Co-evolution of virulence and resistance in heterogeneous wheat populations

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Introduction

In a population of wheat with divers genetic composition, natural selection will favour resistant varieties as susceptible lines will produce less seed. On the other hand, there will also be a selection pressure towards more spores with virulence to the resistance genes within the population. Little is known about the dynamics between these two forces in the co-evolution between resistance and virulence.

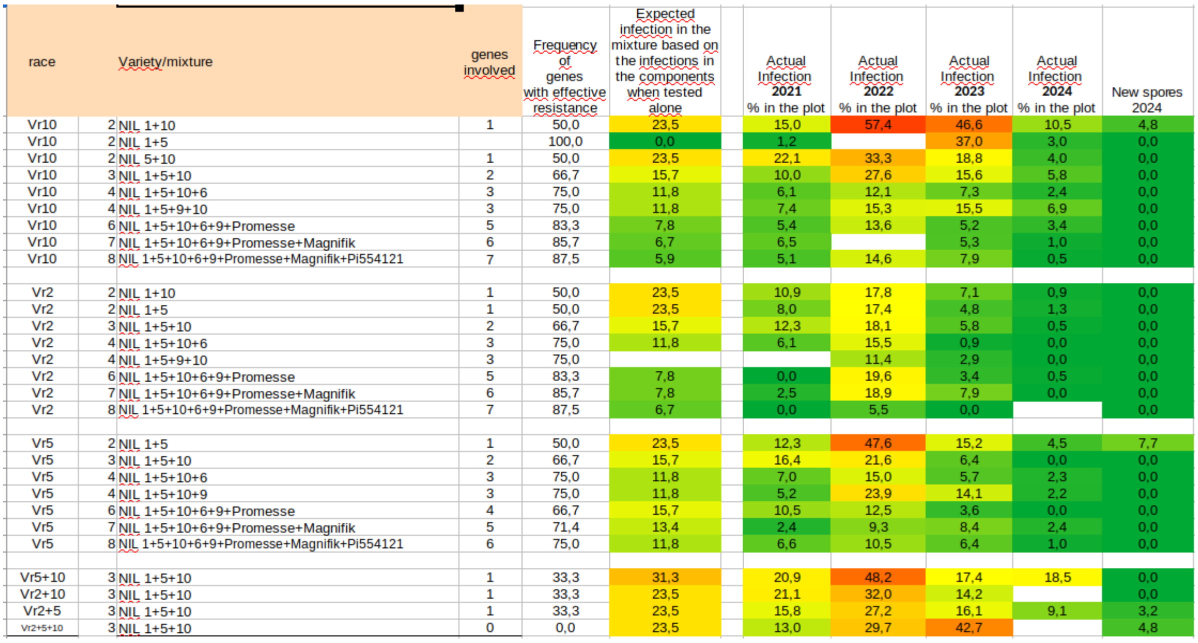
Materials and methods

8 mixtures were composed of wheat lines with known resistance genes. Each mixture included from one to 6 different resistance genes. Each mixture were contaminated with a race of common bunt (*Tilletia caries*) with virulence to one of the resistance genes in the mixture. Each year, the infection level in the field was recorded, and grain and spores were harvested and resown.

Results and discussion

Over a four year period of regrowing mixtures, the infection level of common bunt gradually decreased, demonstrating that selection towards resistance in the mixture dominate over selection for virulence in the fungal spores. However, after four years, bunt infection were still detectable in most mixtures, also in mixtures with a high degree of diversity in resistance genes. The bunt selection pressure in the experiment was much higher that what would be acceptable in commercial agriculture conditions. The experiment can therefore only explain dominating tendencies over time, and cannot be recommended as a strategy to control common bunt for practical farming.

In the last year of the experiment, the mixtures were also contaminated with new spores of the initial race instead of the spores from previous year. This resulted in decreased infection level compared with spores from natural selection. This demonstrate that some selection and adaptation to the wheat resistance has taken place, and the mixtures had become more resistant to primary infection from external spores.



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	2	NIL 1+10	1	50,0	23,5	15,0	57,4	46,6	10,5	4,8
Vr10	2	NIL 1+5		100,0	0,0	1,2		37,0	3,0	0,0
Vr10	2	NIL 5+10	1	50,0	23,5	22,1	33,3	18,8	4,0	0,0
Vr10	3	NIL 1+5+10	2	66,7	15,7	10,0	27,6	15,6	5,8	0,0
Vr10	4	NIL 1+5+10+6	3	75,0	11,8	6,1	12,1	7,3	2,4	0,0
Vr10	4	NIL 1+5+9+10	3	75,0	11,8	7,4	15,3	15,5	6,9	0,0
Vr10	6	NIL 1+5+10+6+9+Promesse	5	83,3	7,8	5,4	13,6	5,2	3,4	0,0
Vr10	7	NIL 1+5+10+6+9+Promesse+Magnifik	6	85,7	6,7	6,5		5,3	1,0	0,0
Vr10	8	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	2	NIL 1+10	1	50,0	23,5	10,9	17,8	7,1	0,9	0,0
Vr2	2	NIL 1+5	1	50,0	23,5	8,0	17,4	4,8	1,3	0,0
Vr2	3	NIL 1+5+10	2	66,7	15,7	12,3	18,1	5,8	0,5	0,0
Vr2	4	NIL 1+5+10+6	3	75,0	11,8	6,1	15,5	0,9	0,0	0,0
Vr2	4	NIL 1+5+9+10	3	75,0			11,4	2,9	0,0	0,0
Vr2	6	NIL 1+5+10+6+9+Promesse	5	83,3	7,8	0,0	19,6	3,4	0,5	0,0
Vr2	7	NIL 1+5+10+6+9+Promesse+Magnifik	6	85,7	7,8	2,5	18,9	7,9	0,0	0,0
Vr2	8	NIL 1+5+10+6+9+Promesse+Magnifik+Pi554121	7	87,5	6,7	0,0	5,5	0,0		0,0
Vr5	2	NIL 1+5	1	50,0	23,5	12,3	47,6	15,2	4,5	7,7
Vr5	3	NIL 1+5+10	2	66,7	15,7	16,4	21,6	6,4	0,0	0,0
Vr5	4	NIL 1+5+10+6	3	75,0	11,8	7,0	15,0	5,7	2,3	0,0
Vr5	4	NIL 1+5+10+9	3	75,0	11,8	5,2	23,9	14,1	2,2	0,0
Vr5	6	NIL 1+5+10+6+9+Promesse	4	66,7	15,7	10,5	12,5	3,6	0,0	0,0
Vr5	7	NIL 1+5+10+6+9+Promesse+Magnifik	5	71,4	13,4	2,4	9,3	8,4	2,4	0,0
Vr5	8	NIL 1+5+10+6+9+Promesse+Magnifik+Pi554121	6	75,0	11,8	6,6	10,5	6,4	1,0	0,0
Vr5+10	3	NIL 1+5+10	1	33,3	31,3	20,9	48,2	17,4	18,5	0,0
Vr2+10	3	NIL 1+5+10	1	33,3	23,5	21,1	32,0	14,2		0,0
Vr2+5	3	NIL 1+5+10	1	33,3	23,5	15,8	27,2	16,1	9,1	3,2
Vr2+5+10	3	NIL 1+5+10	0	0,0	23,5	13,0	29,7	42,7		4,8

Acknowledgments

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