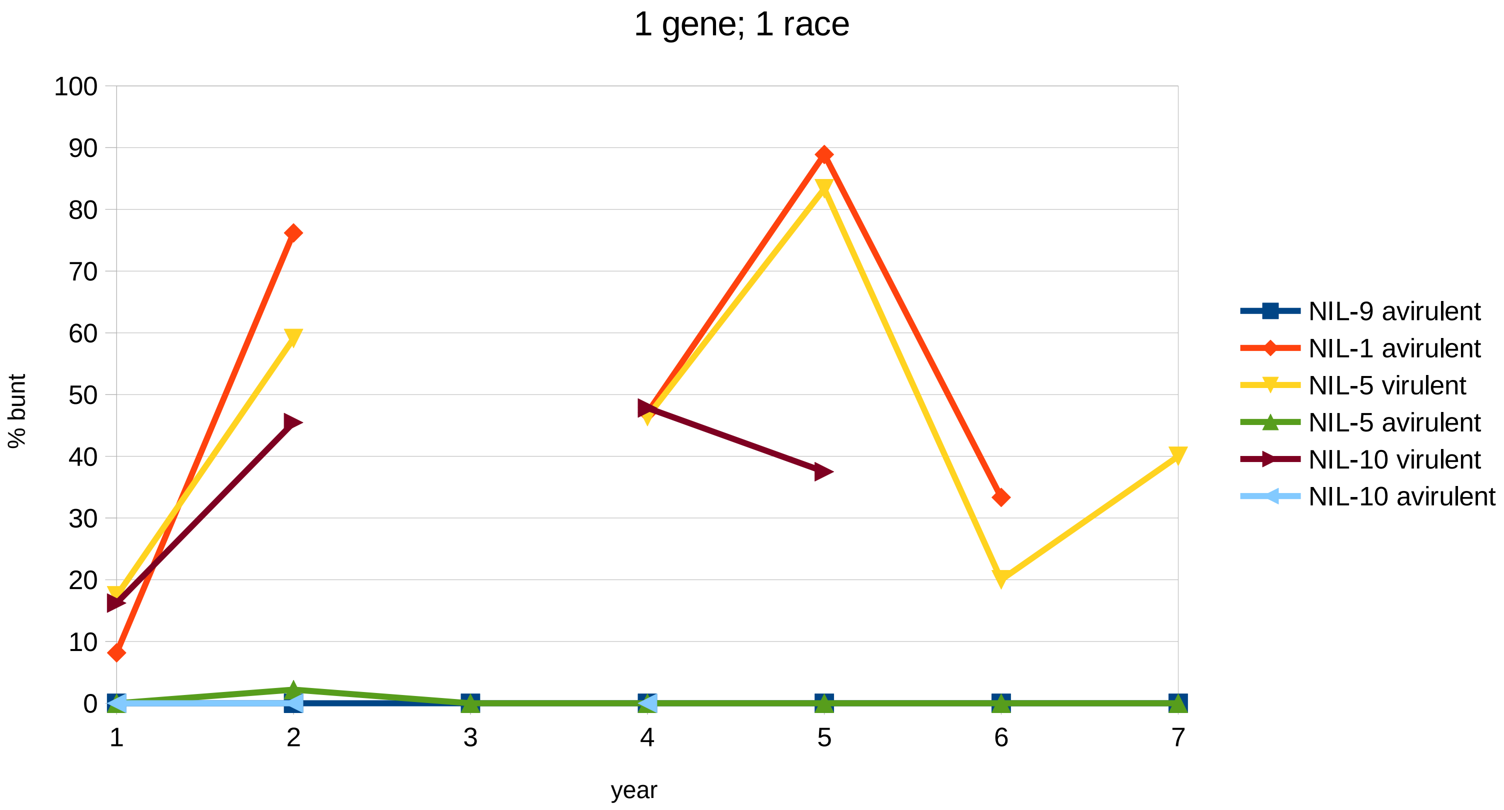
Results from the Danish National trials from 2021 to 2022. Trials were prompted to support the promoting of variety mixtures (SEGES 2022)

Major differences

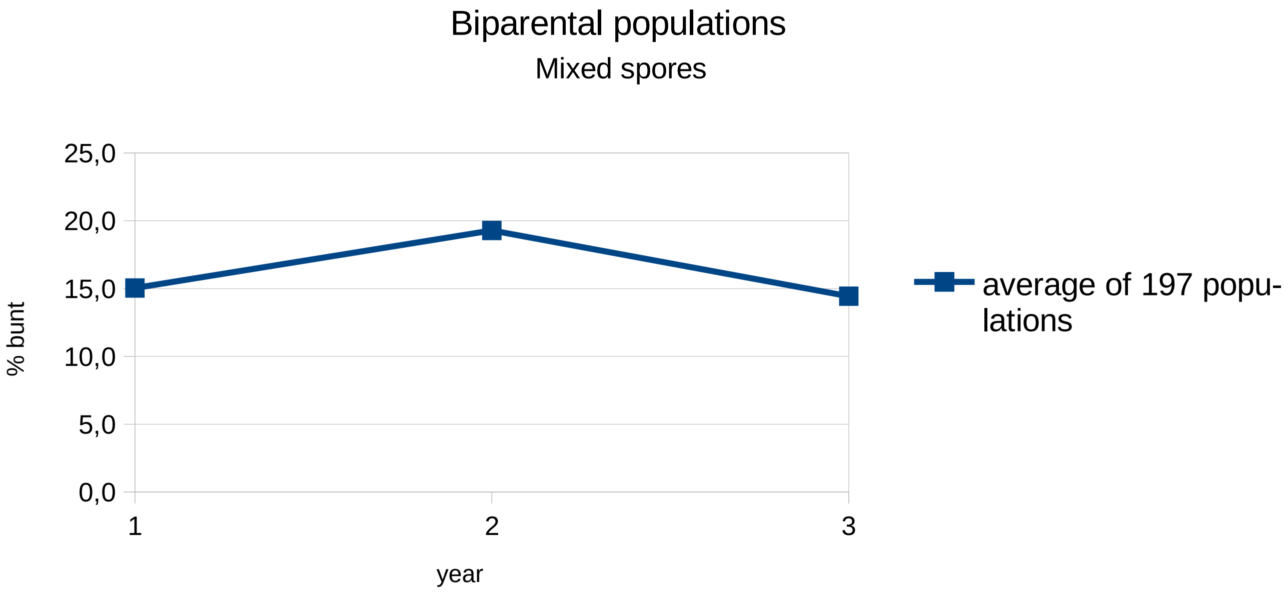
Leaf diseases starts from scratch every year with multiple life-circles on the plants and between plants

- Common bunt is perennial
- Common bunt is almost lethal
- Only one life-circle per year

1 gene; 1 race

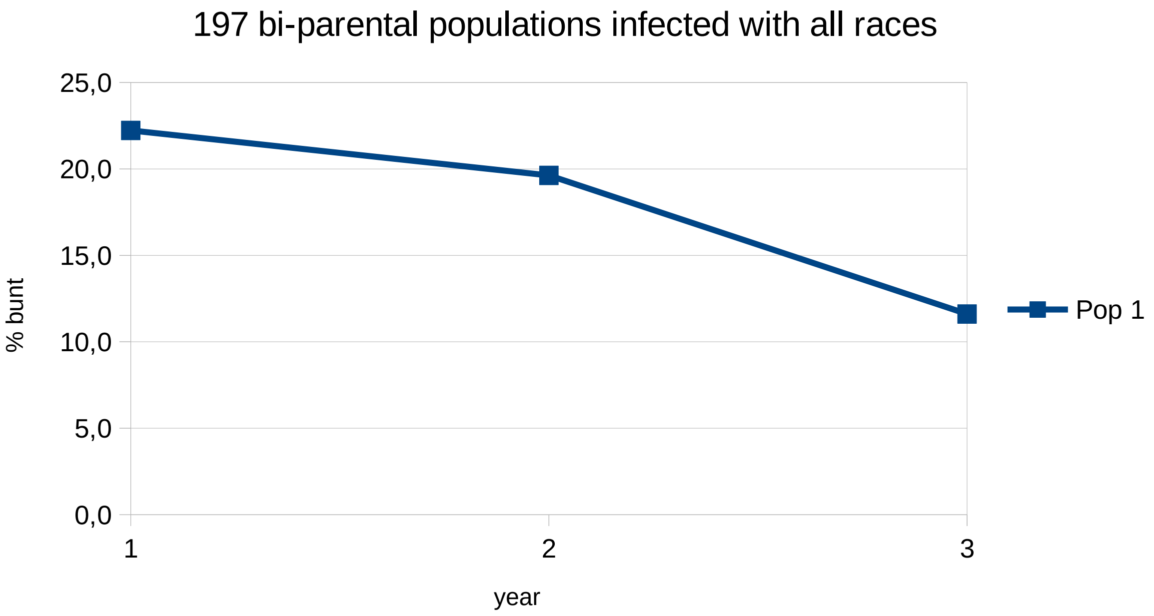

1 gene; 1 race
100
90
80
70
60
50
40
30
20
10
0
% bunt
1
2
3
4
5
6
7
year
NIL-9 avirulent
NIL-1 avirulent
NIL-5 virulent
NIL-5 avirulent
NIL-10 virulent
NIL-10 avirulent

2 genes; many races



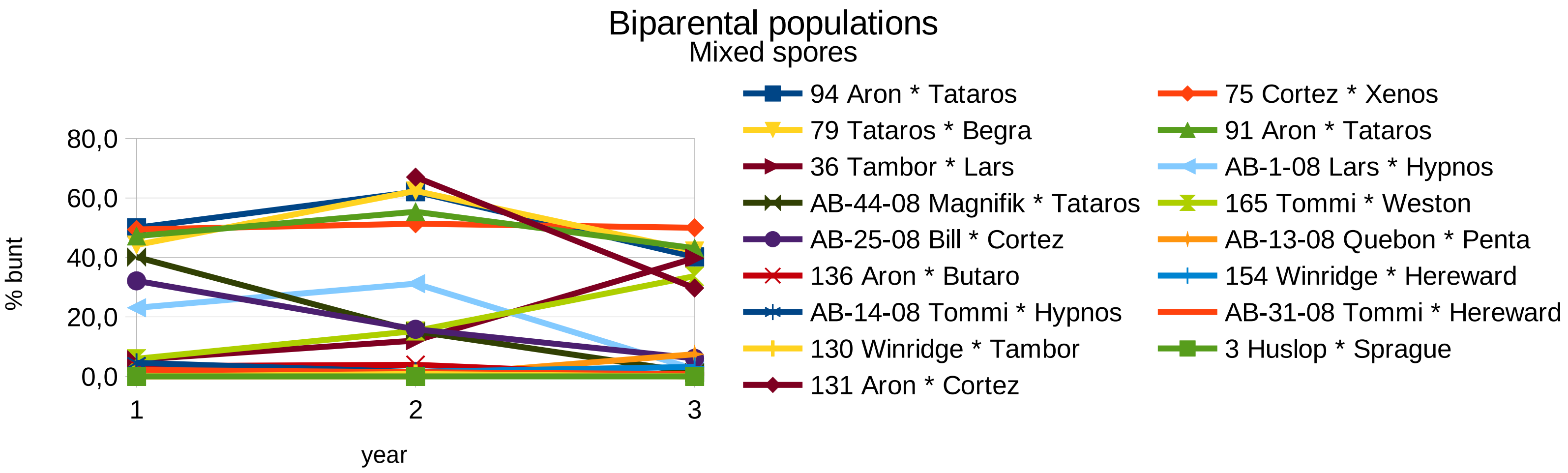
COBRA project
2013-2015

Mix of many genes and many races



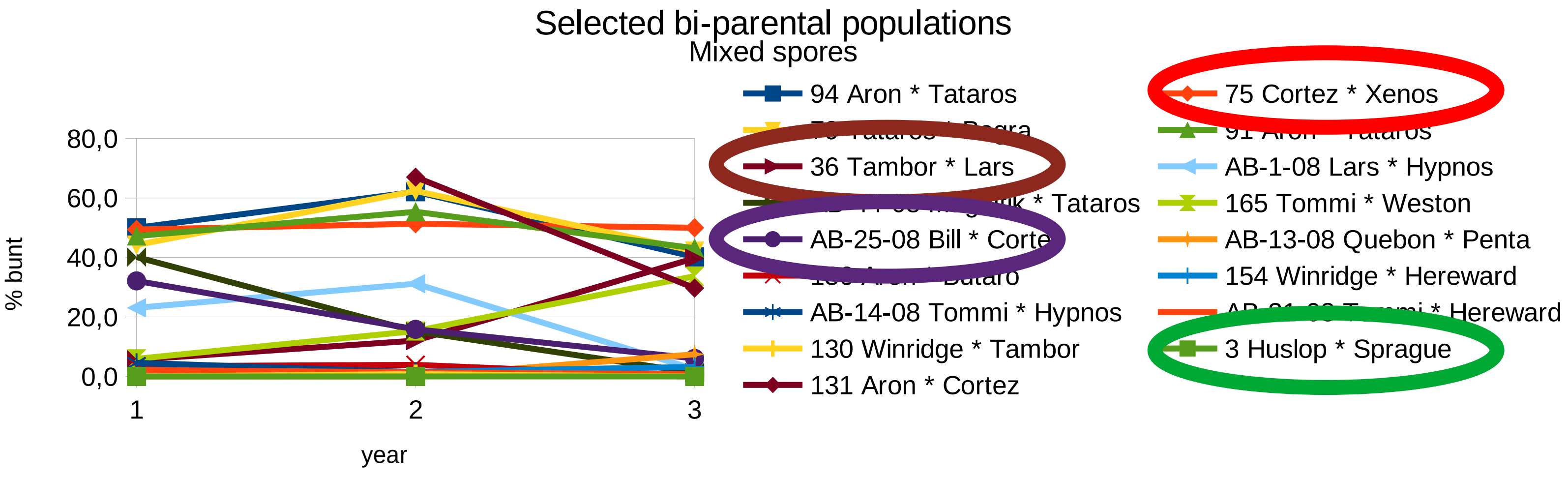
COBRA project
2013-2015

2 genes; many races



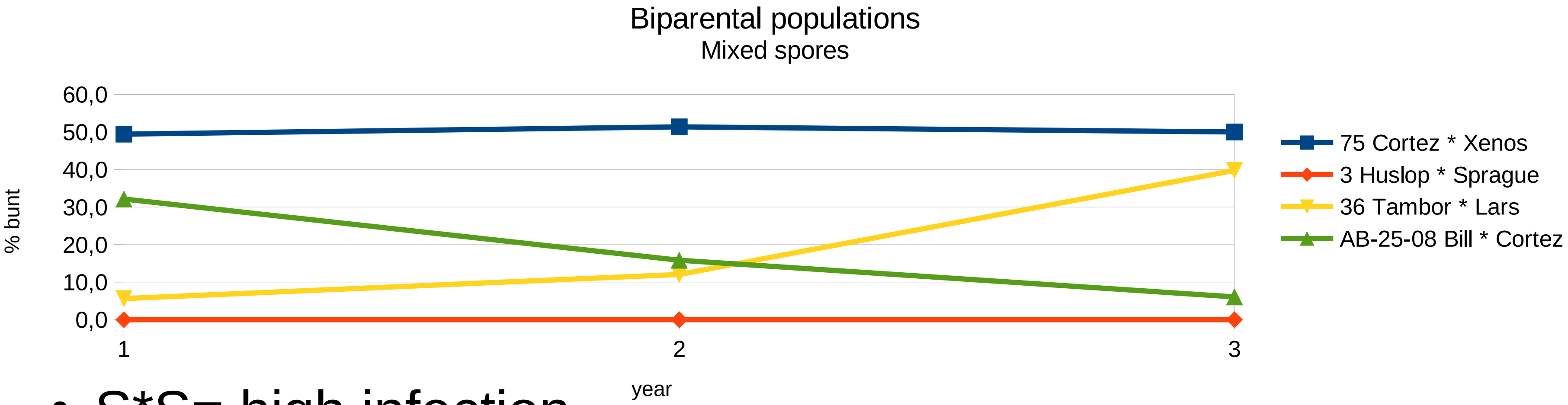
COBRA project
2013-2015

2 genes; many races



COBRA project
2013-2015

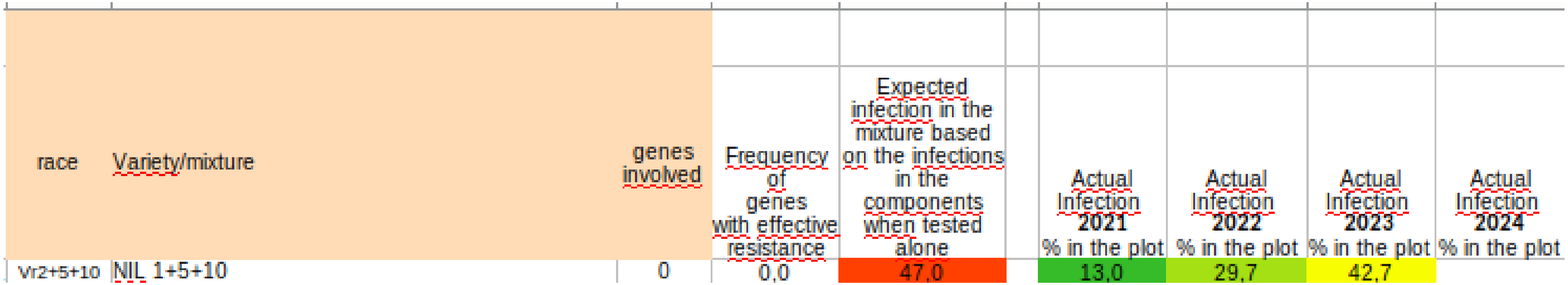
Selected idiotypes
2 genes; many races



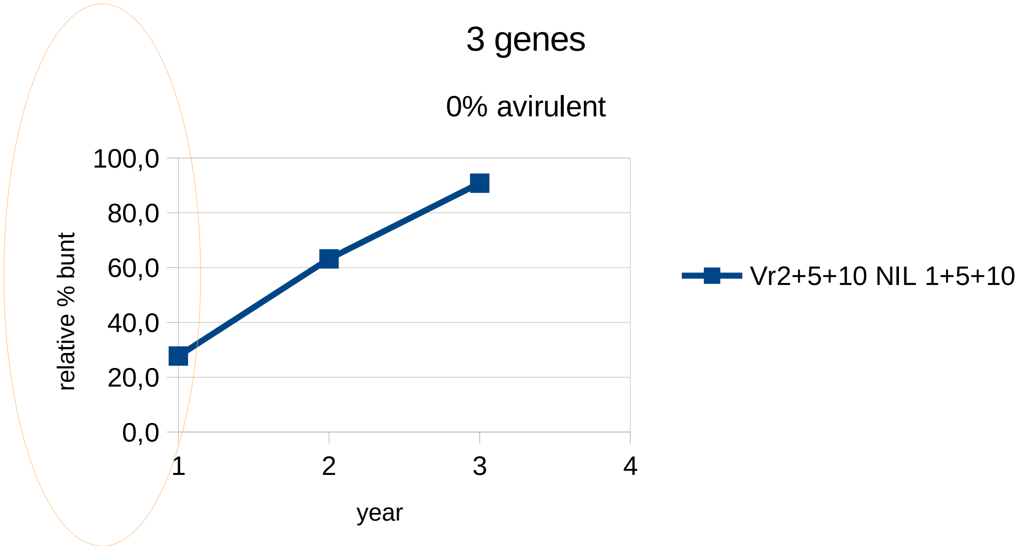
- S*S= high infection
- R*R= low infection
- (r)*(r)= increasing infection
- R*S= decreasing infection

COBRA project
2013-2015

3 genes; 3 races



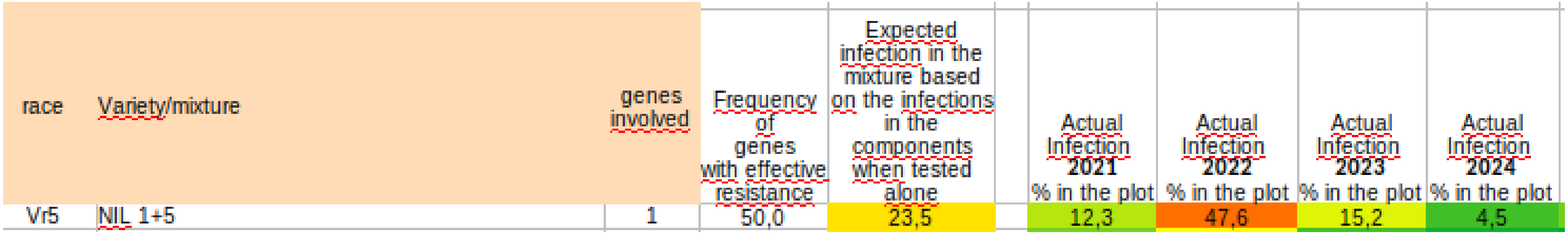
race	Variety/mixture	genes involved	Frequency of genes with effective resistance	Expected infection in the mixture based on the infections in the components when tested alone		Actual Infection **2021** % in the plot	Actual Infection **2022** % in the plot	Actual Infection **2023** % in the plot	Actual Infection **2024** % in the plot
Vr2+5+10	NIL 1+5+10	0	0,0	47,0		13,0	29,7	42,7	



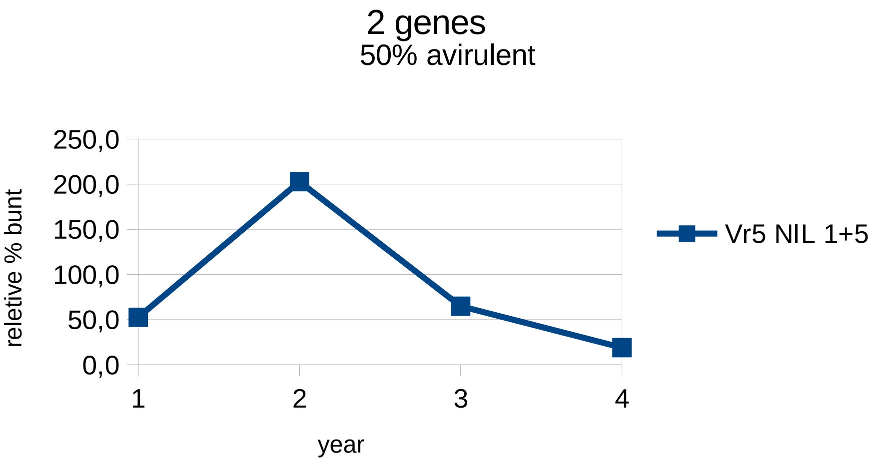
DIVERSILIENCE
project 2022-24

Confirming the results
from the COBRA project

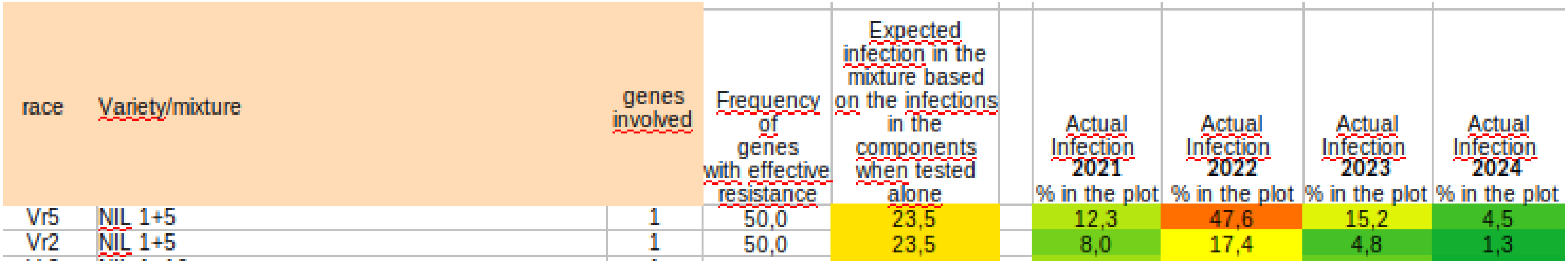
2 genes; 1 race



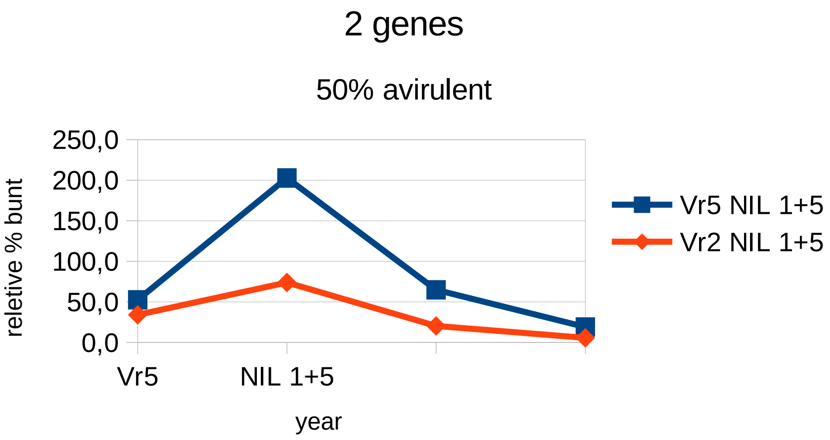
race	Variety/mixture	genes involved	Frequency of genes with effective resistance	Expected infection in the mixture based on the infections in the components when tested alone		Actual Infection **2021** % in the plot	Actual Infection **2022** % in the plot	Actual Infection **2023** % in the plot	Actual Infection **2024** % in the plot
Vr5	NIL 1+5	1	50,0	23,5		12,3	47,6	15,2	4,5



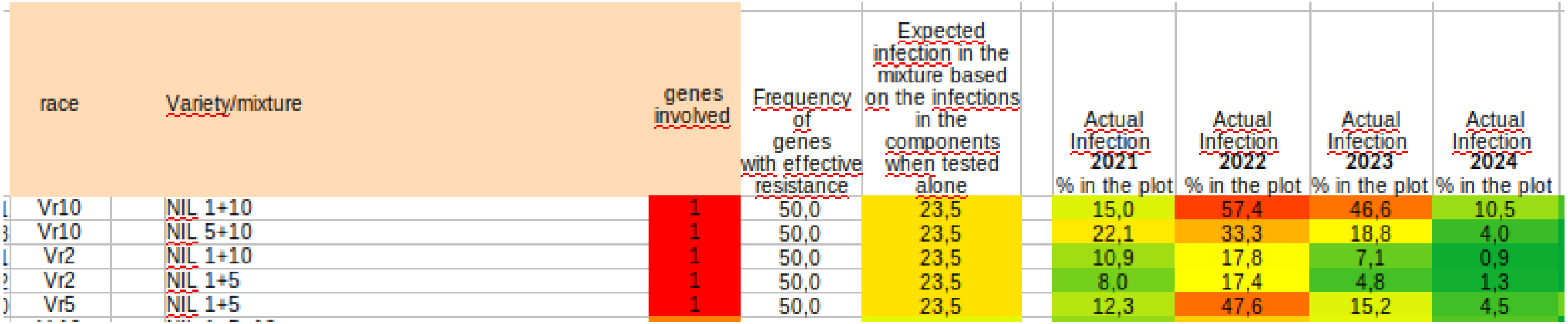
2 genes; 1 race



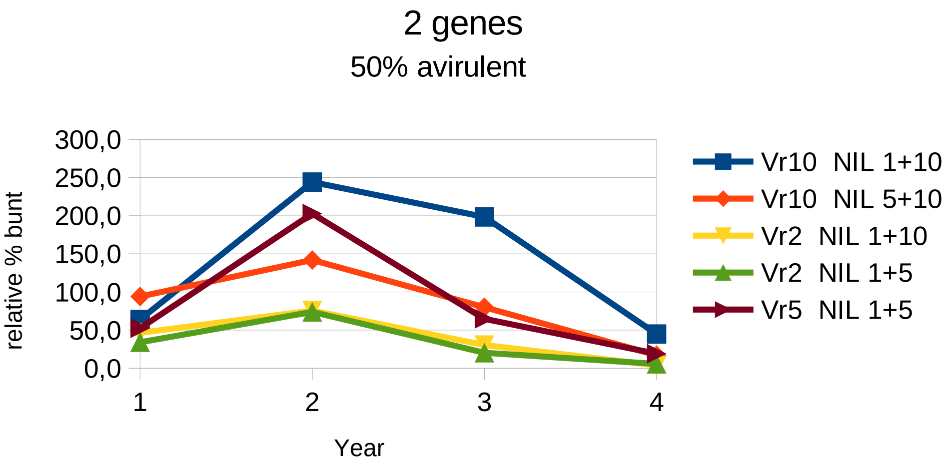
race	Variety/mixture	genes involved	Frequency of genes with effective resistance	Expected infection in the mixture based on the infections in the components when tested alone		Actual Infection 2021 % in the plot	Actual Infection 2022 % in the plot	Actual Infection 2023 % in the plot	Actual Infection 2024 % in the plot
Vr5	NIL 1+5	1	50,0	23,5		12,3	47,6	15,2	4,5
Vr2	NIL 1+5	1	50,0	23,5		8,0	17,4	4,8	1,3



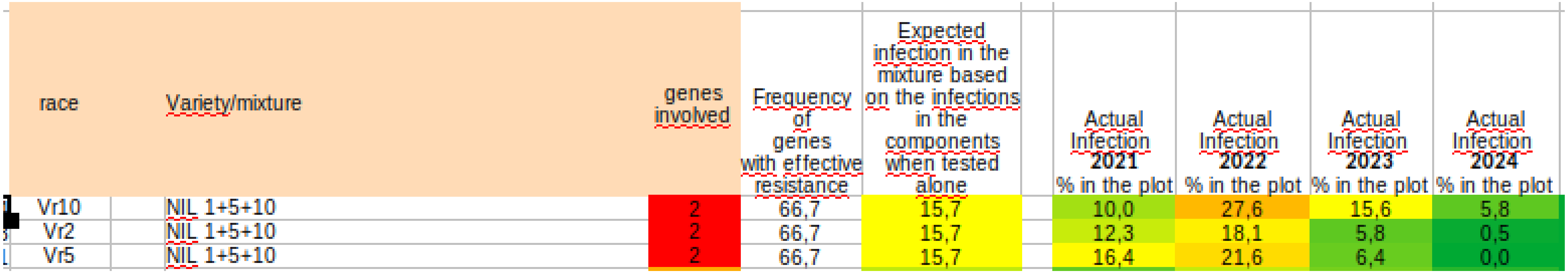
2 genes; 1 race



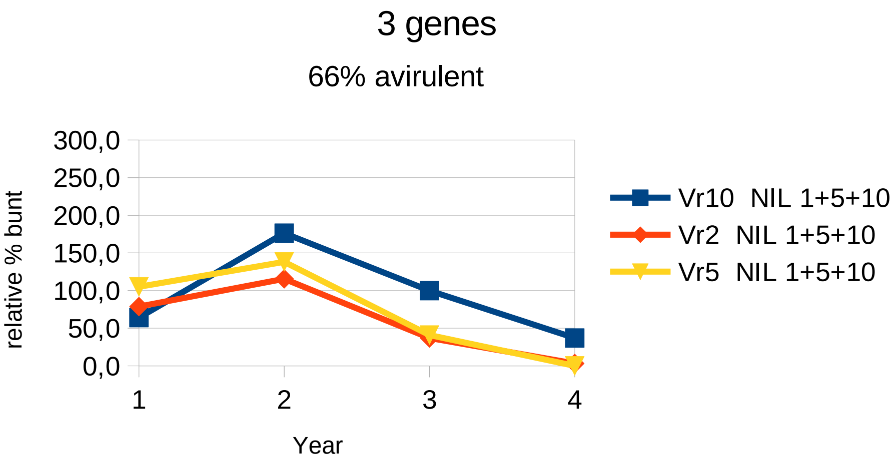
race		Variety/mixture	genes involved	Frequency of genes with effective resistance	Expected infection in the mixture based on the infections in the components when tested alone		Actual Infection **2021** % in the plot	Actual Infection **2022** % in the plot	Actual Infection **2023** % in the plot	Actual Infection **2024** % in the plot
Vr10		NIL 1+10	1	50,0	23,5		15,0	57,4	46,6	10,5
Vr10		NIL 5+10	1	50,0	23,5		22,1	33,3	18,8	4,0
Vr2		NIL 1+10	1	50,0	23,5		10,9	17,8	7,1	0,9
Vr2		NIL 1+5	1	50,0	23,5		8,0	17,4	4,8	1,3
Vr5		NIL 1+5	1	50,0	23,5		12,3	47,6	15,2	4,5



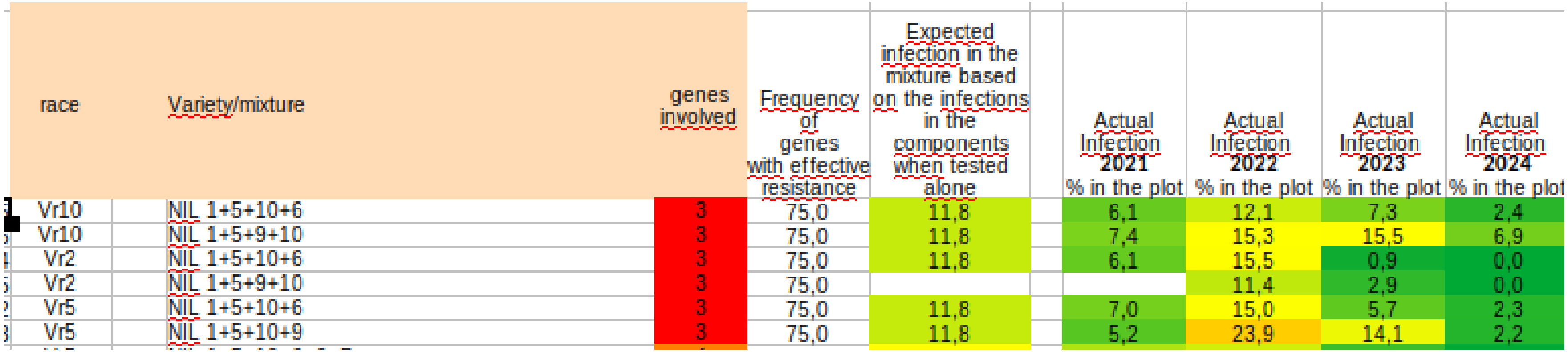
3 genes; 1 race



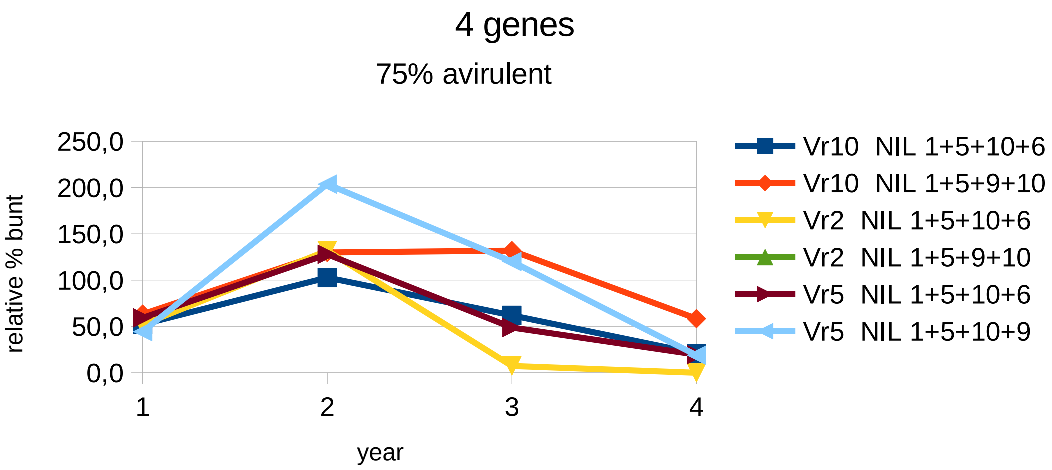
race	Variety/mixture	genes involved	Frequency of genes with effective resistance	Expected infection in the mixture based on the infections in the components when tested alone		Actual Infection **2021** % in the plot	Actual Infection **2022** % in the plot	Actual Infection **2023** % in the plot	Actual Infection **2024** % in the plot
Vr10	NIL 1+5+10	2	66,7	15,7		10,0	27,6	15,6	5,8
Vr2	NIL 1+5+10	2	66,7	15,7		12,3	18,1	5,8	0,5
Vr5	NIL 1+5+10	2	66,7	15,7		16,4	21,6	6,4	0,0



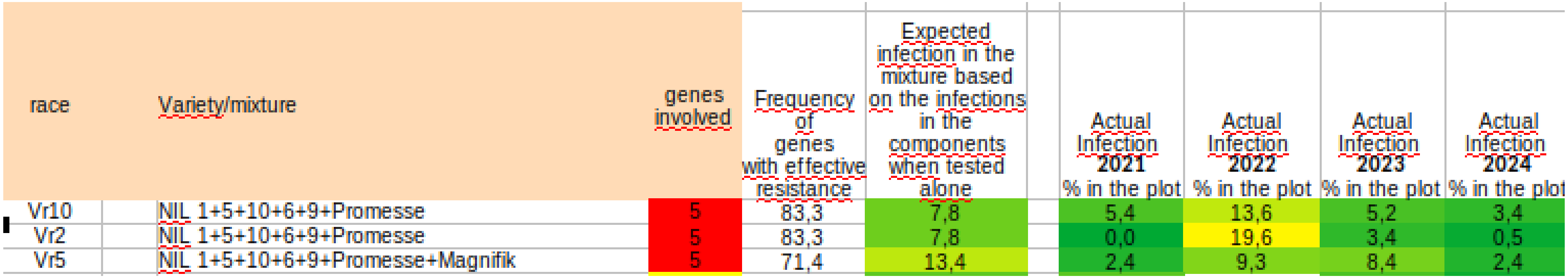
4 genes; 1 race



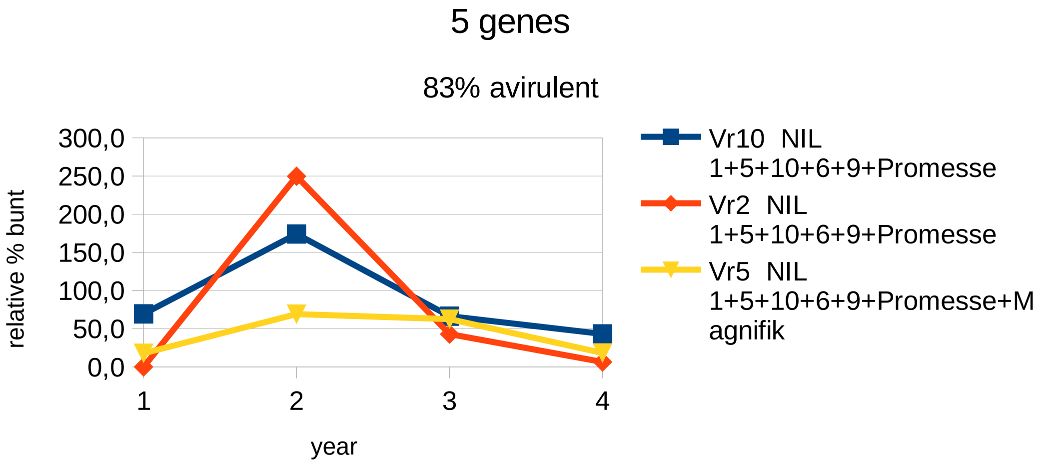
race	Variety/mixture	genes involved	Frequency of genes with effective resistance	Expected infection in the mixture based on the infections in the components when tested alone		Actual Infection 2021 % in the plot	Actual Infection 2022 % in the plot	Actual Infection 2023 % in the plot	Actual Infection 2024 % in the plot
Vr10	NIL 1+5+10+6	3	75,0	11,8		6,1	12,1	7,3	2,4
Vr10	NIL 1+5+9+10	3	75,0	11,8		7,4	15,3	15,5	6,9
Vr2	NIL 1+5+10+6	3	75,0	11,8		6,1	15,5	0,9	0,0
Vr2	NIL 1+5+9+10	3	75,0				11,4	2,9	0,0
Vr5	NIL 1+5+10+6	3	75,0	11,8		7,0	15,0	5,7	2,3
Vr5	NIL 1+5+10+9	3	75,0	11,8		5,2	23,9	14,1	2,2



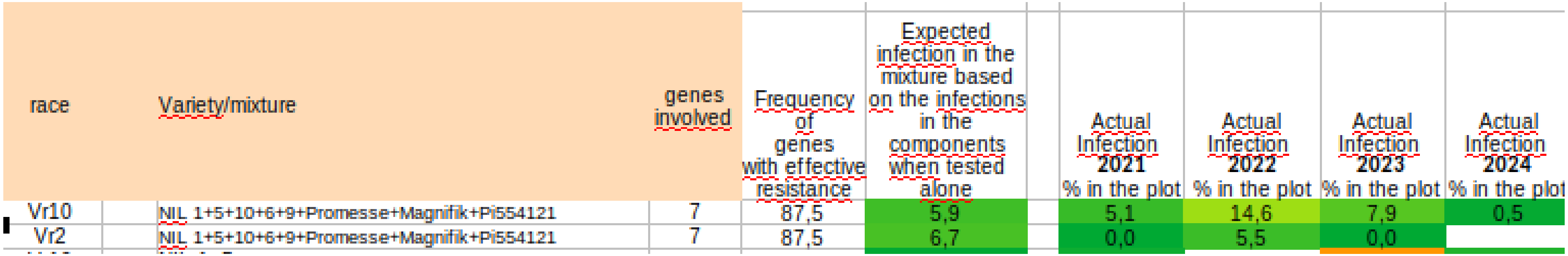
5 genes; 1 race



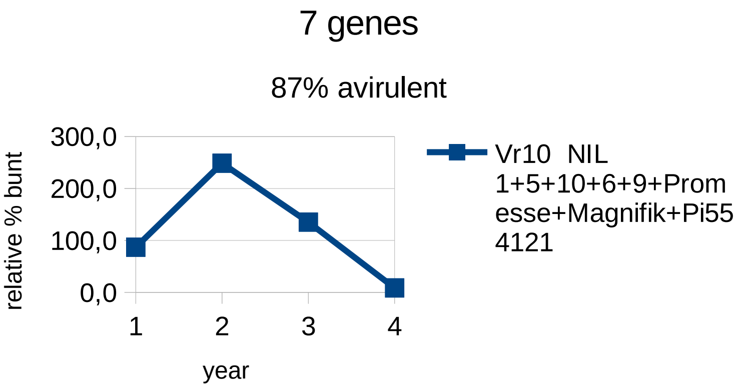
race	Variety/mixture	genes involved	Frequency of genes with effective resistance	Expected infection in the mixture based on the infections in the components when tested alone		Actual Infection **2021** % in the plot	Actual Infection **2022** % in the plot	Actual Infection **2023** % in the plot	Actual Infection **2024** % in the plot
Vr10	NIL 1+5+10+6+9+Promesse	5	83,3	7,8		5,4	13,6	5,2	3,4
Vr2	NIL 1+5+10+6+9+Promesse	5	83,3	7,8		0,0	19,6	3,4	0,5
Vr5	NIL 1+5+10+6+9+Promesse+Magnifik	5	71,4	13,4		2,4	9,3	8,4	2,4

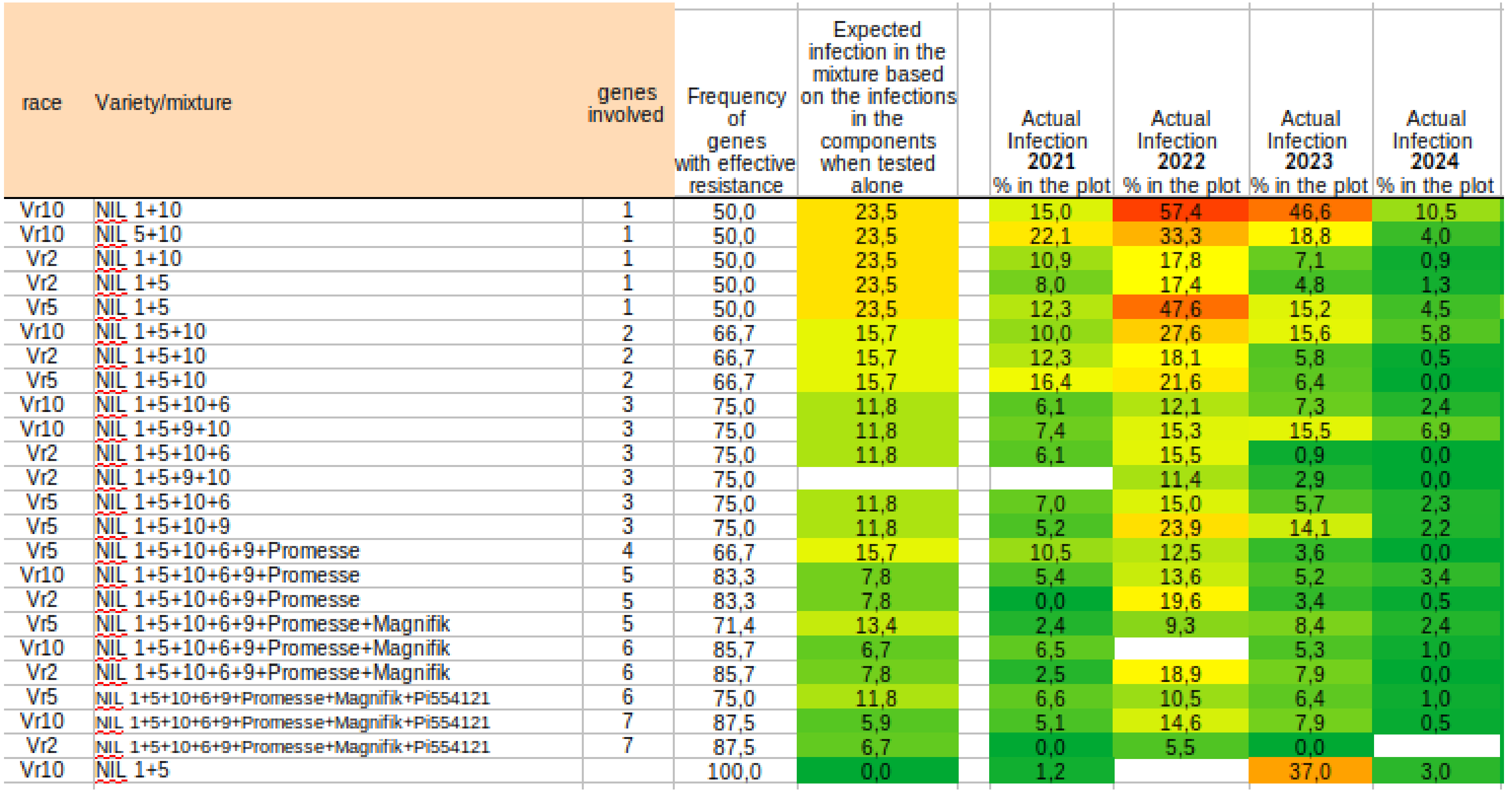


7 genes; 1 race

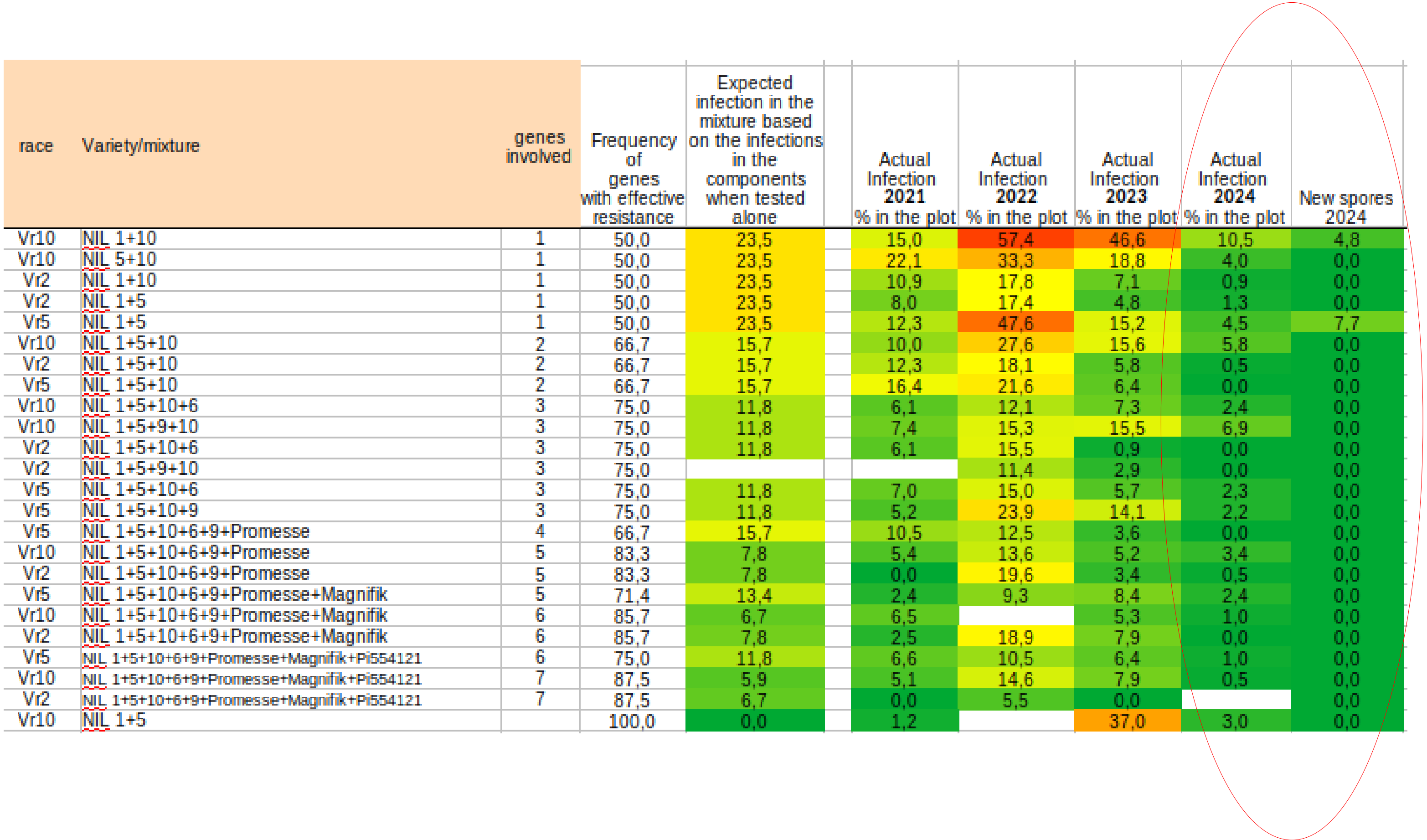


race		Variety/mixture	genes involved	Frequency of genes with effective resistance	Expected infection in the mixture based on the infections in the components when tested alone		Actual Infection **2021** % in the plot	Actual Infection **2022** % in the plot	Actual Infection **2023** % in the plot	Actual Infection **2024** % in the plot
Vr10		NIL 1+5+10+6+9+Promesse+Magnifik+Pi554121	7	87,5	5,9		5,1	14,6	7,9	0,5
Vr2		NIL 1+5+10+6+9+Promesse+Magnifik+Pi554121	7	87,5	6,7		0,0	5,5	0,0	



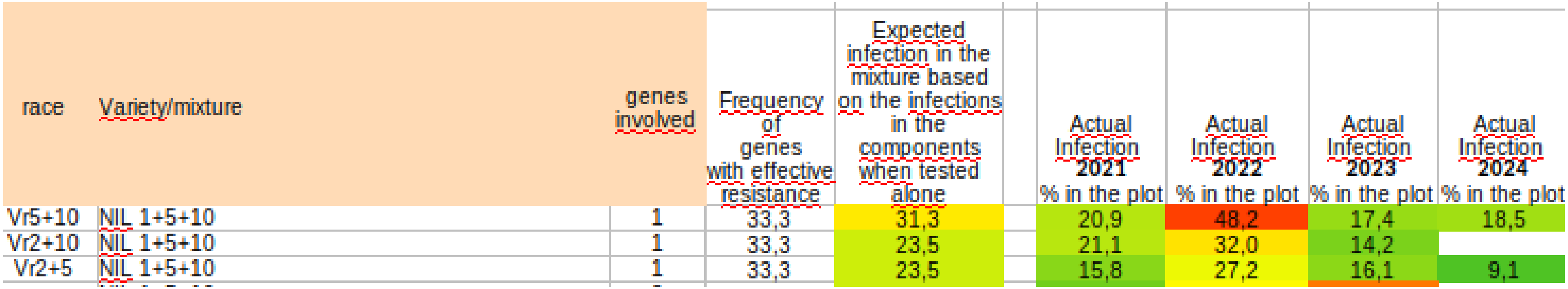


race	Variety/mixture	genes involved	Frequency of genes with effective resistance	Expected infection in the mixture based on the infections in the components when tested alone		Actual Infection **2021** % in the plot	Actual Infection **2022** % in the plot	Actual Infection **2023** % in the plot	Actual Infection **2024** % in the plot
Vr10	NIL 1+10	1	50,0	23,5		15,0	57,4	46,6	10,5
Vr10	NIL 5+10	1	50,0	23,5		22,1	33,3	18,8	4,0
Vr2	NIL 1+10	1	50,0	23,5		10,9	17,8	7,1	0,9
Vr2	NIL 1+5	1	50,0	23,5		8,0	17,4	4,8	1,3
Vr5	NIL 1+5	1	50,0	23,5		12,3	47,6	15,2	4,5
Vr10	NIL 1+5+10	2	66,7	15,7		10,0	27,6	15,6	5,8
Vr2	NIL 1+5+10	2	66,7	15,7		12,3	18,1	5,8	0,5
Vr5	NIL 1+5+10	2	66,7	15,7		16,4	21,6	6,4	0,0
Vr10	NIL 1+5+10+6	3	75,0	11,8		6,1	12,1	7,3	2,4
Vr10	NIL 1+5+9+10	3	75,0	11,8		7,4	15,3	15,5	6,9
Vr2	NIL 1+5+10+6	3	75,0	11,8		6,1	15,5	0,9	0,0
Vr2	NIL 1+5+9+10	3	75,0				11,4	2,9	0,0
Vr5	NIL 1+5+10+6	3	75,0	11,8		7,0	15,0	5,7	2,3
Vr5	NIL 1+5+10+9	3	75,0	11,8		5,2	23,9	14,1	2,2
Vr5	NIL 1+5+10+6+9+Promesse	4	66,7	15,7		10,5	12,5	3,6	0,0
Vr10	NIL 1+5+10+6+9+Promesse	5	83,3	7,8		5,4	13,6	5,2	3,4
Vr2	NIL 1+5+10+6+9+Promesse	5	83,3	7,8		0,0	19,6	3,4	0,5
Vr5	NIL 1+5+10+6+9+Promesse+Magnifik	5	71,4	13,4		2,4	9,3	8,4	2,4
Vr10	NIL 1+5+10+6+9+Promesse+Magnifik	6	85,7	6,7		6,5		5,3	1,0
Vr2	NIL 1+5+10+6+9+Promesse+Magnifik	6	85,7	7,8		2,5	18,9	7,9	0,0
Vr5	NIL 1+5+10+6+9+Promesse+Magnifik+Pi554121	6	75,0	11,8		6,6	10,5	6,4	1,0
Vr10	NIL 1+5+10+6+9+Promesse+Magnifik+Pi554121	7	87,5	5,9		5,1	14,6	7,9	0,5
Vr2	NIL 1+5+10+6+9+Promesse+Magnifik+Pi554121	7	87,5	6,7		0,0	5,5	0,0	
Vr10	NIL 1+5		100,0	0,0		1,2		37,0	3,0

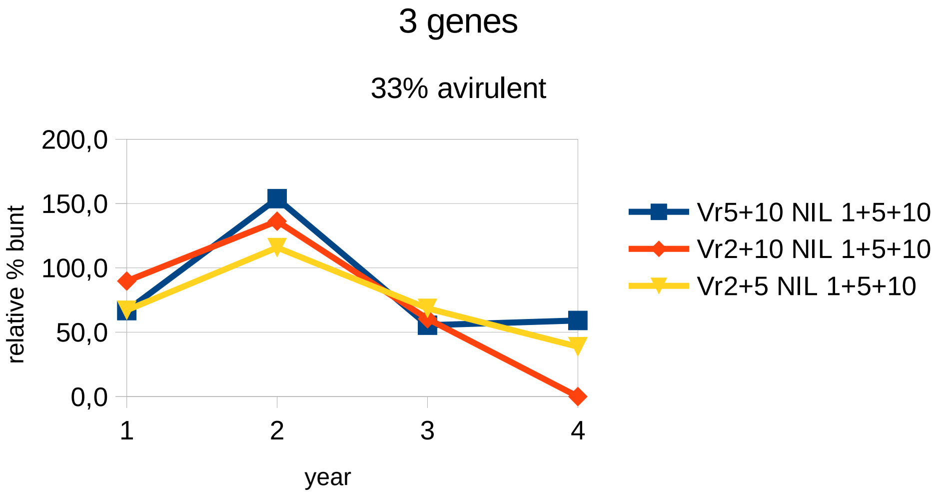


race	Variety/mixture	genes involved	Frequency of genes with effective resistance	Expected infection in the mixture based on the infections in the components when tested alone		Actual Infection **2021** % in the plot	Actual Infection **2022** % in the plot	Actual Infection **2023** % in the plot	Actual Infection **2024** % in the plot	New spores 2024
Vr10	NIL 1+10	1	50,0	23,5		15,0	57,4	46,6	10,5	4,8
Vr10	NIL 5+10	1	50,0	23,5		22,1	33,3	18,8	4,0	0,0
Vr2	NIL 1+10	1	50,0	23,5		10,9	17,8	7,1	0,9	0,0
Vr2	NIL 1+5	1	50,0	23,5		8,0	17,4	4,8	1,3	0,0
Vr5	NIL 1+5	1	50,0	23,5		12,3	47,6	15,2	4,5	7,7
Vr10	NIL 1+5+10	2	66,7	15,7		10,0	27,6	15,6	5,8	0,0
Vr2	NIL 1+5+10	2	66,7	15,7		12,3	18,1	5,8	0,5	0,0
Vr5	NIL 1+5+10	2	66,7	15,7		16,4	21,6	6,4	0,0	0,0
Vr10	NIL 1+5+10+6	3	75,0	11,8		6,1	12,1	7,3	2,4	0,0
Vr10	NIL 1+5+9+10	3	75,0	11,8		7,4	15,3	15,5	6,9	0,0
Vr2	NIL 1+5+10+6	3	75,0	11,8		6,1	15,5	0,9	0,0	0,0
Vr2	NIL 1+5+9+10	3	75,0				11,4	2,9	0,0	0,0
Vr5	NIL 1+5+10+6	3	75,0	11,8		7,0	15,0	5,7	2,3	0,0
Vr5	NIL 1+5+10+9	3	75,0	11,8		5,2	23,9	14,1	2,2	0,0
Vr5	NIL 1+5+10+6+9+Promesse	4	66,7	15,7		10,5	12,5	3,6	0,0	0,0
Vr10	NIL 1+5+10+6+9+Promesse	5	83,3	7,8		5,4	13,6	5,2	3,4	0,0
Vr2	NIL 1+5+10+6+9+Promesse	5	83,3	7,8		0,0	19,6	3,4	0,5	0,0
Vr5	NIL 1+5+10+6+9+Promesse+Magnifik	5	71,4	13,4		2,4	9,3	8,4	2,4	0,0
Vr10	NIL 1+5+10+6+9+Promesse+Magnifik	6	85,7	6,7		6,5		5,3	1,0	0,0
Vr2	NIL 1+5+10+6+9+Promesse+Magnifik	6	85,7	7,8		2,5	18,9	7,9	0,0	0,0
Vr5	NIL 1+5+10+6+9+Promesse+Magnifik+Pi554121	6	75,0	11,8		6,6	10,5	6,4	1,0	0,0
Vr10	NIL 1+5+10+6+9+Promesse+Magnifik+Pi554121	7	87,5	5,9		5,1	14,6	7,9	0,5	0,0
Vr2	NIL 1+5+10+6+9+Promesse+Magnifik+Pi554121	7	87,5	6,7		0,0	5,5	0,0		0,0
Vr10	NIL 1+5		100,0	0,0		1,2		37,0	3,0	0,0

3 genes; 2 race



race	Variety/mixture	genes involved	Frequency of genes with effective resistance	Expected infection in the mixture based on the infections in the components when tested alone		Actual Infection **2021** % in the plot	Actual Infection **2022** % in the plot	Actual Infection **2023** % in the plot	Actual Infection **2024** % in the plot
Vr5+10	NIL 1+5+10	1	33,3	31,3		20,9	48,2	17,4	18,5
Vr2+10	NIL 1+5+10	1	33,3	23,5		21,1	32,0	14,2	
Vr2+5	NIL 1+5+10	1	33,3	23,5		15,8	27,2	16,1	9,1



Sorry, no surprising conclusions

- Mixtures have lower infection compared to the theoretical expected infection level, most likely due to delusion of virulent spores
- Increasing numbers of resistant genes decreases infection levels in mixtures
- Infection level decreases over time at high infection levels due to selection
- Selection of resistant lines is faster than selection of virulence development
- At low infection levels, the effect of selection for improved resistance is expected to be low

Tank you for your attention