NETWORK-BASED GWAS OF RASE-SPECIFIC RESISTANCES TO COMMON BUNT (*TILLETIA CARIES*) IN WHEAT

Jelena Baćanović-Šišić, Dominic Dennenmoser and Gunter Backes

University of Kassel, Section of Organic Plant Breeding and Agrobiodiversity, Germany

Aim of the research

- Lack of the knowledege about genetic basis of the resistance
- Gene – for – gene concept
- Until now 3 resistance genes have been mapped – Bt 9 on 6DL, Bt10 on 6DS and Bt 12 on 7DS
- Resistant cultivars mean of the disease control in organic agriculture
- Goal - development of molecular markers (KASP) for range of resistance genes against common bunt (*Tilletia caries)* in wheat
- To be used in MAS in wheat

Materials and Methods

- 455 wheat varieties and breeding lines were phenotyped in 2018 and 2019 in Denmark by Agrologica
- 274 selected lines were genotyped with 25K SNP micro array chip (TraitGenetics, Germany)
- Infected with 8 to 13 races of common bunt

Isolate	2018	2019	Virulent against	Comment
Vr0	●			
Vr1	●		Bt-1, Bt-2, Bt-7	= Vr2
Vr2	●	●	Bt-1, Bt-2, Bt-7	
VrR	●	●	Bt-2, Bt-3	=Vr3
Vr4	●		(Bt-2)	
VrG	●	●	Bt-7	=Vr5
Vr8	●	●	Bt-7, Bt-11	
Vr10	●	●	Bt-7. Bt-11, Bt-Z	
Vr13	●	●	Bt-13	
Vr341	●	●	Bt-Z	
Vr3540	●		Bt1?	
VrDot	●		Bt-2	Dottenfelderhof
VrP	●	●		

Materials and Methods

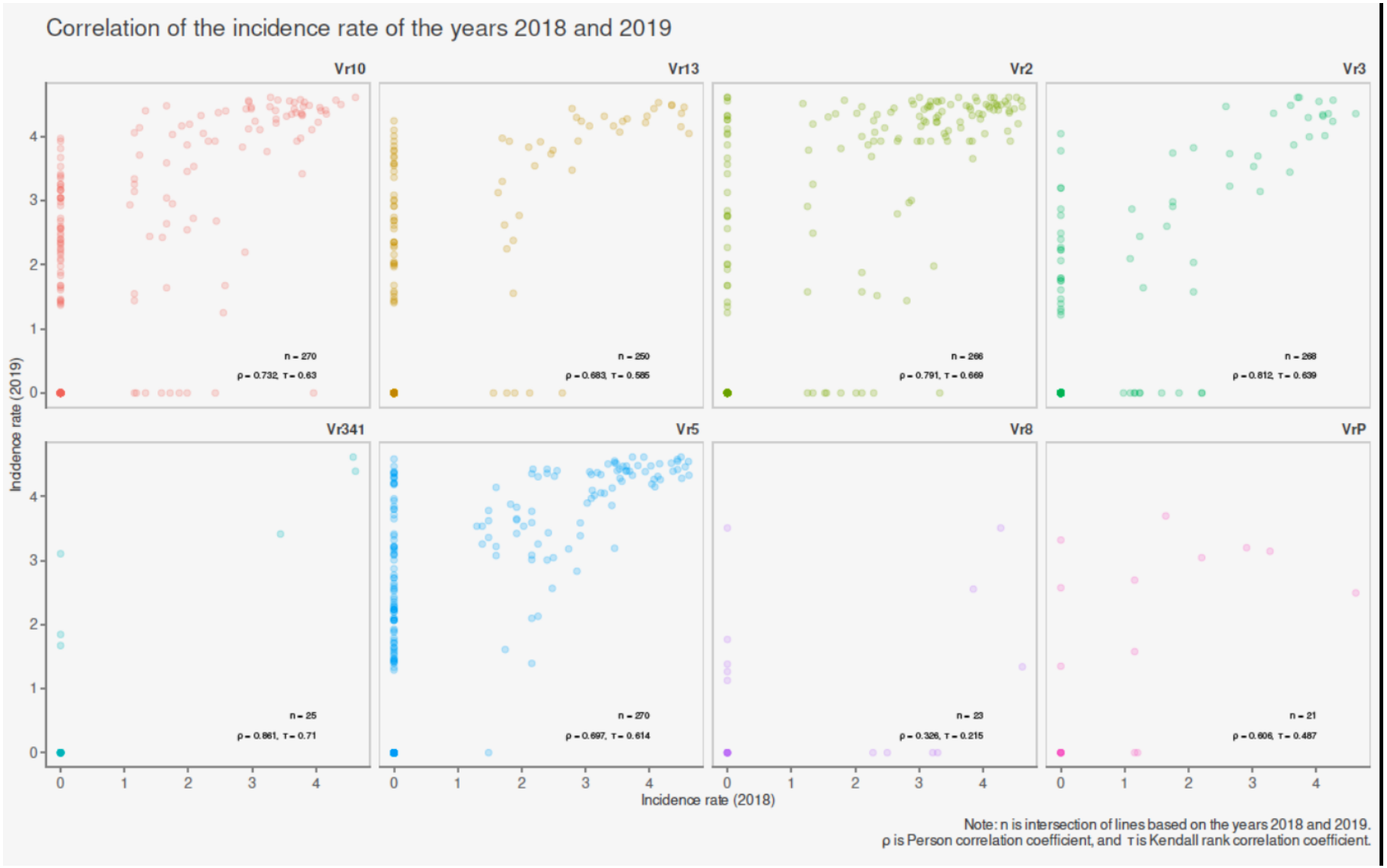
- Lines with the gene postulation Bt1 to Bt 13 have been phenotyped
- Lines presented in one experimental year and Vr tested on small numbers of lines were excluded
- Only Vr13, Vr10, Vr5, Vr2 and Vr3 icluded in the analysis
- Network-based GWAS

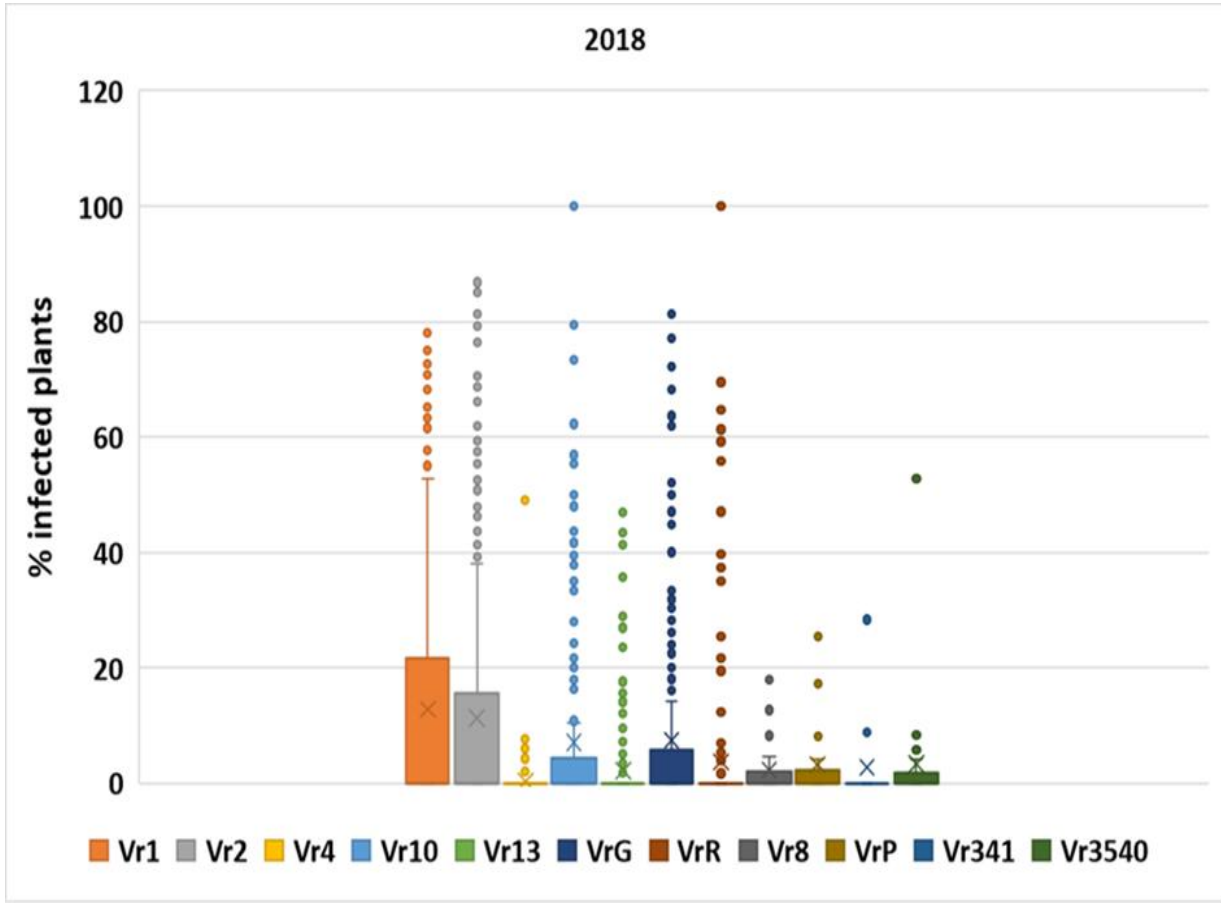
Gene postulation	Number of lines
Bt5	75
Bt7	59
Bt13	32
Bt1	30
Bt2	30
BtZ	26
BtQ	16
Bt6	2
Bt10	2
Bt+	2
Bt0	1
Bt9	1

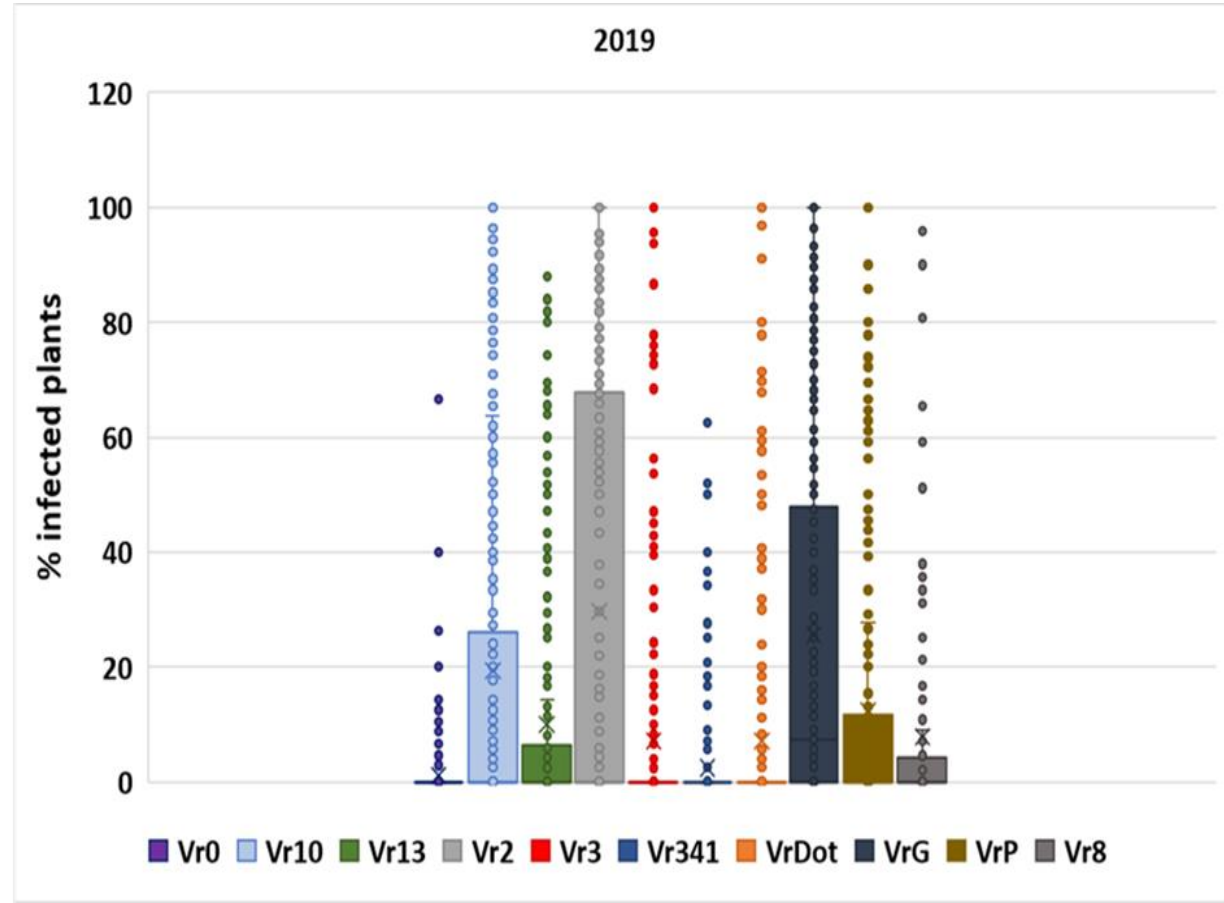
GWAS Methodology

- Problems occuring

  - Due to large number of 0, data were not normaly distributed
  - Big differences in infection rate of wheat in 2018 and 2019


Correlation of the incidence rate of the years 2018 and 2019
Vr10
n = 270
ρ = 0.732, τ = 0.63
Vr13
n = 250
ρ = 0.683, τ = 0.585
Vr2
n = 266
ρ = 0.791, τ = 0.669
Vr3
n = 268
ρ = 0.812, τ = 0.639
Vr341
n = 25
ρ = 0.861, τ = 0.71
Vr5
n = 270
ρ = 0.697, τ = 0.614
Vr8
n = 23
ρ = 0.326, τ = 0.215
VrP
n = 21
ρ = 0.606, τ = 0.487
Inddence rate (2019)
Incidence rate (2018)
Note: n is intersection of lines based on the years 2018 and 2019.
ρ is Person correlation coefficient, and τ is Kendall rank correlation coefficient.


2018
% infected plants
120
100
80
60
40
20
0
Vr1
Vr2
Vr4
Vr10
Vr13
VrG
VrR
Vr8
VrP
Vr341
Vr3540


2019
% infected plants
120
100
80
60
40
20
0
Vr0
Vr10
Vr13
Vr2
Vr3
Vr341
VrDot
VrG
VrP
Vr8

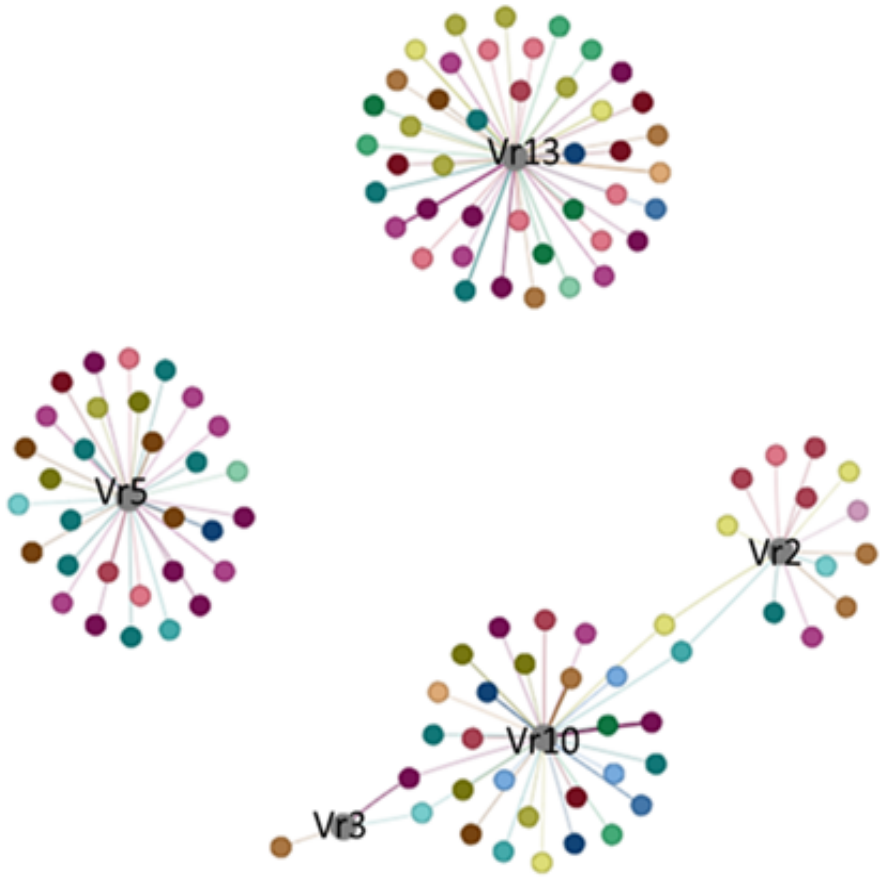
GWAS Methodology

- Maxima values of the standardized and log+1 transformed data of both years
- Network-based GWAS
  - can handle ordinal, non-Gaussian continuous data, and mixed discrete-and-continuous data
  - adjusts for the effect of all other SNPs and phenotypes while measuring the pairwise associations between them (accounting for population structure)
- Complex network of interactions among: (i) genetic markers, (ii) phenotypes, and (iii) between genetic markers and phenotypes

- Genetic maps of Allen et al. (2017) and Wang et al. (2014) have been utilised

Results

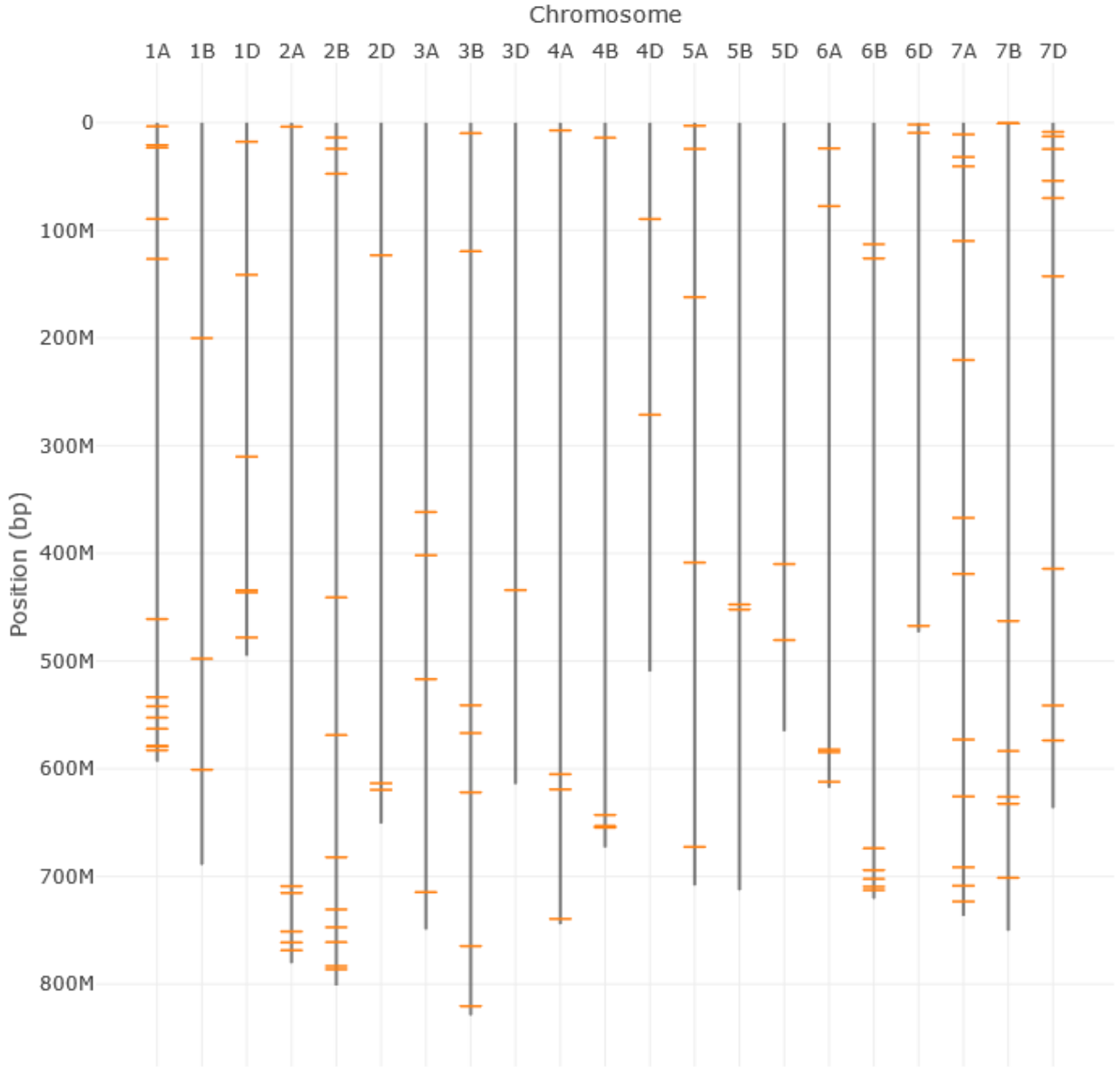
- 120 associated SNP markers ($r^2 \leq 0.2$)
  - 43 SNPs for the Vr13,
  - 31 for the Vr5,
  - 29 for the Vr10,
  - 14 for the Vr2 and
  - 3 for the Vr3.



Each edge represents the connection between two nodes, where each node is a SNP marker (colored, where each color represent a chromosome on which marker is located) or a virulence race (grey)

(r^2=0.20)

	Vr10	Vr13	Vr2	Vr3	Vr5	Total
1A	3	5		1	5	14
1B	2				1	3
1D	2	2	3			7
2A	1	1			4	6
2B	1	4	1		5	11
2D	1		1	1	1	4
3A	1	3				4
3B	1	3	2	1		7
3D			1			1
4A	2	1			1	4
4B	1	3				4
4D	1	1				2
5A	1	3			1	5
5B	1	1				2
5D		1			1	2
6A	3				2	5
6B	2	1	3		1	7
6D	3					3
7A	2	3	1		6	12
7B	1	5	1		1	8
7D		6	1		2	9



Distributiona and position of associated markers accross wheat genome

Next steps

- Still ongoing research
- Selection of promising candidate SNPs
- Development of the KASP markers
- To be tested in the laboratory

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