

Towards the Selection of RILs for Lodging, Anchorage and Drought Trials

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DALP – to assess Lodging and test Anchorage



DALP - DROUGHT, ANCHORAGE and LODGING PANEL

CIMMYT lines and SATYN panel

Elite varieties

Roth Res and JIC lines

DFW Breeders TK H17 and H18

EMS semi-dwarves

Selected Paragon x Garcia RILs

Watkins – all founder parents of NAM populations

Other parents of available populations

DALP – to assess Lodging and test Anchorage



- All (except one) founder parents of NAM populations present in DALP
- ~ 230 lines + / - irrigation
- Spaced plants (~ 5.5. cm apart)
- 6m plots so able to irrigate with boom
- Usual field phenotyping (DTEM / HT / YLD)
- Lodging scores (after early June severe weather, will assess again)
- Will sacrifice specified segment of plots to anchorage tests

Assessing lodging traits from Paragon NAM background



- An additional year of the Paragon x Garcia Drought Trial was essential as only one spring drought occurred in the first three seasons
- Fortunately had strong spring drought in April 2019 so decision vindicated
- But this delayed scheduled exploration of new populations for lodging, anchorage and drought.
- Needed to compensate for this and explore more populations than originally planned
- Decided on mixed trial of a number of RIL populations the results of which should allow us a number of potential suitable populations to drill in autumn 2020

Assessing lodging traits from Paragon NAM background



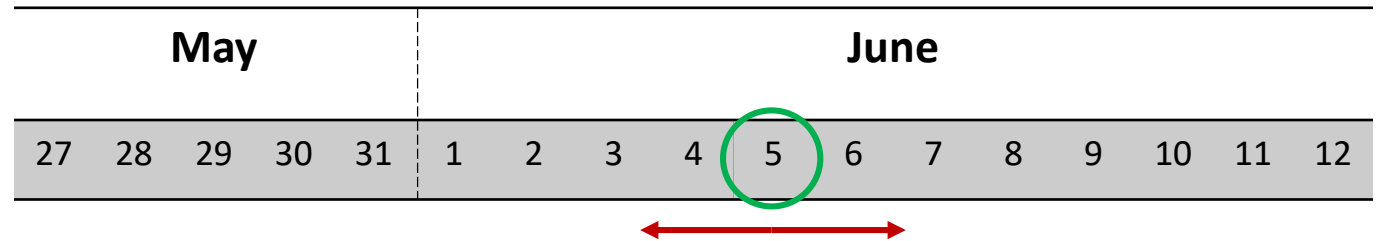
- Nested association mapping (NAM) populations
- WGIN and DFW have 80+ populations of crosses between Paragon and founder parents (including the Watkins collection)
- Minimum of 96 RILs per founder parent
- Find marker associated traits for lodging with high accuracy
- Need to select 1-3 populations for autumn 2020 trials

RIL Selection – 3-step process – Paragon is benchmark



- Selected RILs with phenotypes similar to Paragon, where possible

1) DTEM – very similar heading date



2) Height

3) Yield

From each population up to 11 lines were selected

1) DTEM

2) Height – similar or slightly smaller

3) Yield



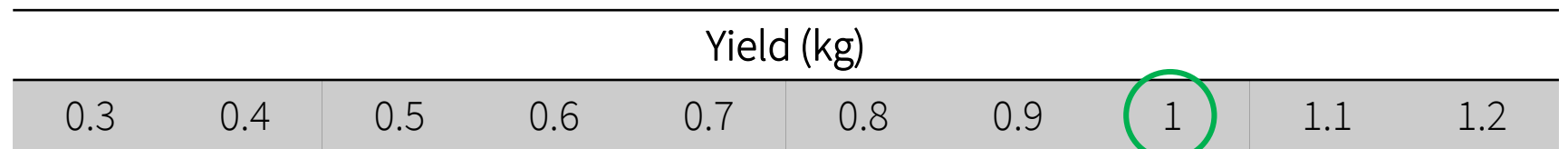
cm
93
92
91
90
89
88
87
86
85
84
83
82
81
80



From each population up to 11 lines were selected

1) DTEM

2) Height



3) Yield – similar or slightly greater

Trial design and measurements



- 466 RILs selected from 52 crosses (up to 11 lines / population)
- Drilled in 1 m plots, randomized design, single rep
- Phenotyping:
 - DTEM, HT, YLD
 - Lodging (after early June severe weather, will assess again)
 - Stiffness (currently concentrating on populations where some RILs lodged and some not)

Scoring Lodging and Stem Stiffness



- Lodging scored 2-3 times over 10 days in all lines (NAM and DALP) after severe weather in early June
- Trying to identify a population(s) where lodging is a segregating trait
- Looked at NAM populations where some RILs had lodged but not many – 13+ currently identified
- Some completely lodged, some no lodging
- Variation in severity of lodging, some lines recovered, others didn't
- Stem stiffness compared to Paragon

Latest Lodging and Stem Stiffness Results



RIL popn	DALP		RILs			
	DTEM from 1st May	Parent	Lodging	Stiffness (partial data)		
				1 (<P)	2 (=P)	3 (>P)
Paragon x Bacard Kachu	9.5	1	3 of 11	2	2	1
Paragon x Fiorello	21	x	3 of 11		4	
Paragon x Super 152	11.5	1	2 of 11	1	4	
Paragon x Waxwing	9	x	2 of 7	2		1
Paragon x Watkins 94	31	2	7 of 9		2	2
Paragon x Watkins 126	17	2	4 of 11	2	3	3
Paragon x Watkins 199	19.5	1	4 of 9	1	2	
Paragon x Watkins 224	28	3	5 of 10		1	4
Paragon x Watkins 471	24.5	3	4 of 11			6
Paragon x Watkins 496	25.5	x	3 of 11	1	2	2
Paragon x Watkins 560	26	3	5 of 10	1		3
Paragon x Watkins 694	21	2	6 of 11		1	4
Paragon x Watkins 749	26	3	3 of 10			4
Paragon	33.5	x				
		x - no lodging				
		1 - slight lodging				
		2 - medium lodging				
		3 - severe lodging				

Selection of RIL population(s)



- Want to identify as many potential populations as possible having a range of 'lodgability' and stem stiffness
- Will need to do germination tests on these to check good level of viability
- Will select 1-3 population to drill this autumn +/- irrigation

Diversity Update July 2020



Andrew Riche



ROTHAMSTED
RESEARCH

Diversity 2020



Sown end Oct

Rather thin – not expecting good yields

Hyperspectral reflectance & UAV flights weekly from end-May

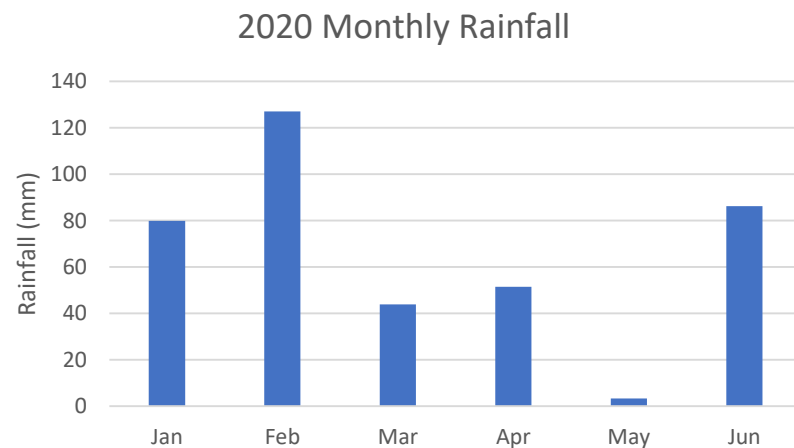
Disease assessments:

14-16 May

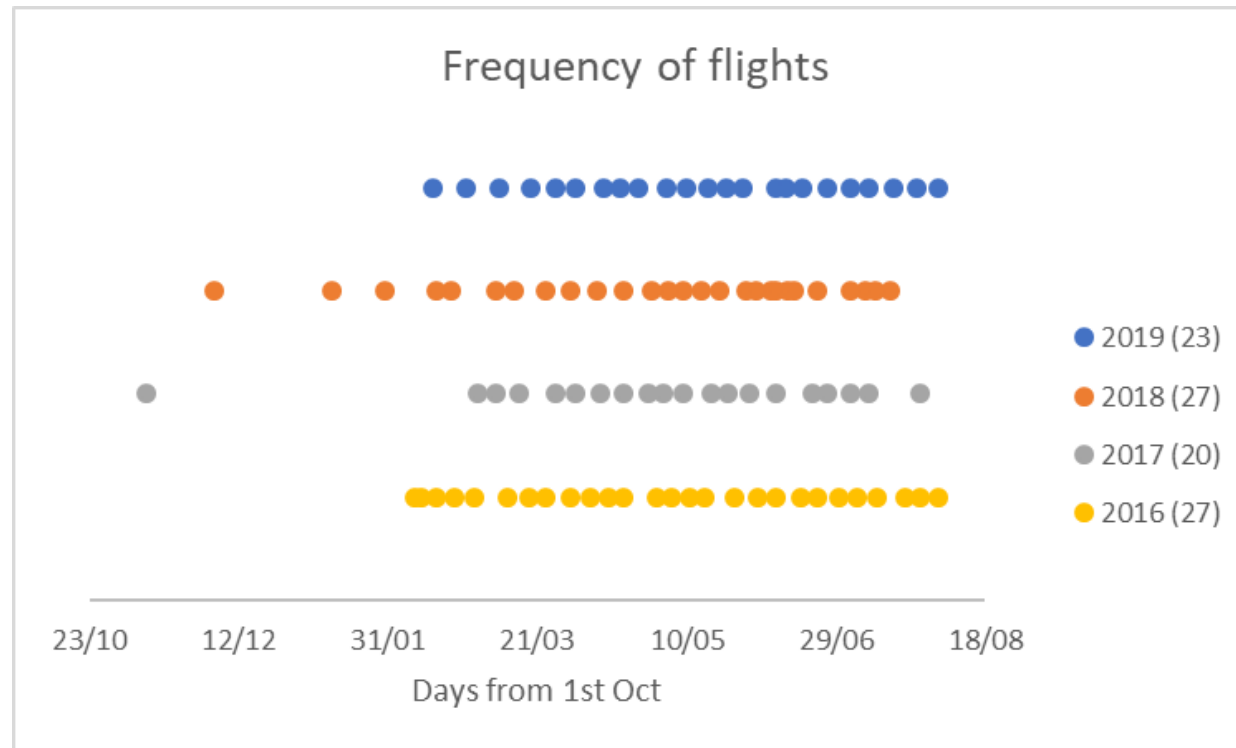
27-29 May

15 June

02 July



UAV Data processing



Timings

For each experiment:

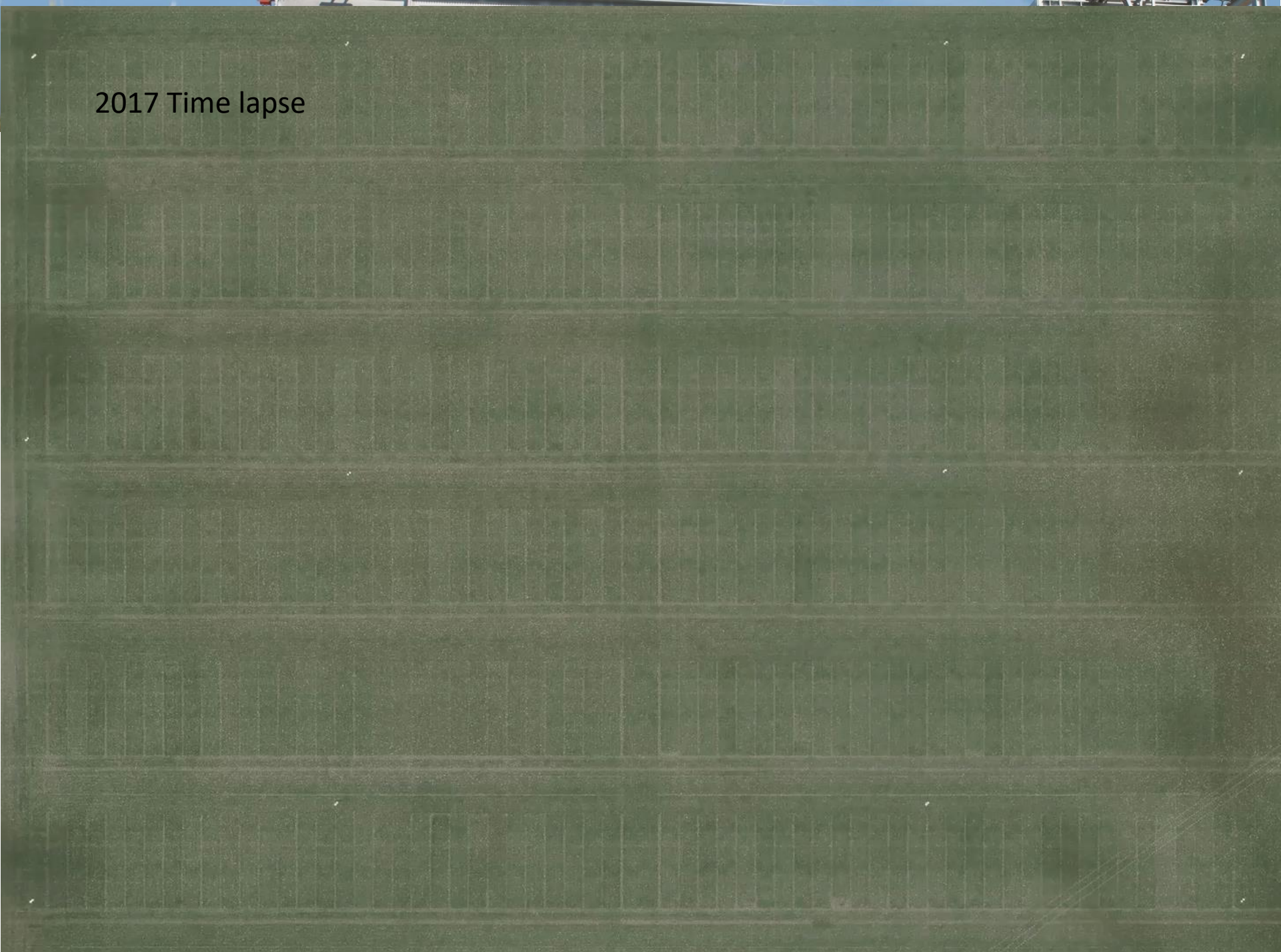
Operation	Hr	Notes
Planning flight	1	
Setting out GCPs & logging position, remove end of season	4 (incl two people)	Usually 2 people
Clear round GCPs	1	
Drawing shape file	2-8	

For each flight:

Operation	Time	
Flying time	1	Including charging batteries
Assigning GCPs & running software	0.5 * 2 for RGB + NIR	

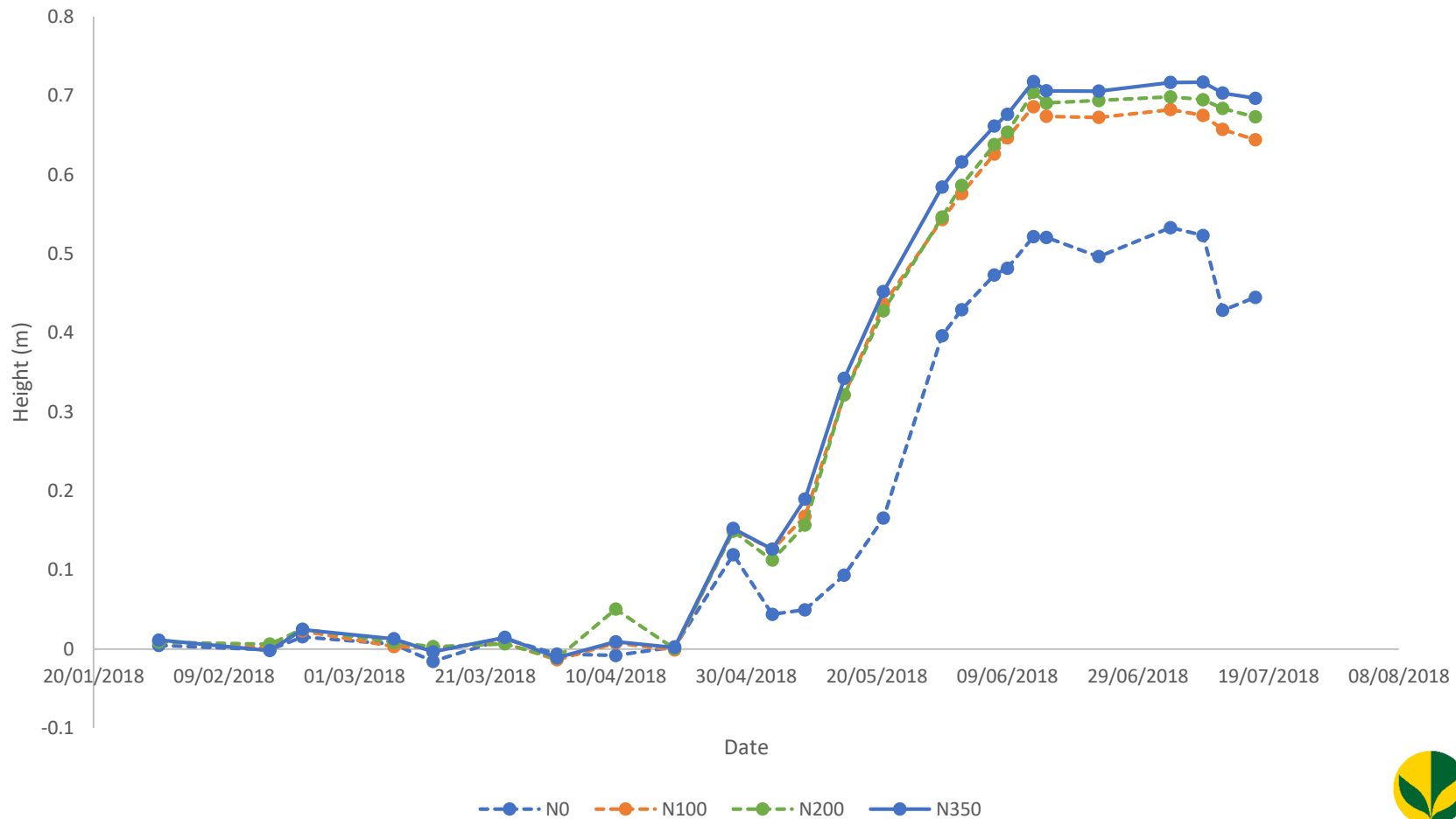
Plus 18-32hrs computer time per image set (600 images) x2 for RGB and NIR

2017 Time lapse



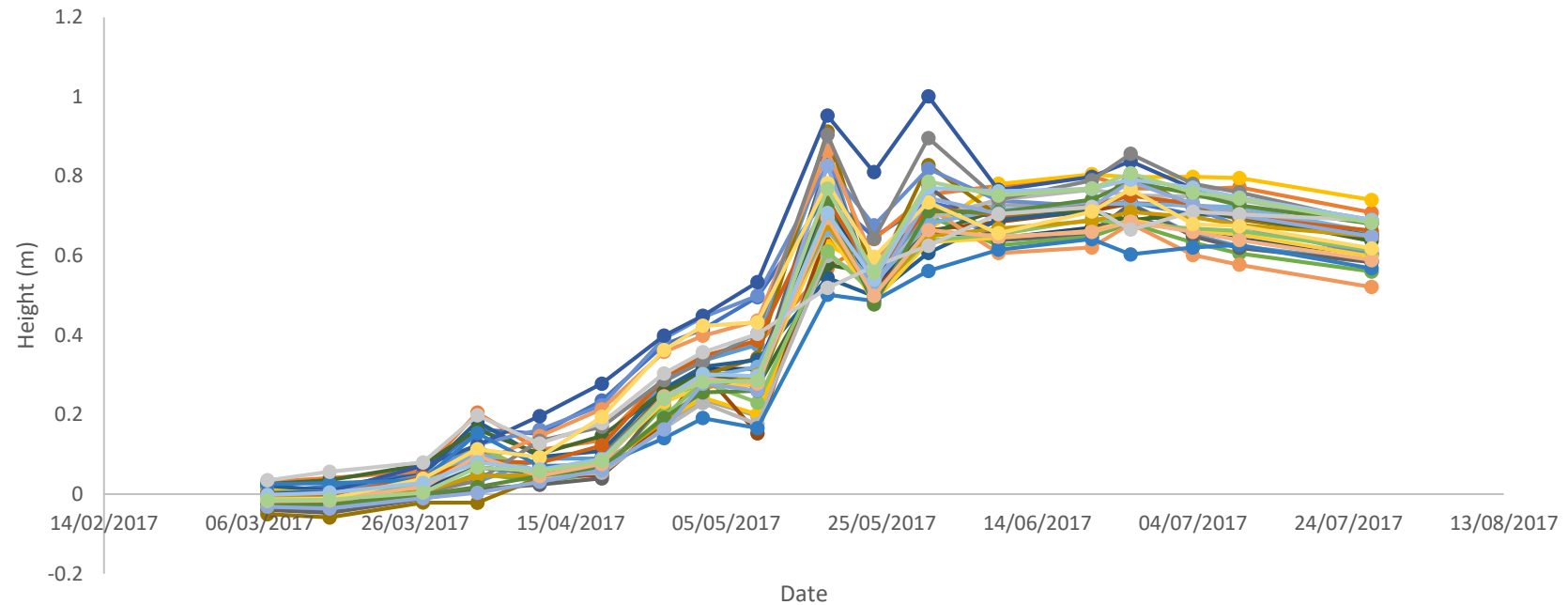
Diversity 2018 UAV data

2018 Plant height meaned across varieties



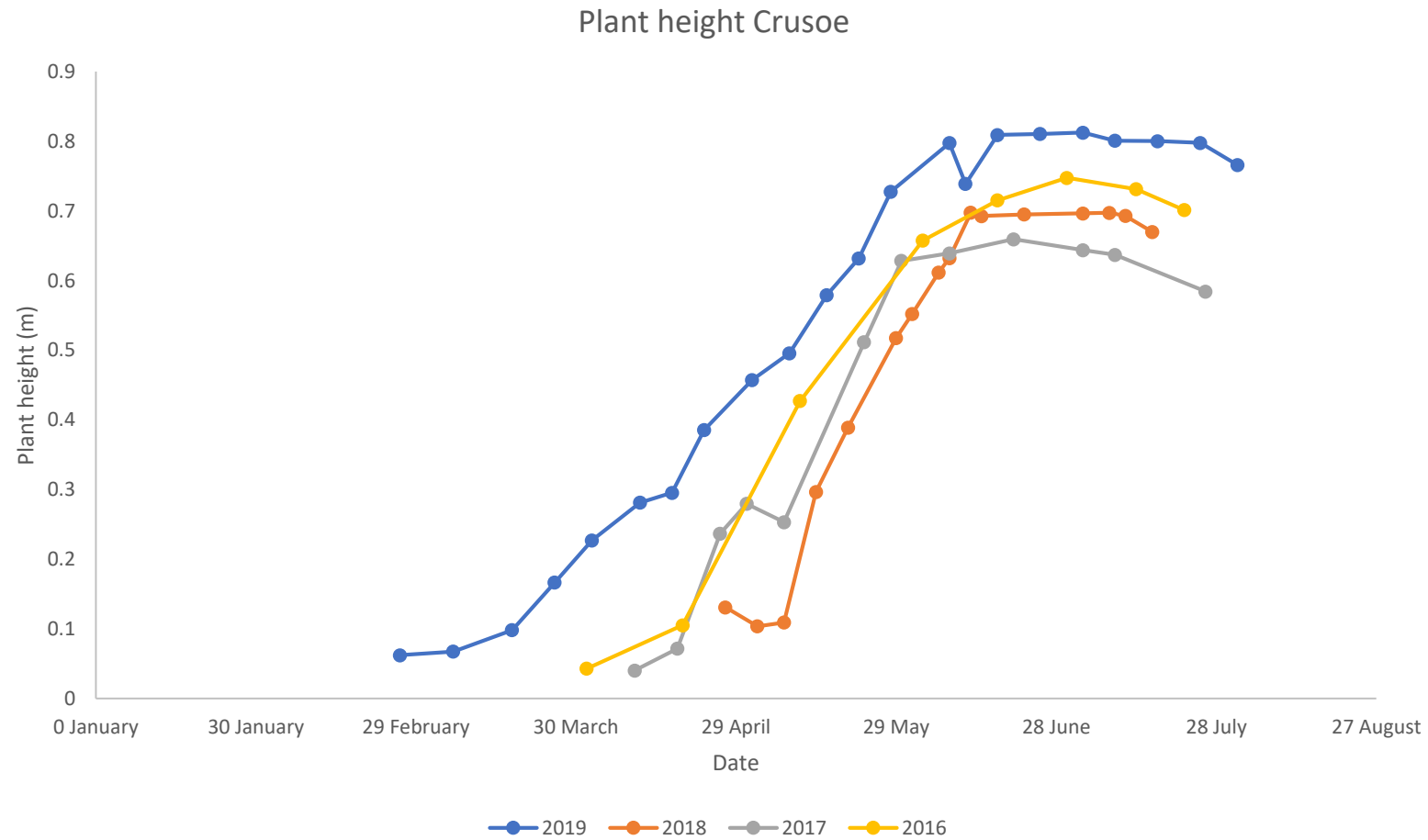
Diversity 2017 UAV data

2017 Plant height N200 SFP

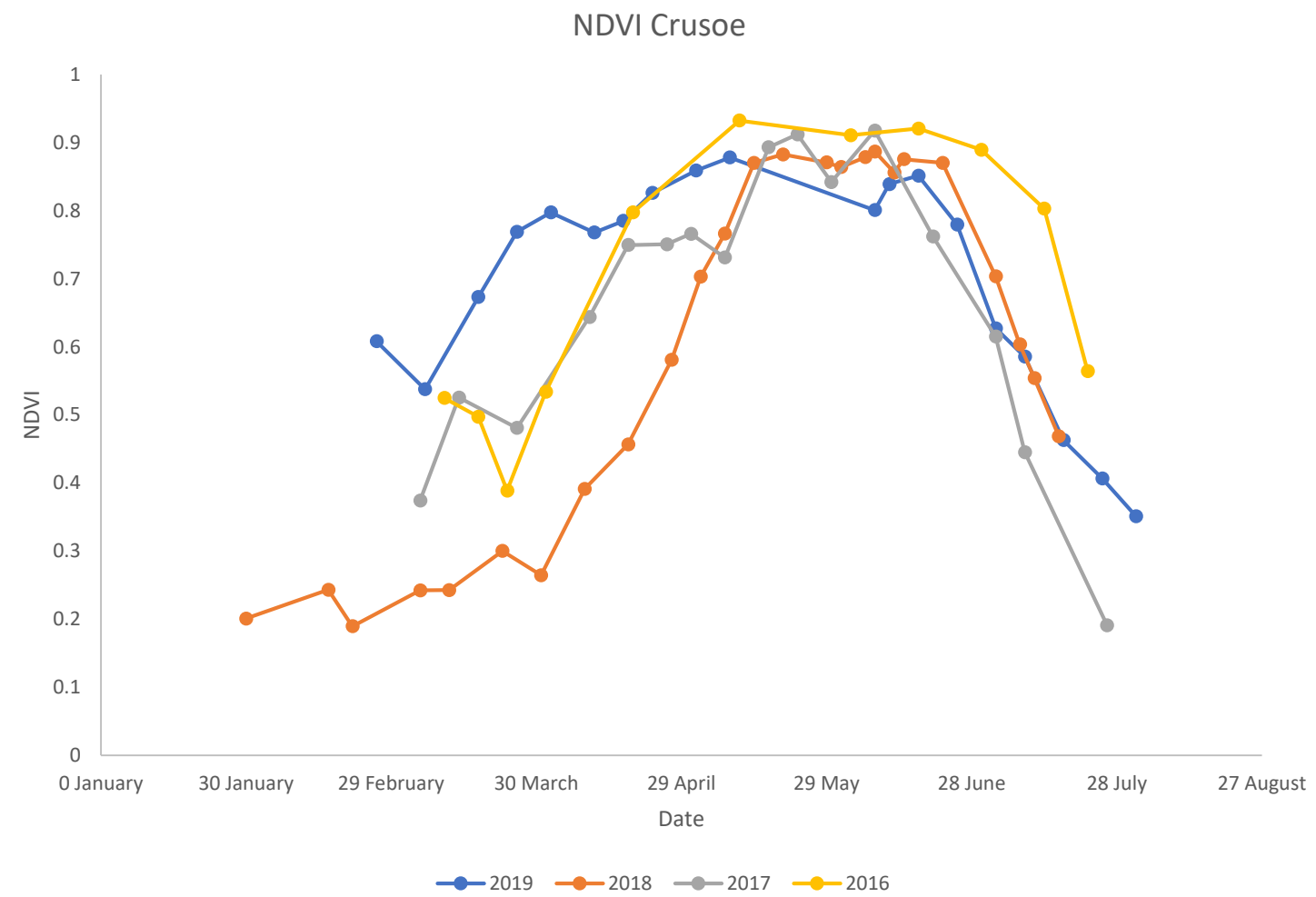


- Avalon
- Cadenza
- Claire
- Cocoon
- Conqueror
- Cordiale
- Crusoe
- Evolution
- Gallant
- Graham
- Hereford
- Hereward
- Hylux
- KWS Lili
- LEEDS
- Malacca
- Maris Widgeon
- Mercia
- Paragon
- RAGT Illustrious
- Reflection
- Riband
- Robigus
- Siskin
- Skyfall
- Soissons + Solstice Mix
- Solstice
- Xi19

Crop height – growth patterns between yrs

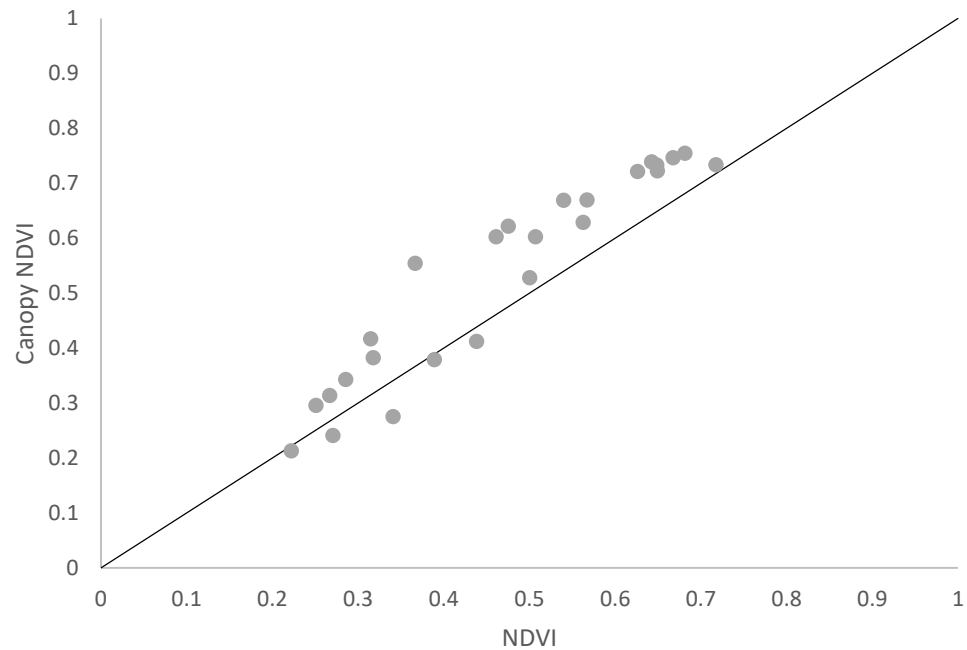


Crop NDVI

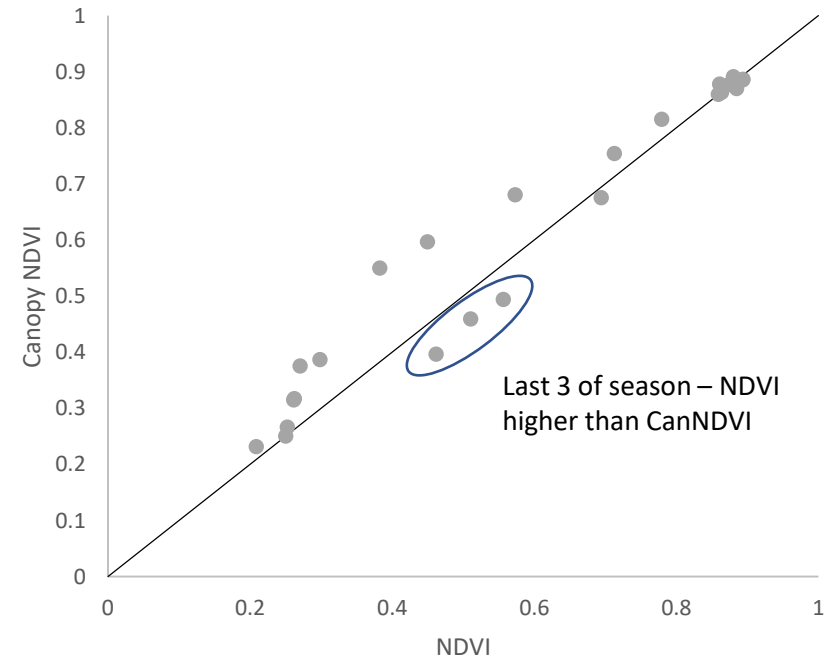


Diversity 2018 Canopy NDVI

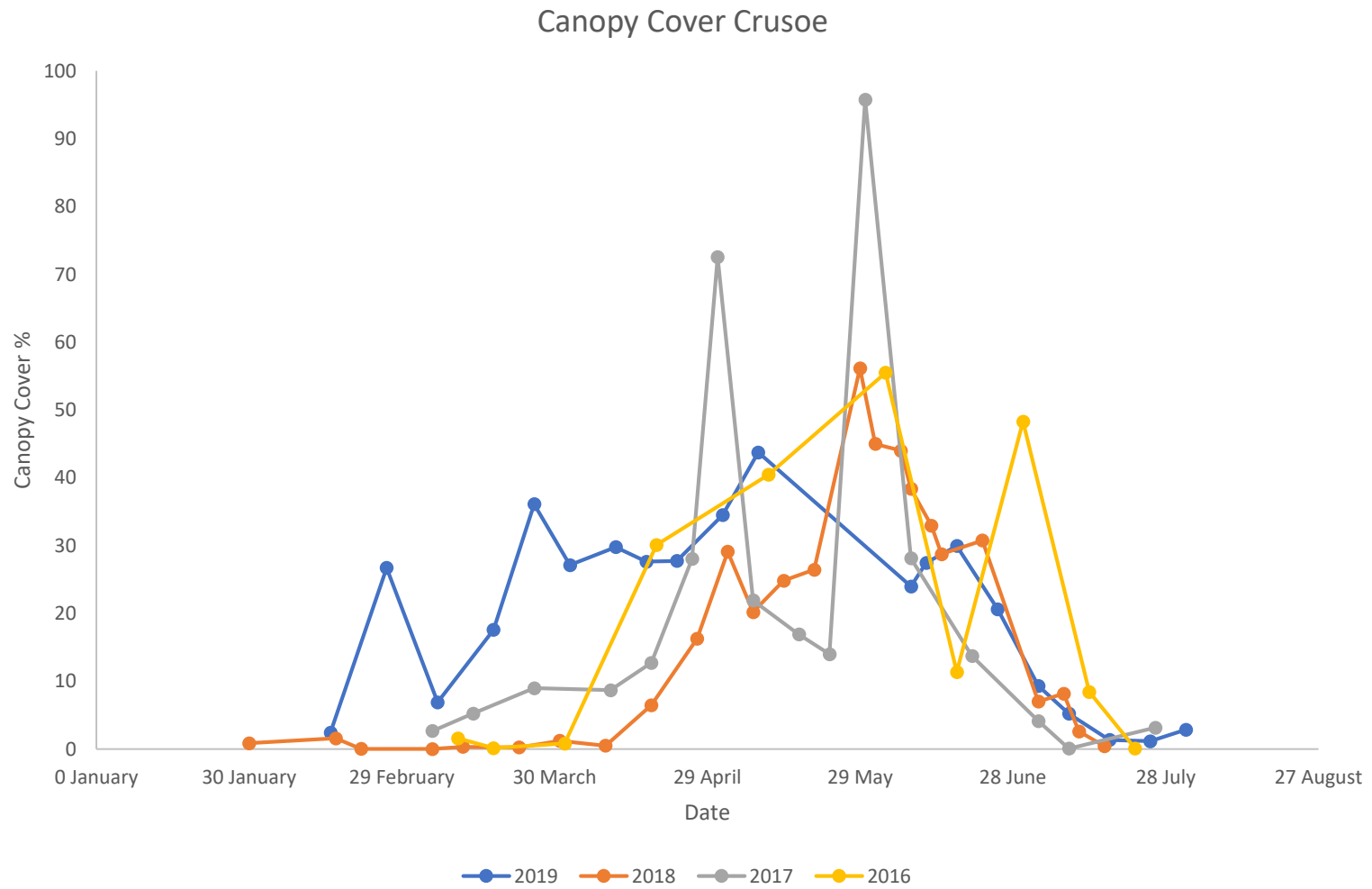
2018 SFP N0 NDVI v Canopy NDVI



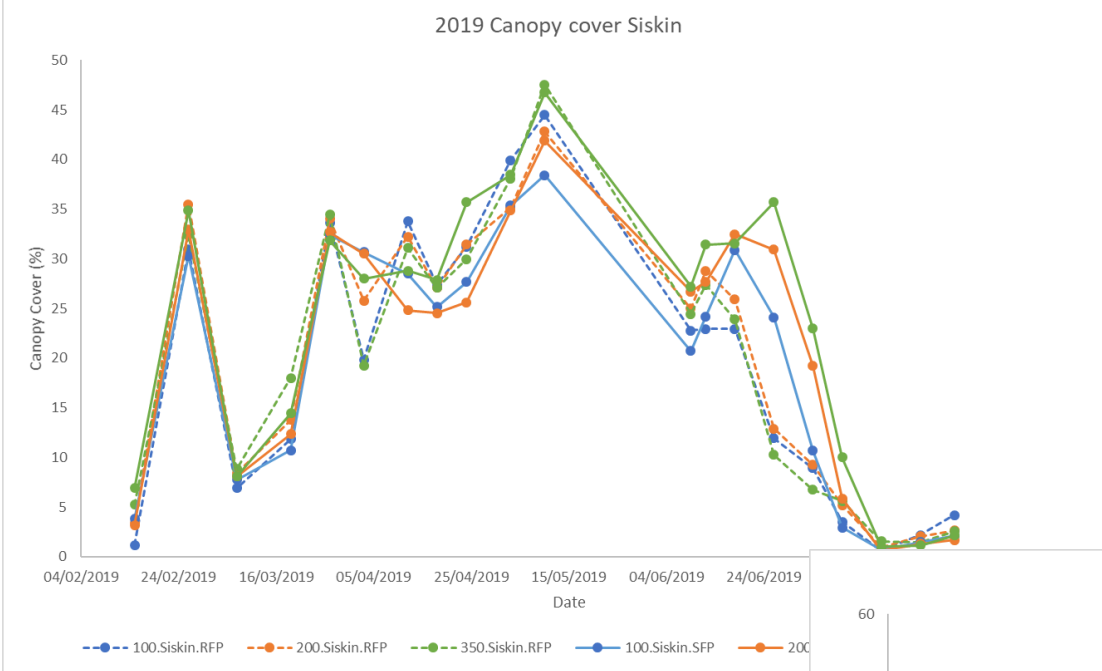
2018 SFP N200 NDVI v Canopy NDVI



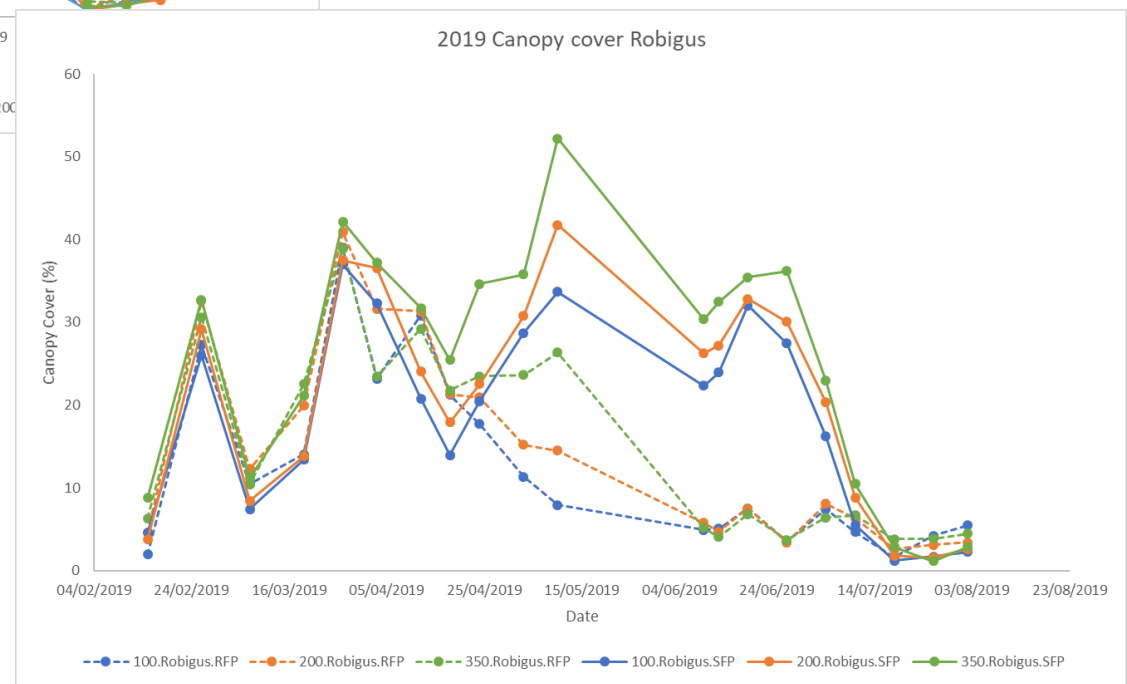
Canopy cover



Crop Growth – Canopy Cover



Reduced canopy of Robigus RFP shows



UAV - New uses



Ear counts

Acknowledgments:

Malcolm Hawkesford

March Castle

Fenner Holman

Chris Mackay

Deborah Wright



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Triticum monococcum Introgression

(update 563.4)

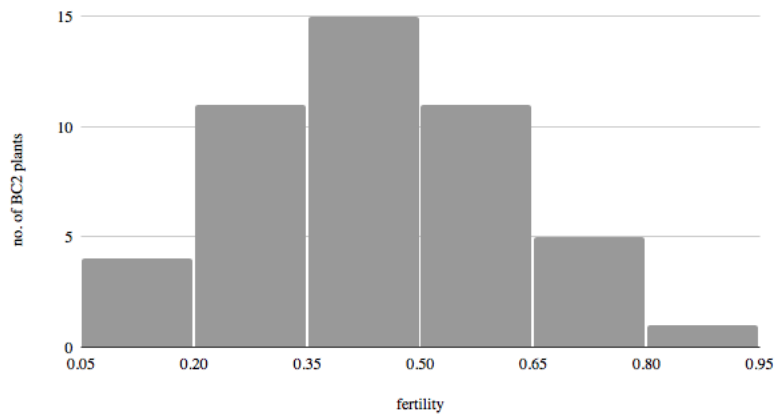
virtual WGIN MM July 8th 2020

Michael Hammond-Kosack (RRes)

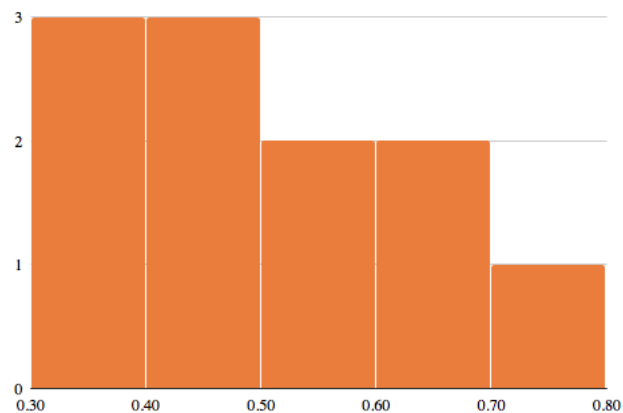
fertility for BC3 crosses for MDR031 derived plants

Kronos

BC3 crossing fertility for F1C24 descendants

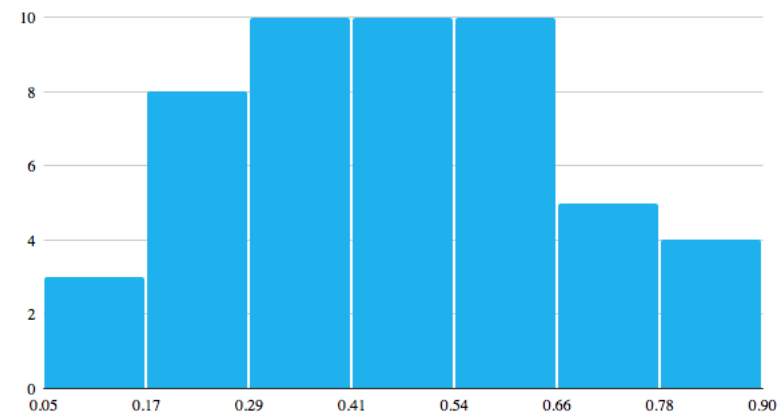


BC3 crossing fertility for F1C47-1 descendants

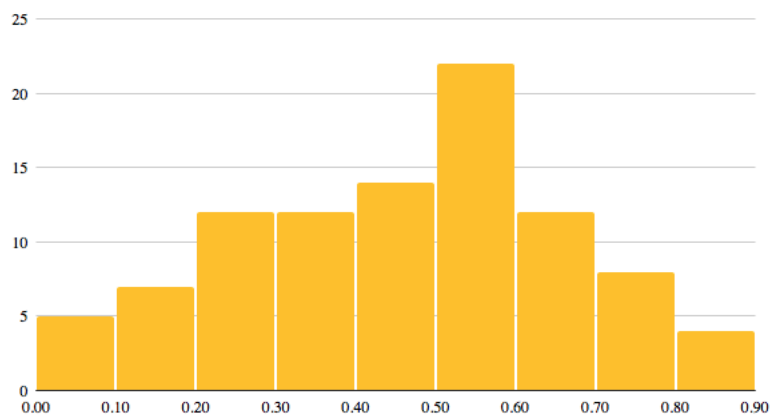


Hoh501

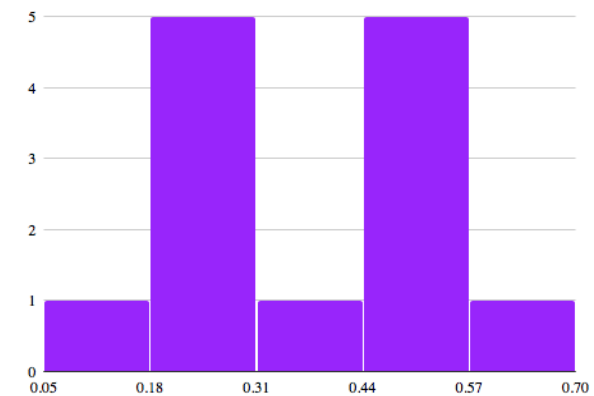
BC3 crossing fertility for F1C86-1 descendants



BC3 crossing fertility for F1C94 descendants



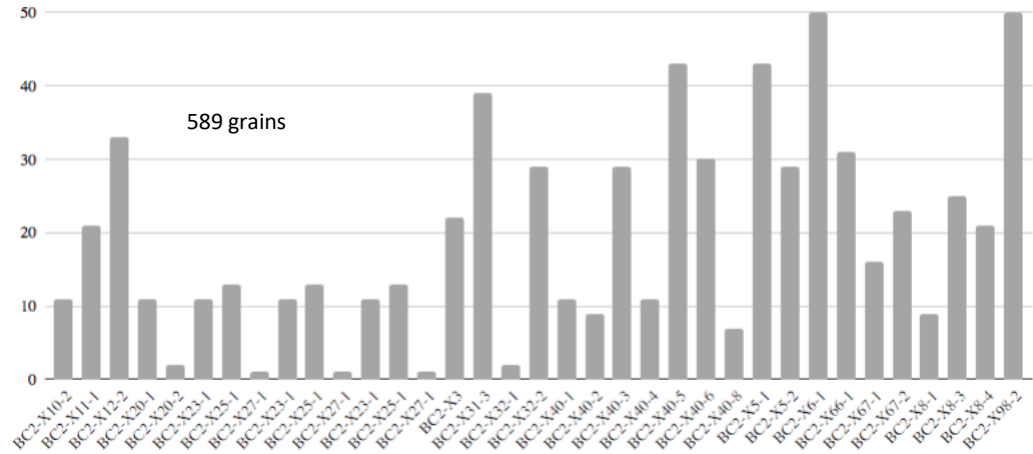
BC3 crossing fertility for F1C86-2 descendants



Summary of BC3 yields for MDR031

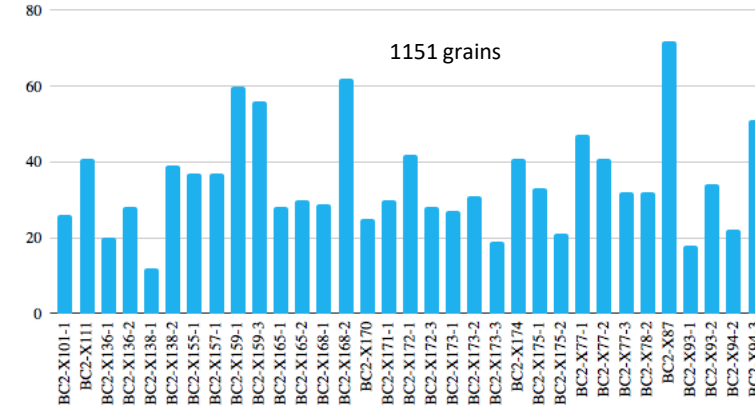
Kronos

BC3 grains obtained from each F1C24-BC2 plant

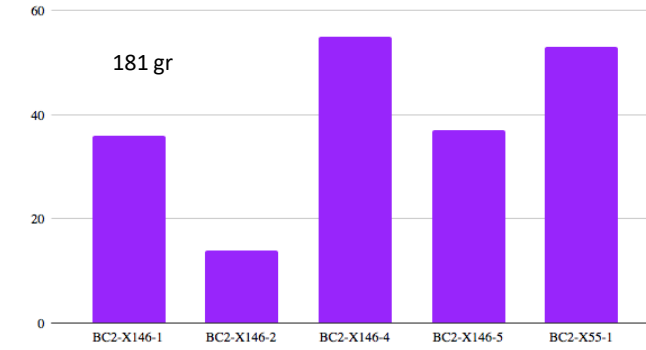


Hoh501

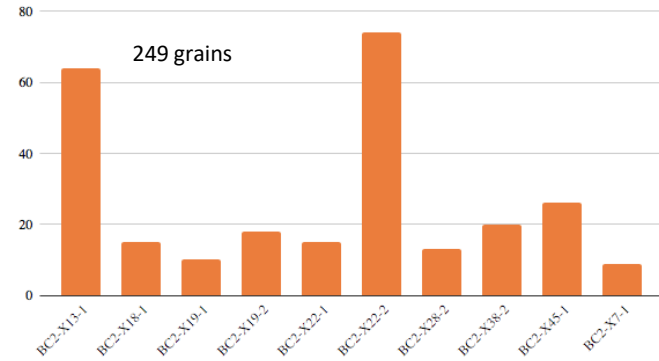
BC3 grains obtained from each F1C86-1-BC2 plant



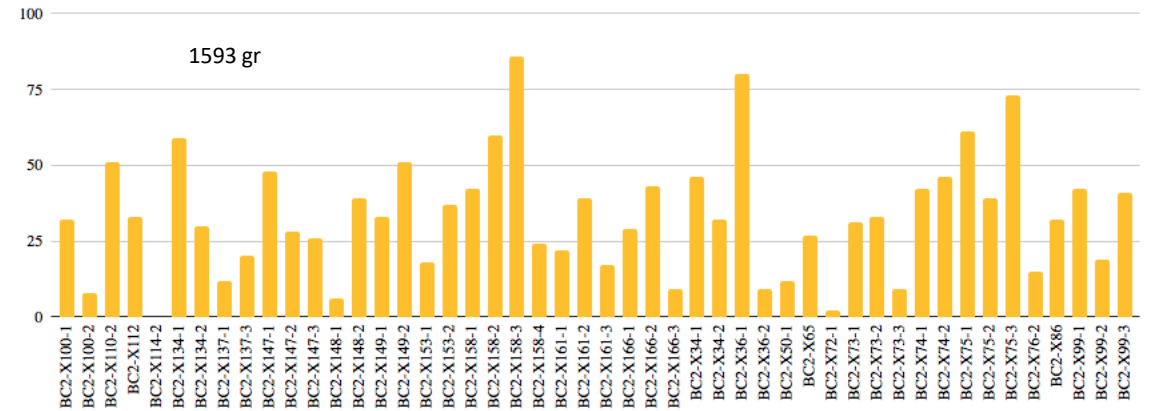
BC3 grains obtained from each F1C86-2-BC2 plant



BC3 grains obtained from each F1C47-1-BC2 plant



BC3 grains obtained from each F1C94-BC2 plant



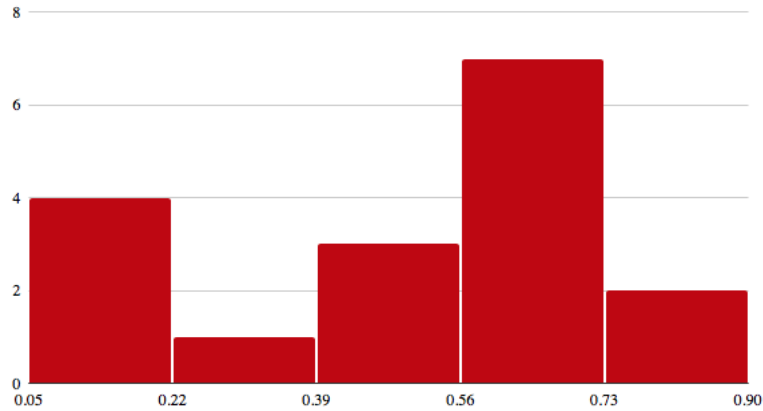
838 grains total

2925 grains total

Summary of BC2 fertilities and yields for MDR049 and MDR308

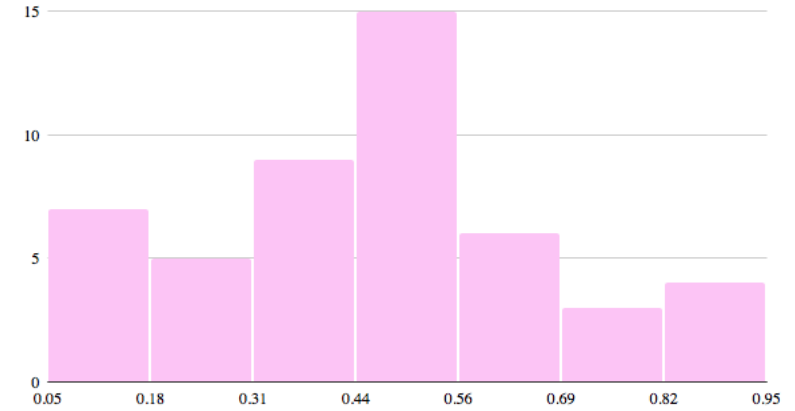
MDR049

BC2 crossing fertility for F1C[MDR049] descendants

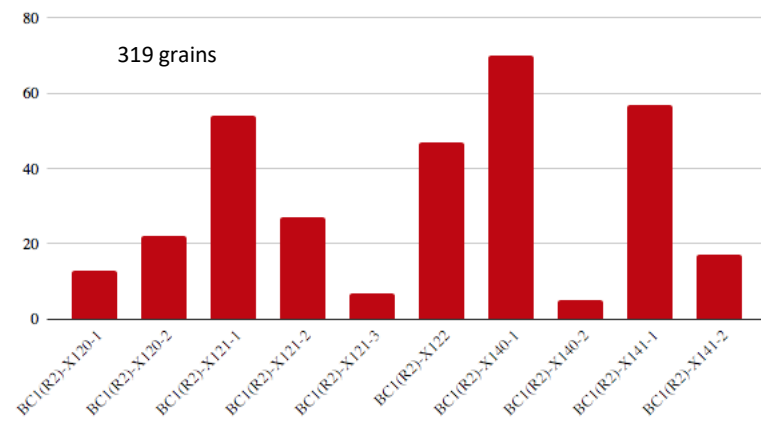


MDR308

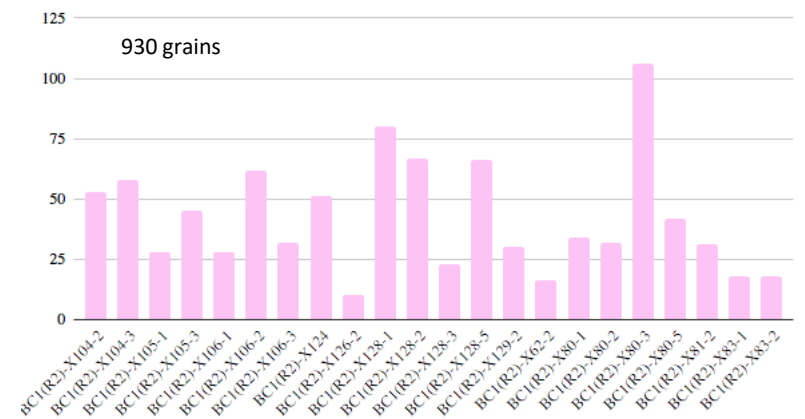
BC2 crossing fertility for F1C[MDR308] descendants



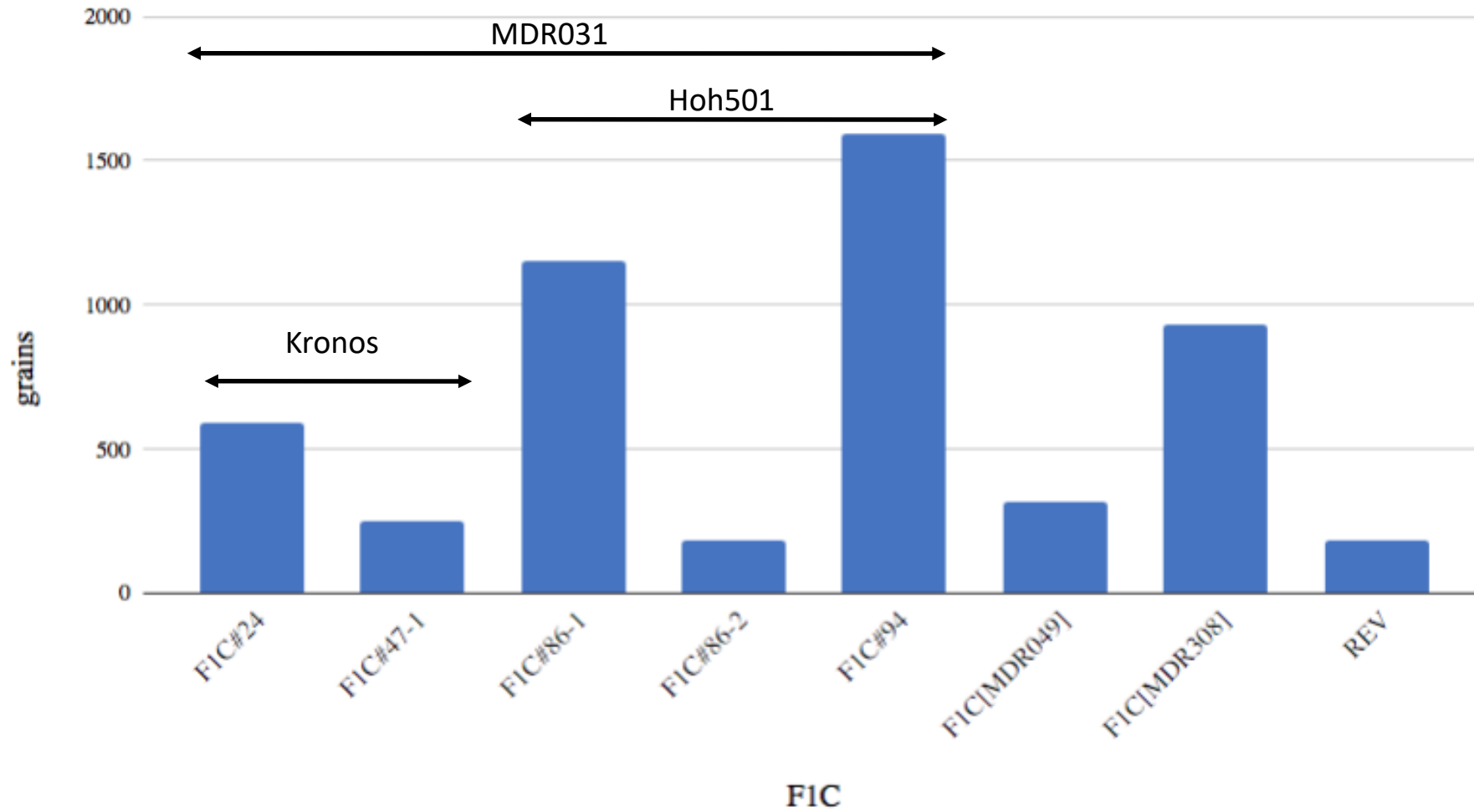
BC2 grains obtained from each F1C[MDR049]-BC1 plant



BC2 grains obtained from each F1C[MDR308]-BC1 plant



BC3 (BC2) grains for each F1C parent



many thanks to Jess Spong (Take-all PhD student with Javier / Kim) for help with crossing

Ear shapes of parent plants



T.mon MDR031



diploid



MDR049



MDR308



Kronos



tetraploid

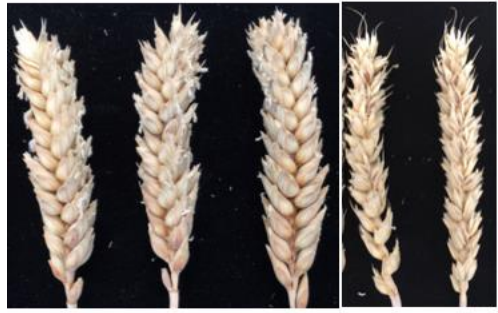


Paragon



hexaploid

selfed BC2 ears from MDR031 derived plants



selfed BC1 ears from MDR049 & MDR308 derived plants



***T. monococcum* introgression field trial April 2020 onwards**

Purpose : 1. To assess various traits as a 1st wheat crop

- Plant growth
- **Plant development**
- Responses to Yellow Rust and Septoria
- Ear **morphology and grain shape**

2. **Seed multiplication for Oct 2020 Take-all trial (3rd wheat)**

WGIN's 1st *Triticum monococcum* Introgression Field Trial

Design #	ALL SELFS (S-#)	F1hybrid	F1C	BC1	BC2	Design #		
1	BC1-X12-1	Kronos	Fielder	Paragon	Paragon	33-36	Paragon	
2	BC1-X12-3						37	Fielder
3	BC1-X87-1					38	Cadenza	
4	BC1-X173-1					39	Kronos	
5	BC1-X27-1					40	Hoh501	
6	BC1-X147-1					30	MDR031	
7	BC1-X75-1		Hoh501			Paragon	31	MDR049
8	BC1-X88-1	MDR031					32	MDR308
9	BC1-X122-1							
10	BC1-X161-3							
11	BC1-X186-2							
12	BC1-X187-1							
13	BC1-X187-2							
14	BC1-X187-3							
15	BC1-X74-1							
16	BC1-X115-1							
17	BC1-X189-2							
18	BC1-X224-1							
19	BC1-X224-2							
20	R2#2-7	MDR049						
21	R2#13-1-1	MDR308						
22	R2#14-1-1							
23	R2#16-7	MDR031						
24	BC2-X65-1							
25	BC2-X113-1							
26	BC2-X113-3							
27	BC2-X150-1							
28	BC2-X150-2							
29	BC2-X150-3							

Take-all R
Aphid R
Septoria R

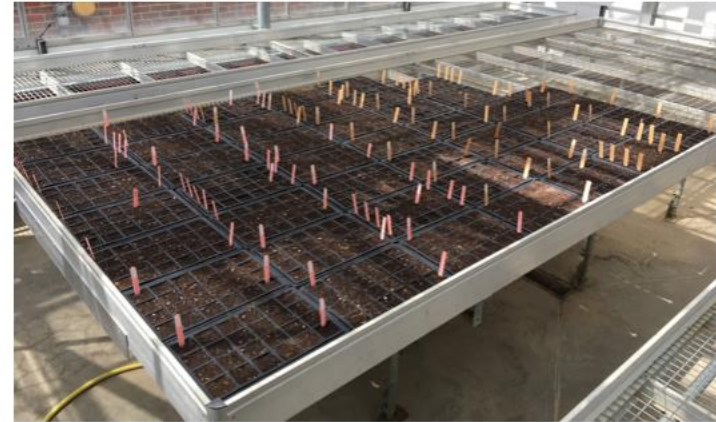
Late April

1. Lockdown pre-germination

@ home

Early to late May

2. Nursery (RRes glass house)



25th May 2020

3A Trial site preparation (3 weeks after glyphosate treatment) and then cultivated 28th May



29th May 2020

3. trial lay-out



Water
bowser

4. the first row planted



5. getting there



6. All done...



**7. ...apart from watering
twice a day (2 x 100l)**



3,500 litres so far, plus the occasional rain

Disease development - Septoria – none

Yellow rust – a lot

Basal leaves heavily YR infected

1 control + 4 lines

40. Hoh501

2. BC1 – X12-3

6. BC1 - X147-1

8. BC1 – X88-1

29. BC2 – X150-3

3 *Tm* lines – no yellow rust lesions



Design #	ALL SELFS (S-#)	F1hybrid	F1C	BC1	BC2
1	BC1-X12-1	Kronos	Fielder		
2	BC1-X12-3				
3	BC1-X87-1				
4	BC1-X173-1				
5	BC1-X27-1				
6	BC1-X147-1				
7	BC1-X75-1				
8	BC1-X88-1	Hoh501	MDR031	Paragon	Paragon
9	BC1-X122-1				
10	BC1-X161-3				
11	BC1-X186-2				
12	BC1-X187-1				
13	BC1-X187-2				
14	BC1-X187-3				
15	BC1-X74-1				
16	BC1-X115-1				
17	BC1-X189-2				
18	BC1-X224-1				
19	BC1-X224-2				
20	R2#2-7		MDR049		
21	R2#13-1-1		MDR308		
22	R2#14-1-1				
23	R2#16-7				
24	BC2-X65-1		MDR031		
25	BC2-X113-1				
26	BC2-X113-3				
27	BC2-X150-1				
28	BC2-X150-2				
29	BC2-X150-3				

Plant development – as of 7th July 2020

Most plants **in anthesis (GS60 onwards)**

3 controls and 5 lines

30. MDR031

33. Paragon

39. Kronos

1. BC1 – X12-1

6. BC1 - X147-1

8. BC1 – X88-1

17. BC1 – X189-2

27. BC2- X150-1

[Also](#) have high YR in basal leaves



Design #	ALL SELFS (S-#)	F1hybrid	F1C	BC1	BC2				
1	BC1-X12-1	Kronos	Fielder						
2	BC1-X12-3								
3	BC1-X87-1								
4	BC1-X173-1								
5	BC1-X27-1	MDR031		Paragon	Paragon				
6	BC1-X147-1								
7	BC1-X75-1								
8	BC1-X88-1								
9	BC1-X122-1								
10	BC1-X161-3								
11	BC1-X186-2								
12	BC1-X187-1								
13	BC1-X187-2								
14	BC1-X187-3								
15	BC1-X74-1								
16	BC1-X115-1								
17	BC1-X189-2					Hoh501	Paragon		
18	BC1-X224-1								
19	BC1-X224-2								
20	R2#2-7	MDR049							
21	R2#13-1-1	MDR308							
22	R2#14-1-1								
23	R2#16-7								
24	BC2-X65-1								
25	BC2-X113-1								
26	BC2-X113-3	MDR031							
27	BC2-X150-1								
28	BC2-X150-2								
29	BC2-X150-3								

Plant development – as of 7th July 2020

Most plants **only up to GS 37** (i.e. flag leaf visible)

1 control and 5 lines

37. Fielder

10. BC1 – X161-3

12. BC1 – X187-1

13. BC1 – X187-2

14. BC1 - X187-3

18. BC1 – X224-1

19. BC1 – X224.2

25. BC2- X113-1

26. BC2 - X113-3

Design #	ALL SELFS (S-#)	F1hybrid	F1C	BC1	BC2
1	BC1-X12-1	Kronos	Fielder		
2	BC1-X12-3				
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5	BC1-X27-1				
6	BC1-X147-1				
7	BC1-X75-1				
8	BC1-X88-1	Hoh501	MDR031	Paragon	Paragon
9	BC1-X122-1				
10	BC1-X161-3				
11	BC1-X186-2				
12	BC1-X187-1				
13	BC1-X187-2				
14	BC1-X187-3				
15	BC1-X74-1				
16	BC1-X115-1				
17	BC1-X189-2				
18	BC1-X224-1				
19	BC1-X224-2				
20	R2#2-7	MDR049			
21	R2#13-1-1	MDR308			
22	R2#14-1-1	MDR031			
23	R2#16-7				
24	BC2-X65-1				
25	BC2-X113-1				
26	BC2-X113-3				
27	BC2-X150-1				
28	BC2-X150-2				
29	BC2-X150-3				



What's next ?

Ear morphology

Yellow Rust assessments on flag leaf and 3 top leaves

Aphid infestations ? **Specifically R2#2-7 vs MDR049**

Flag leaf size

Leaf **senescence**

Total number of flowering tillers / plant

Plant heights

Grain harvest

Grain shape

Prepare the seed for the 3rd wheat – take-all trial to be drilled Oct 2020

7th July 2020 – Field trial 40 days old



Questions for the Breeders

- **What is the consensus for introgressed plant labelling ?**
To help the dissemination of seeds
- **When to start the SSD ?**
- Which plants / lines to nominate for DFW Breeders Observation Panel ?

Many thanks to

Glasshouse staff – Jill Maple, Fiona Gilzean & Tom Yaxley - Phase 1 lockdown

Field staff - Chris Mackay, Ben Flannery - Phase 1 & 2 lockdown

Statistician – Suzanne Clark - Phase 1 lockdown

**Gail Canning – location of seed stocks in the seed store
and advice on GS scoring - Phase 1 & 2 lockdown**

Resilience to foliar pathogens

Kim Hammond-Kosack

Vanessa McMillan

Gail Canning

Deborah Wright



Department
for Environment
Food & Rural Affairs

WGIN MM 8th July 2020



WGIN 4 objectives



- To explore whether *mlo* mediated resistance to powdery mildew is also effective against other fungal pathogens
- To explore the genetic basis of Yellow Rust resistance in two Watkins lines

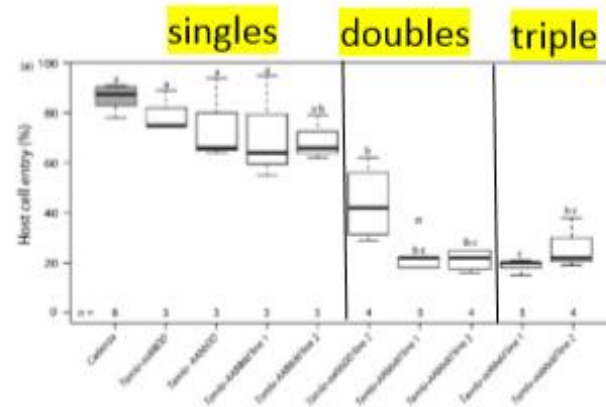
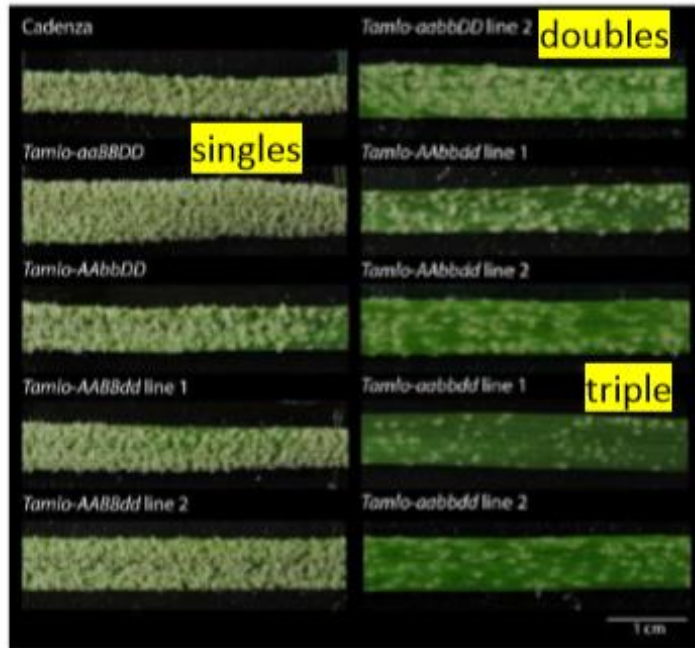
Powdery Mildew



ROTHAMSTED
RESEARCH

ROTHAMSTED
RESEARCH

TILLING wheat for *mlo* mediated mildew resistance



Seedling
glasshouse
screen

Cv Cadenza

Initially WGIN
funded



Plant Biotechnology Journal (2017) 15, pp. 367–376

doi: 10.1111/plb.12621

mlo-based powdery mildew resistance in hexaploid bread wheat generated by a non-transgenic TILLING approach

Johanna Acevedo-García¹, David Spencer¹, Hannah Thierion¹, Anja Reinstädler¹, Kim Hammond-Kosack², Andrew L. Phillips² and Ralph Panstruga^{1*}

Funders: German Federal Ministry of Food and Agriculture

Germany Society for the Advancement of Plant Innovation



Department
for Environment
Food & Rural Affairs



2019/ 2020 *mlo* wheat trial – update on progress

Finally drilled in late March 2020

- 72 plots – identical design to 2018/19 trial

Established very well

**Main disease Yellow Rust - scored 3 times on
Flag leaf and top 3 leaves**

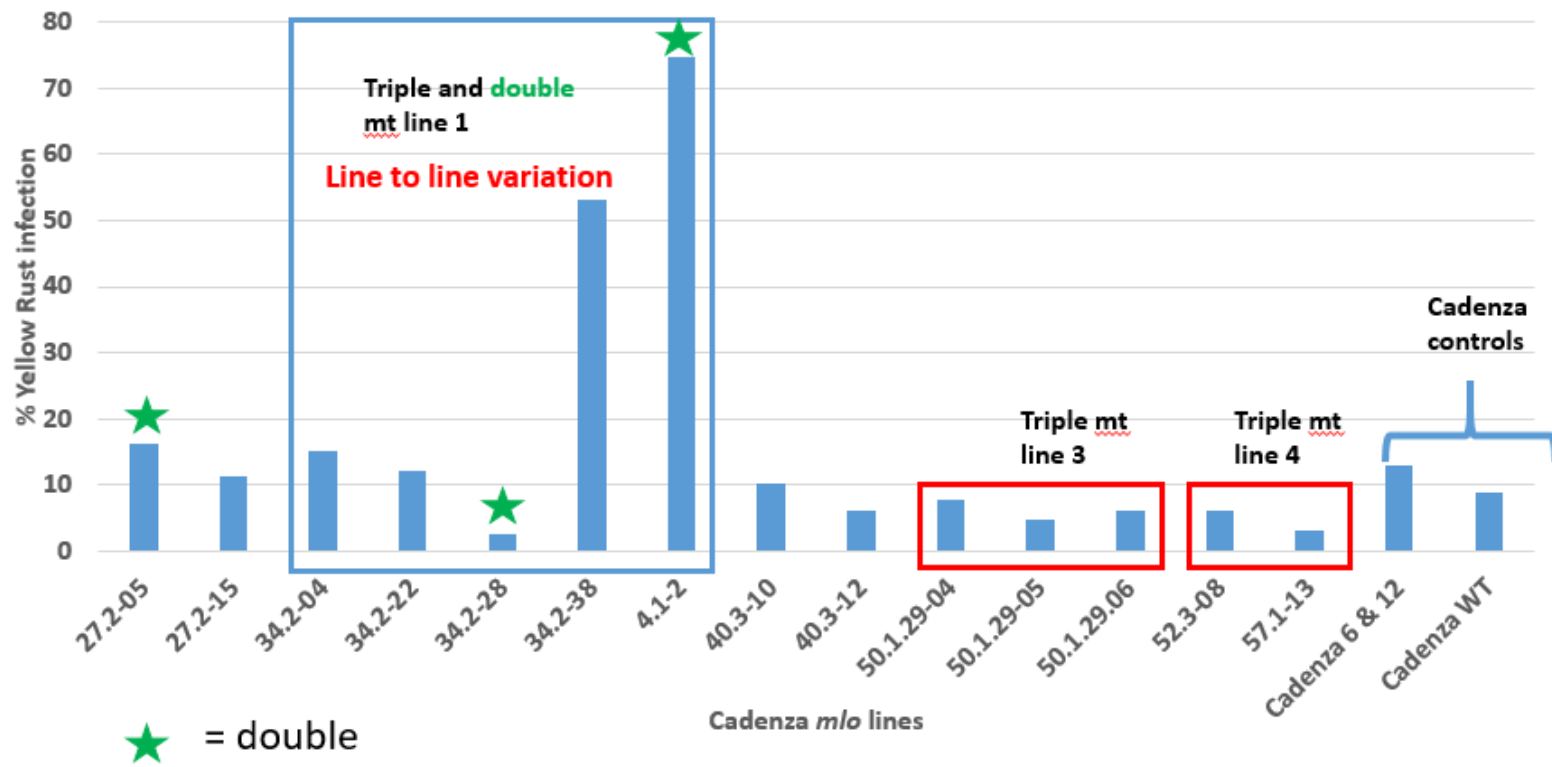
Data gone to statistics dept for analysis



Double *mlo* line 4-1-2 was again the most susceptible line in 2020 trial

Trial 1 -2019

19/R/WW/1925: Average combined Yellow Rust score for leaf 3 and leaf 4



Artificial inoculations with Fusarium done on 15th June 2020 (1 week out of Phase 1 lockdown)

Fusarium inoculations – 15th and 19th June



Image DJI_0174

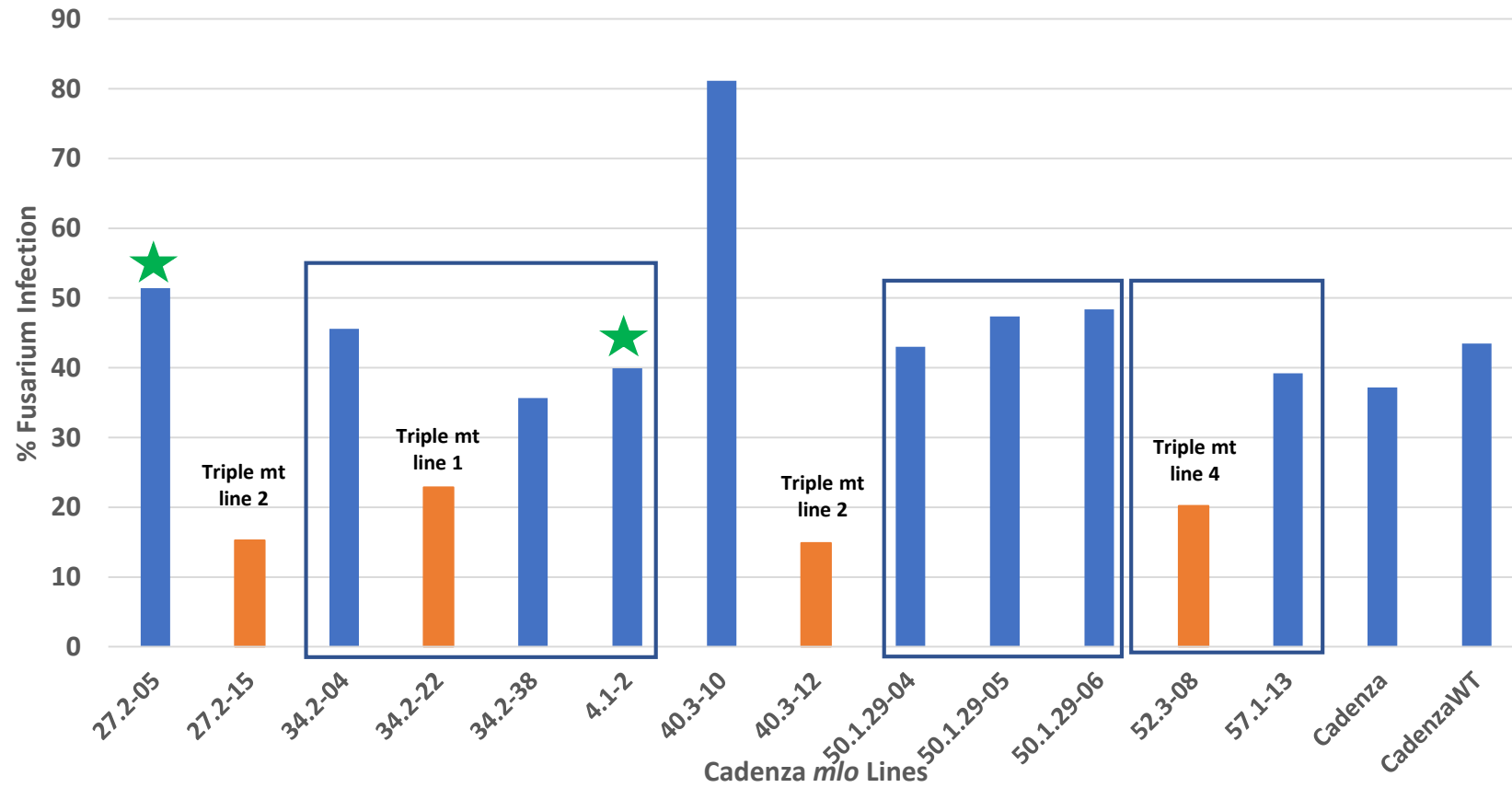
16th June 2020 , Andrew Riche

Scored 20 ears per plot at 21 days
– 6th and 10th July



Trial 2 -2019

19RWW1926: *Fusarium graminearum* infection



★ = double

WGIN 4 objectives



- To explore whether *mlo* mediated resistance to powdery mildew is also effective against other fungal pathogens
 - To explore the genetic basis of Yellow Rust resistance in two Watkins lines
 - W 733 – dominant resistance
 - W786 – recessive resistance
- High disease in 2020 trial and both Watkins lines still provide high levels of resistance
- Evaluated a larger F₂ population and more F₃ lines**

Many thanks to



Wheat *mlo* project and Watkins YR project

Gail Canning

Deborah Wright

Jessica Hammond (Plant Pathology Apprentice)

Martin Urban - Fusarium inoculations

2019 - Tania Chancellor (2nd year PhD student)

2019 - Vanessa McMillan

Statistics

Rodger White, Stephen Powers

and **Suzanne Clark**

RRes Farm and glasshouse staff



Aphids and BYDV

Resistance Screening and Diversity Trial Update

Lawrence Bramham

8th July 2020



Department
for Environment
Food & Rural Affairs





Aphid/BYDV Resistance Screening

Resistance Screening

- Germplasm screened for aphid/BYDV resistance:
 - 20 wheat cultivars from WGIN diversity trial
 - 17 hexaploid lines from the core Watkins landrace collection
 - 33 synthetic wheat lines developed by NIAB EMR
 - 3 additional commercial cultivars (Hereward, Paragon and Solstice), included as control material throughout all testing

Screening Strategy

- 7-day old seedlings (10 per line) challenged with 5 x *Rhopalosiphum padi* reared on BYDV-PAV infected wheat



5 x viruliferous
R. padi



1 week



Insecticide application &



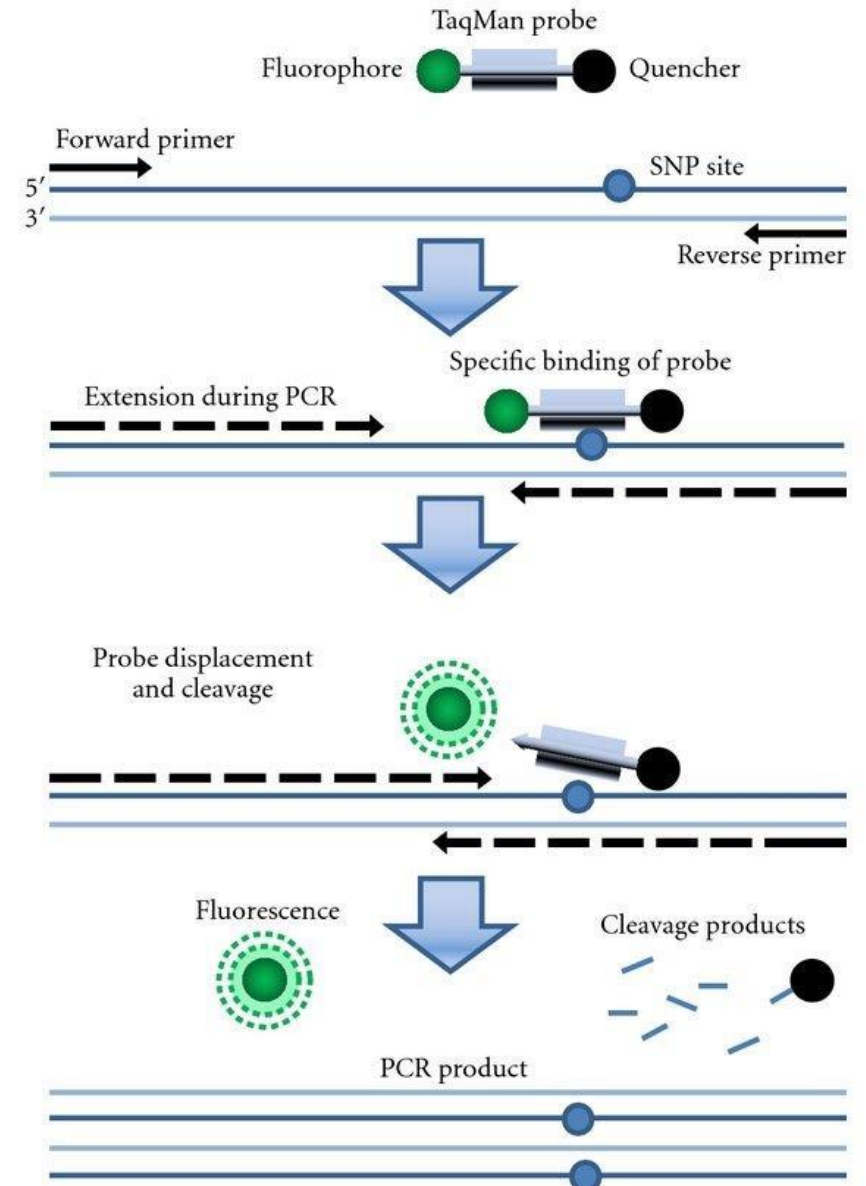
Collect 1st leaf sample



Collect 2nd leaf sample (flag leaf)

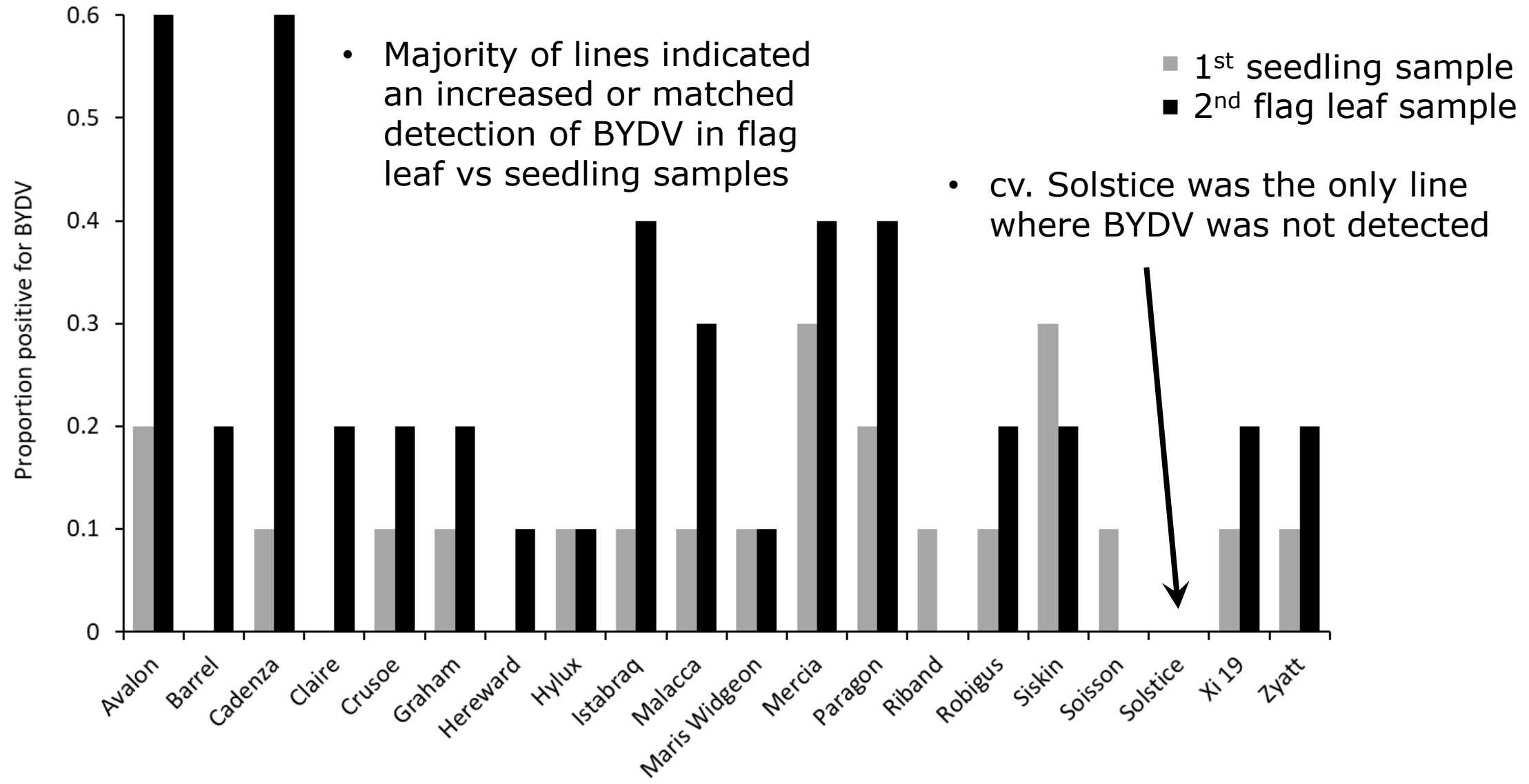
BYDV Assay

- Mid/high-throughput assay developed at Rothamsted (Martin Williamson)
 - designed for use with aphids
 - working for $<0.5 \text{ cm}^2$ foliar samples
- 'TaqMan'/qRT-PCR capable of identifying both the presence and strain of BYDV
- All 1st leaf samples processed
- 2nd leaf samples underway



BYDV Assay Results

- 20 wheat cultivars from WGIN diversity trial (2019):



BYDV Assay Results – 1st Leaves

- 17 Watkins lines:

Watkins core collection designation	Number of <i>R. padi</i> /BYDV-challenged samples			Number of unchallenged control samples		
	R	I	S	R	I	S
WATKINS_0007	10					1
WATKINS_0032	7			2		
WATKINS_0034	8			3		
WATKINS_0042	9			2		
WATKINS_0044	5	1		3		
WATKINS_0045	9			2		1
WATKINS_0079	9			3		
WATKINS_0103	7			2		
WATKINS_0110	8			2		1
WATKINS_0126	6			2		
WATKINS_0127	5			2		
WATKINS_0139	7			3		
WATKINS_0141	6			2		
WATKINS_0145	7			3		
WATKINS_0160	8			2	1	
WATKINS_0468	7	1		2	1	
WATKINS_0729	8			3		

R = Resistant
I = Intermediate
S = Susceptible

- No BYDV detected in 11/17 of 1st leaf samples
- BYDV detected within unchallenged control material, suggesting insecticide treatment was <100% effective

BYDV Assay Results – 1st Leaves

- 33 synthetic NIAB EMR lines (table 1 of 2):

R = Resistant
I = Intermediate
S = Susceptible

Synthetic hexaploid wheat designation	Number of <i>R. padi</i> /BYDV-challenged samples			Number of unchallenged control samples		
	R	I	S	R	I	S
NIAB_SHW_012	9	1		3		
NIAB_SHW_018	3	1	1	3		
NIAB_SHW_027	6	1		2		
NIAB_SHW_028	7	2	1	1		
NIAB_SHW_029	7			1		
NIAB_SHW_030	10			3		
NIAB_SHW_031	5	1		3		
NIAB_SHW_035	7			1		
NIAB_SHW_036	1			1		
NIAB_SHW_042	8		1	2		
NIAB_SHW_051	6	1		2		
NIAB_SHW_054	7			3		
NIAB_SHW_071	5	1	1	1		
NIAB_SHW_072	8			3		
NIAB_SHW_073	6	3		3		
NIAB_SHW_076	7	1	1	1		
NIAB_SHW_077	6		3	3		

- 8/33 lines with no BYDV detected in 1st leaf samples

BYDV Assay Results – 1st Leaves

- 33 synthetic NIAB EMR lines (table 2 of 2):

R = Resistant
I = Intermediate
S = Susceptible

Synthetic hexaploid wheat designation	Number of <i>R. padi</i> /BYDV-challenged samples			Number of unchallenged control samples		
	R	I	S	R	I	S
NIAB_SHW_080	7			2		1
NIAB_SHW_082	8		1	3		
NIAB_SHW_083	7	1		3		
NIAB_SHW_084	5			1		1
NIAB_SHW_085	5	1		1	1	
NIAB_SHW_086	4	1		3		
NIAB_SHW_087	6			2	1	
NIAB_SHW_090	11	1		2	1	
NIAB_SHW_091	8		2	3		
NIAB_SHW_093	9			3		
NIAB_SHW_094	7		2	3		
NIAB_SHW_095	7	1	1	3		
NIAB_SHW_096	8	1		1		
NIAB_SHW_099	7		3	3		
NIAB_SHW_137	4		1	2		
NIAB_SHW_138	9			3		

- 8/33 lines with no BYDV detected in 1st leaf samples
- BYDV detected within some unchallenged control material

BYDV Assay Results – 1st Leaves

- 3 commercial control cultivars:

R = Resistant
I = Intermediate
S = Susceptible

Wheat cultivar	Number of <i>R. padi</i> /BYDV-challenged samples			Number of unchallenged control samples		
	R	I	S	R	I	S
Hereward	16	1	2	8		1
Paragon	13	5	3	7	1	
Solstice	32	1		8		

- Consistent indication that cv. Solstice exhibits some level of BYDV and/or aphid resistance

← 'Intermediate' cv. Solstice 1st leaf sample reassessed 3 times;

2x = R

1x = I

BYDV Assay Results – 2nd Leaves

- 2nd leaf samples of the three control cultivars processed since ease in lockdown restrictions
- Quality control failures due to passive fluorescence reference dye, so data not yet robust
- No indication of BYDV within cv. Solstice 2nd leaf samples (TBC)



Diversity Field Trial Aphid Monitoring

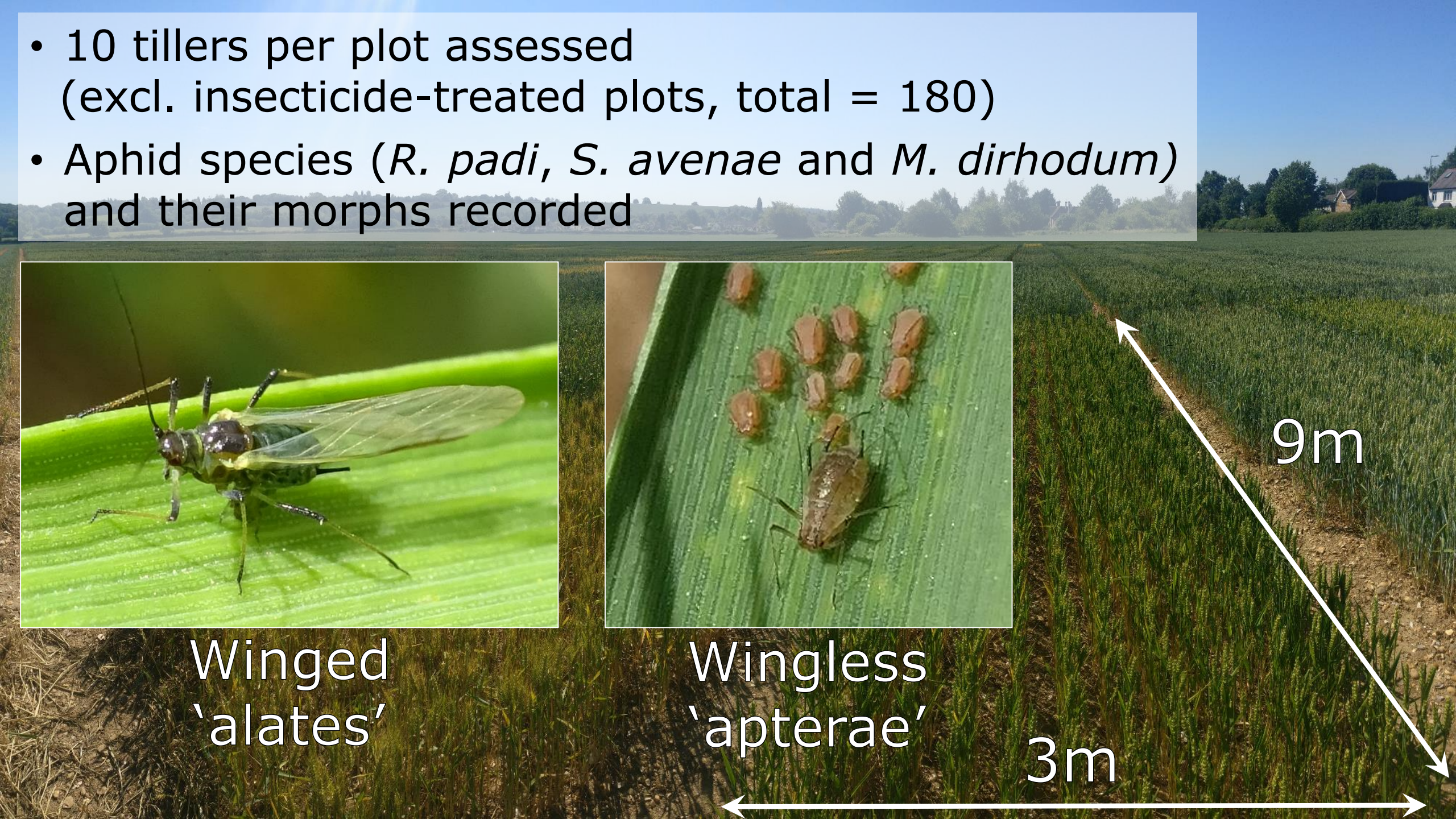
- 10 tillers per plot assessed (excl. insecticide-treated plots, total = 180)
- Aphid species (*R. padi*, *S. avenae* and *M. dirhodum*) and their morphs recorded



Winged
'alates'

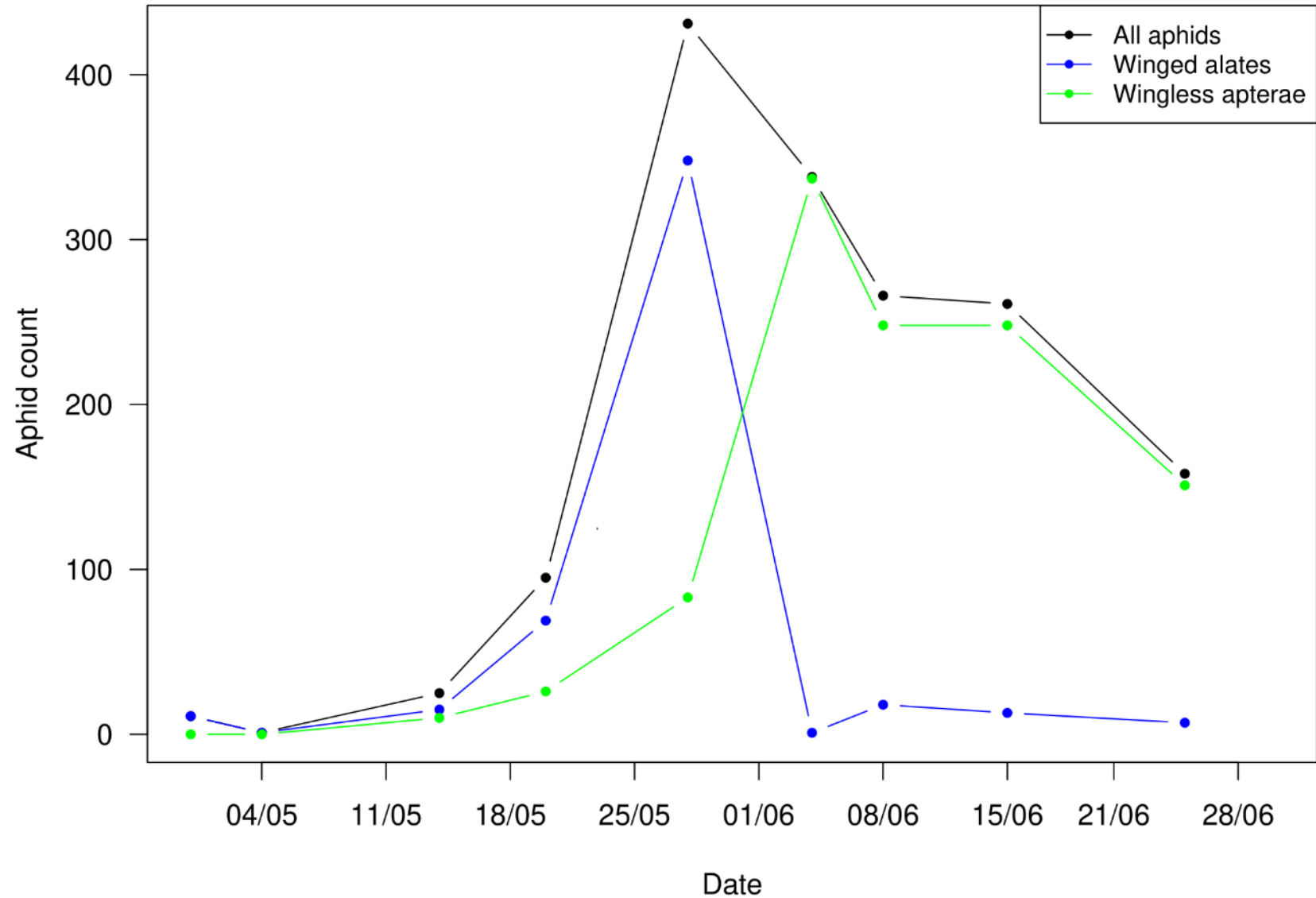


Wingless
'apterae'



Overall Aphid Presence

- Peak in aphid presence around 28th May
 - correlates with weather and RRes suction trap data for most aphid species
- Indication of aphid migration to field trial at this time, followed by curtailing reproduction of wingless apterae



Aphid Presence by Cultivar

- Wingless apterae presenting no clear tendency for survival/higher reproduction on individual cultivars
 - data influenced by tillers with high number of aphids
 - dynamic biological system, exploring data but no correlations to GS, N or clear cultivar



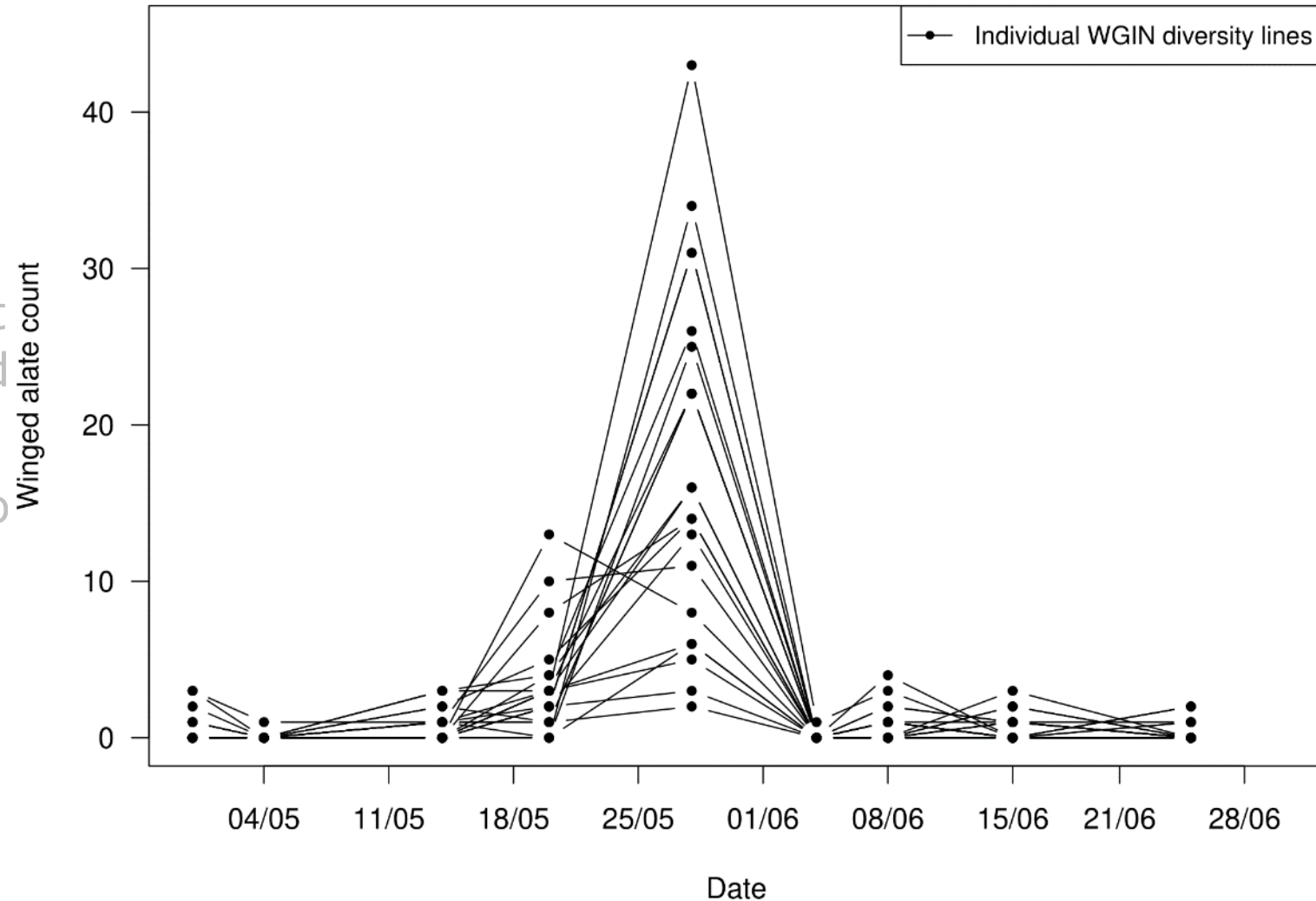
Aphid Presence by Cultivar

- Wingless apterae presenting no clear tendency for survival/higher reproduction on individual cultivars

- data influenced by tillers with high number of aphid
- dynamic biological system, exploring data but no clear cultivar correlations to GS, N

clear cultivar

- Variation in preference of winged alates to cultivars

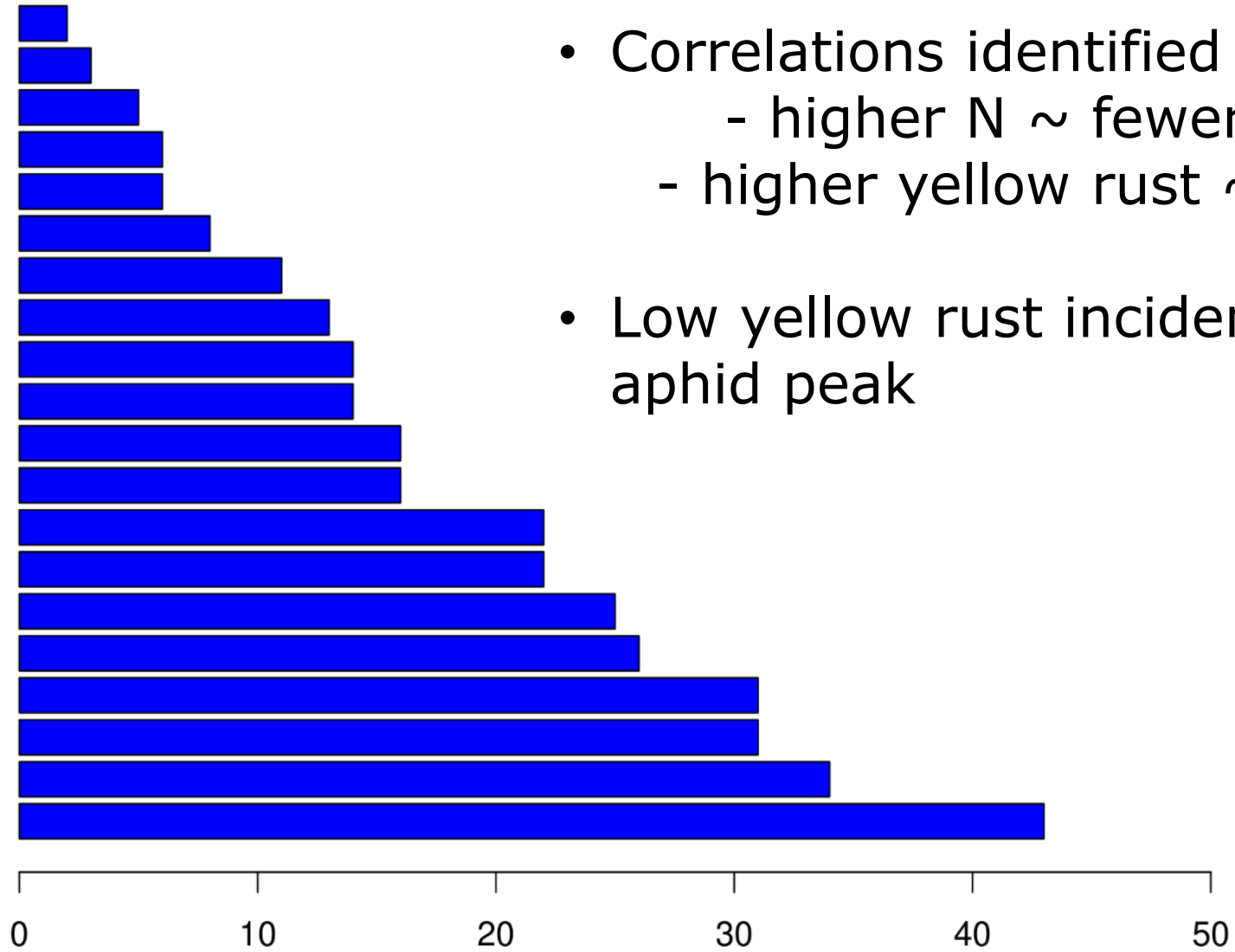


Winged Alates by Cultivar

Yellow Rust:

<5%
0%
<5%
<25%
<5%
0%
<5%
<5%
<5%
<5%
0%
<10%
<10%
<5%
<5%
<5%
0%
0%
0%
0%

Paragon
Theodore
Graham
Robigus
Maris Widgeon
Soissons
Cadenza
Riband
Solstice
Malacca
Mercia
Claire
Istabraq
Avalon
Barrel
Xi19
Zyatt
Hereward
Siskin
Crusoe



Winged alate count on 28/05/20

- Correlations identified previously:
 - higher N ~ fewer aphids
 - higher yellow rust ~ fewer aphids
- Low yellow rust incidence during aphid peak

Summary

- Preliminary BYDV testing has identified lines with potential sources of resistance
 - to be validated in future with 2nd leaf samples
- Notable aphid movement captured in WGIN diversity field trial with indication of what may be BYDV vectors' preference towards/against certain cultivars
 - data to be fully explored, potential for future semiochemical research

WAK bioinformatics update

Kostya Kanyuka



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RESEARCH



Biotechnology and
Biological Sciences
Research Council



Wall-associated receptor like kinases (WAKs)

Cloned WAK genes implicated in pathogen defence

WAK1	Arabidopsis	DAMP (OGs) receptor
RFO1	Arabidopsis	R gene (<i>Fusarium oxysporum</i>)
Htn1	maize	R gene (<i>Exserohilum turcicum</i>)
qHSR1	maize	R gene (<i>Sporisorium reilianum</i>)
Xa4	rice	R gene (<i>Xanthomonas oryzae</i>)
Stb6	wheat	R gene (<i>Zymoseptoria tritici</i>)
Snn1	wheat	S gene (<i>Parastagonospora nodorum</i>)
Sbs1&2	barley	S gene (<i>Bipolaris sorokiniana</i>)
Rlm9	canola	R gene (<i>Leptosphaeria maculans</i>)

- DAMP receptor recognising products of plant cell-wall pectin degradation (**WAK1**)
- broad-spectrum, but partial, quantitative resistance (**Htn1**, **qHSR1**, **RFO1**)
- qualitative pathogen resistance in a gene-for-gene manner (**Stb6**, **Xa4**, **Rlm9**)
- sensitivity to the necrotrophic effector or the pathogen (**Snn1**, **Sbs1&2**)



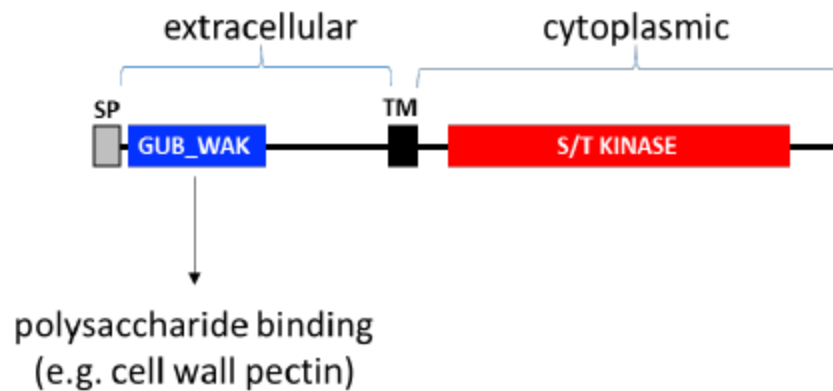
Characterize the WAK gene family in wheat



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Wall-associated receptor like kinases (WAKs)

Structure of a typical WAK protein



WAKs characterised in plants

- Arabidopsis (23)
- Rice (75)
- Poplar (122)

vs

WAKs in wheat cv. Chinese Spring

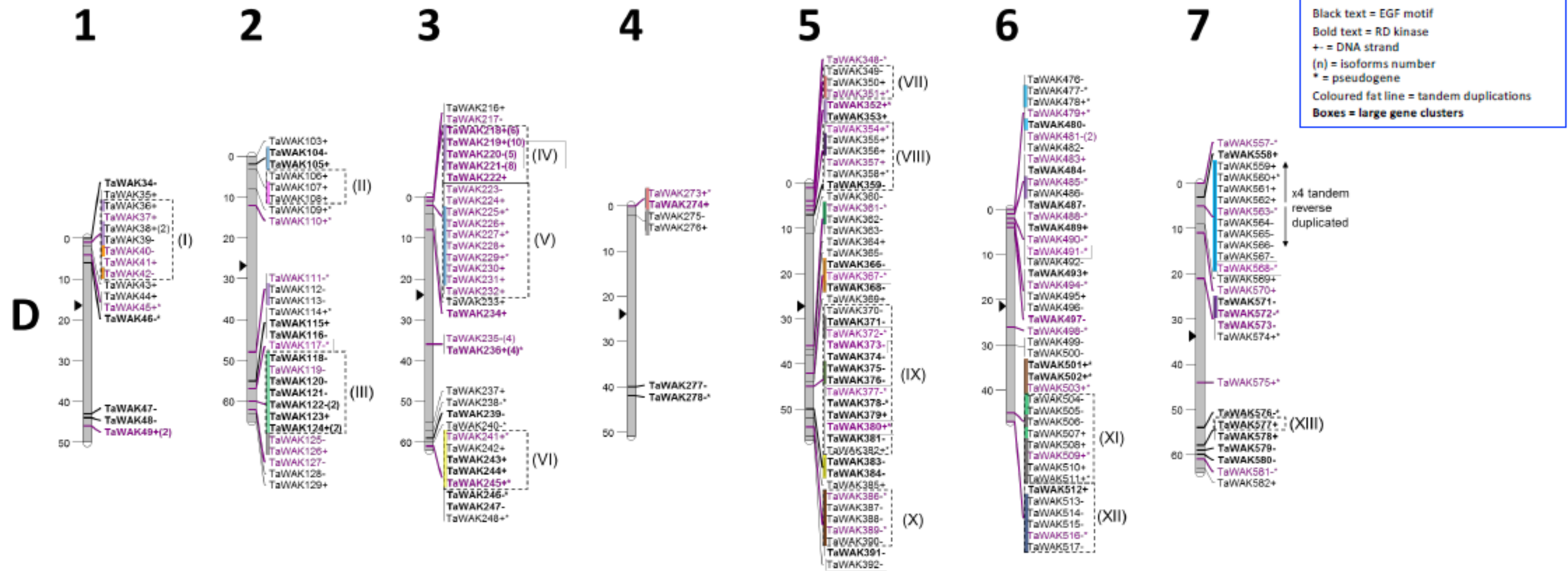
- **406 RLK** and 2 RLP genes
- 193 pseudogenes (**112 RLKs**, and 81 RLPs)
- Total **601** sequences among which **518 are RLKs**

Expansion of WAK gene family in wheat



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Clusterisation and subtelomeric location of WAKs

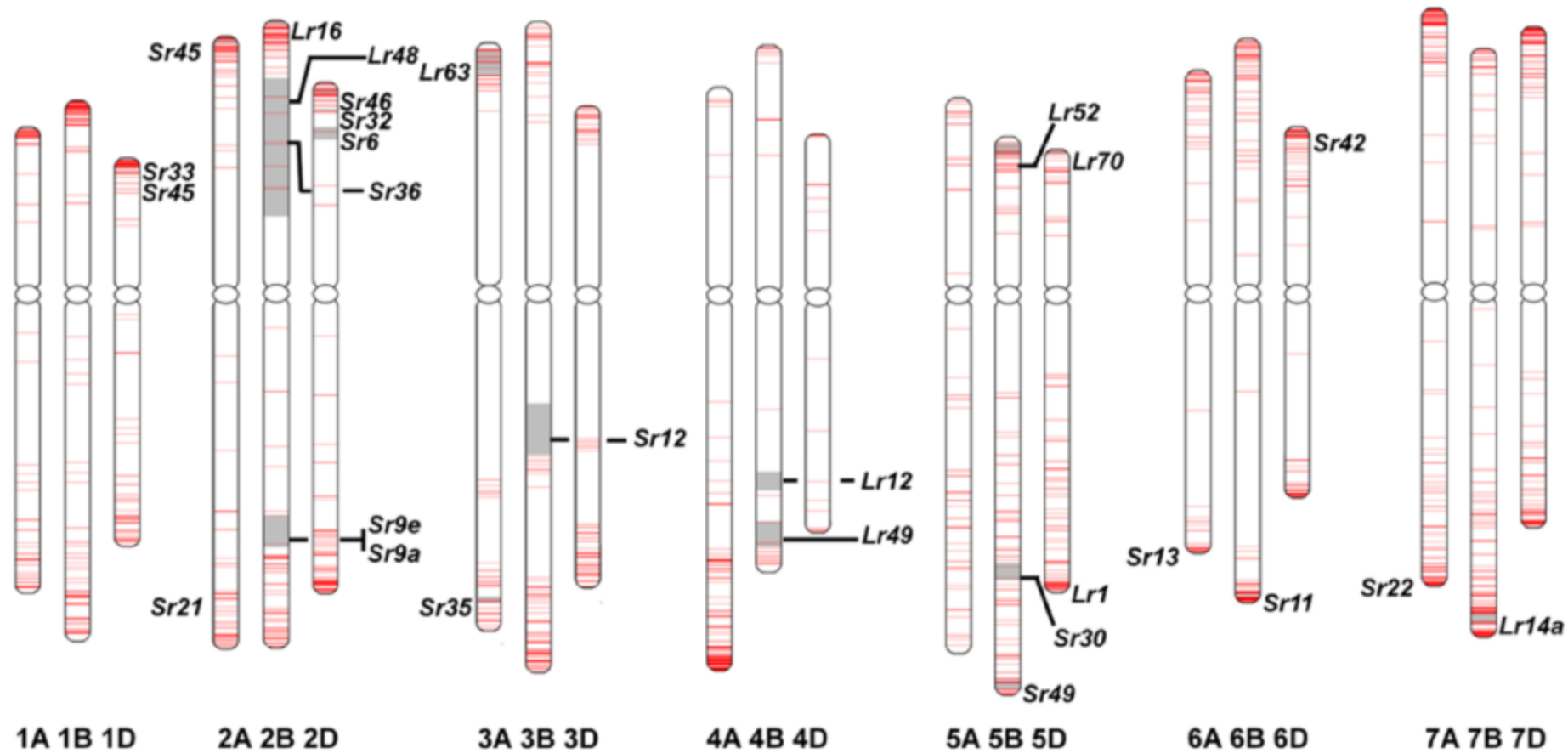


Features shared with NLRs



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Clusterisation and subtelomeric location of NLRs



Steuernagel et al. 2018 bioRxiv



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Are WAKs important players in Septoria resistance?

Gene/QTL	Chromosome	Size of the interval (bp)	Number of WAKs	Candidate WAKs
<i>Stb2</i>	1BS	3,753,304	0	
<i>Stb3</i>	7AS	36,017,764	1	<i>TaWAK530</i>
<i>Stb4</i>	7DS	166,669,925	14	<i>TaWAK557–TaWAK570</i>
<i>Stb5</i>	7DS	96,468,653	13	<i>TaWAK557–TaWAK569</i>
<i>Stb7</i>	4AL	5,073,142	2	<i>TaWAK269, TaWAK270</i>
<i>Stb9</i>	2BL	113,746,383	13	<i>TaWAK88–TaWAK100</i>
<i>Stb10</i>	1D	193,937,871	3	<i>TaWAK44–TaWAK46</i>
<i>Stb11</i>	1BS	73,135,081	15	<i>TaWAK15–TaWAK30</i>
<i>Stb12</i>	4AL	11,685,167	3	<i>TaWAK268–TaWAK270</i>
<i>Stb13</i>	7BL	177,021,373	10	<i>TaWAK547–TaWAK556</i>
<i>Stb14</i>	3BS	2,288,244	8	<i>TaWAK175–TaWAK182</i>
<i>StbSm3</i>	3AS	3,768,577	0	
<i>Stb17</i>	5AL	72,092,188	5	<i>TaWAK293–TaWAK298</i>
<i>StbWW</i>	1BS	73,135,081	15	<i>TaWAK16–TaWAK30</i>
<i>TmStb1</i>	7AS	116,002,803	13	<i>TaWAK518–TaWAK530</i>
<i>QStb.lsa_fb-1A</i>	1A	53,176,139	0	
<i>2DS</i>	2DS	47,410,006	5	<i>TaWAK104–TaWAK108</i>
<i>QStb.lsa_tb-4A</i>	4AL	1,947,740	0	
<i>QStb.lsa_tb-4B</i>	4B	344,665,898	1	<i>TaWAK272</i>
<i>QStb.psr-7D-1</i>	7DS	5,106,019	10	<i>TaWAK559–TaWAK568</i>
<i>7DS</i>	7DS	138,115,519	6	<i>TaWAK569–TaWAK574</i>
<i>7DL</i>	7DL	45,720,815	2	<i>TaWAK576, TaWAK577</i>
<i>QStb.lsa_fb-7D</i>	7DL	3,966,596	1	<i>TaWAK582</i>
<i>QStb.ipk-7D1</i>	7D	440,031,428	6	<i>TaWAK570–TaWAK575</i>
<i>Stb18</i>	6DS	4,765,359	3	<i>TaWAK490–TaWAK492</i>
<i>Stb19</i>	1DS	5,779,654	8	<i>TaWAK35–TaWAK42</i>



Exome/ promotorome capture of wheat WAKs



Array containing 25,810 baits was designed and manufactured



Chinese Spring

- ✓ all exons
- ✓ putative promoters (2-kb sequences)

- 20 exotic wheats carrying known Septoria resistance genes
- 14 Watkins lines showing high level of resistance to multiple foliar diseases
- 60 wheat cultivars mostly of UK/ European origin with known field reaction to Septoria
- 2 *Triticum monococcum* genotypes with contrasting response to Septoria

Used to capture WAK sequences from 96 wheat genotypes

Captured and sequenced DNA

Mapped captured DNA to the wheat Chinese Spring genome

Allelic variation analysis is in progress



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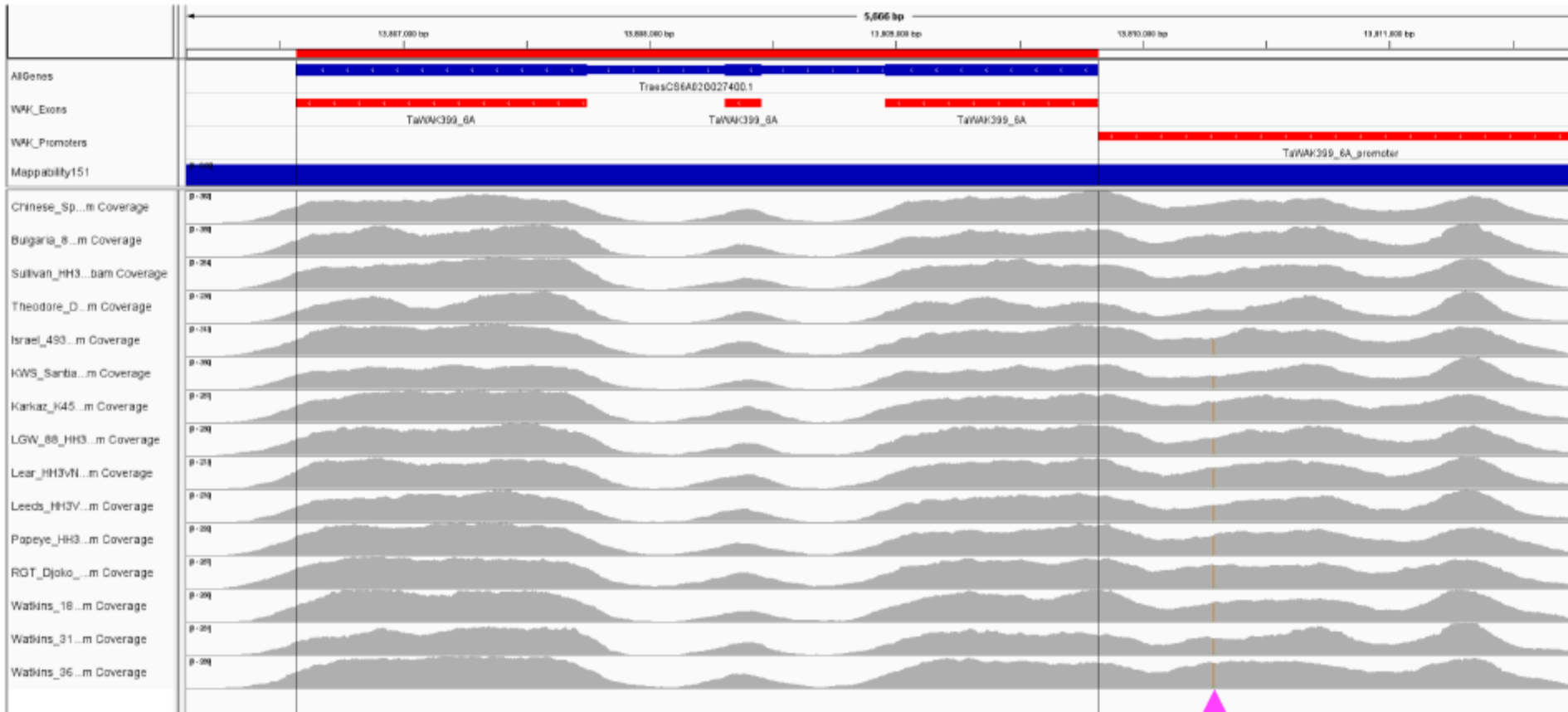
WAKs capture analysis

- Baited and sequenced 601 WAK genes (2,638 bait mappings) for 96 accessions. Read data high quality with good coverage: approximately 300X on average for the baited genes
- **Stringently mapped sequencing reads end-to-end using Bowtie2 & filtered (Q30)*** to allow mapping of each read only to a single best possible location in the genome
- Good gene recall for Chinese Spring reference (<10 genes absent) although some regions not uniquely mappable with 151 base reads (e.g. conserved kinase)
- Annotated sequence variants called at 22,853 loci (FreeBayes; DP \geq 10, variant Q \geq 30)
- Produced a database of gene models & IGV snapshot sets for visualising and exploration of this large genomic dataset
- Clear patterns of gene conservation and haplotype variation across accessions
- Distance between Chinese Spring reference & bait varieties is an obstacle to definitive absence calls in divergent accessions (other [annotated] references pending)

* These, together with the CS WAK genes annotations are available for sharing with breeders and academics. The data could be visualised using IGV and used for example for development of new SNP-based markers (e.g. KASP markers).

Some WAKs are very conserved

TaWAK399



IGV
snapshot

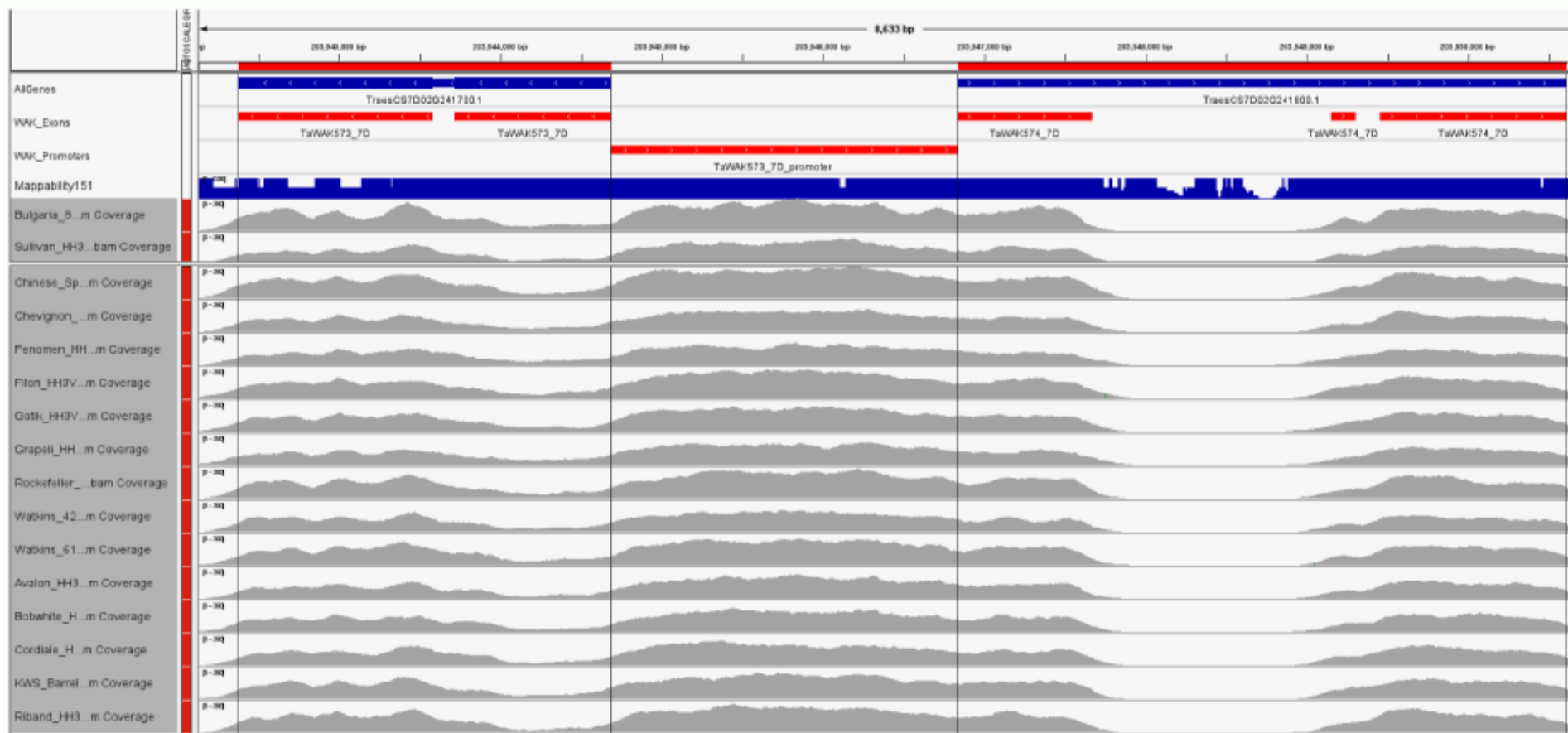
Single SNP in promoter and no SNPs in exons



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Some WAKs are very conserved

TaWAK573 & TaWAK574



IGV
snapshot

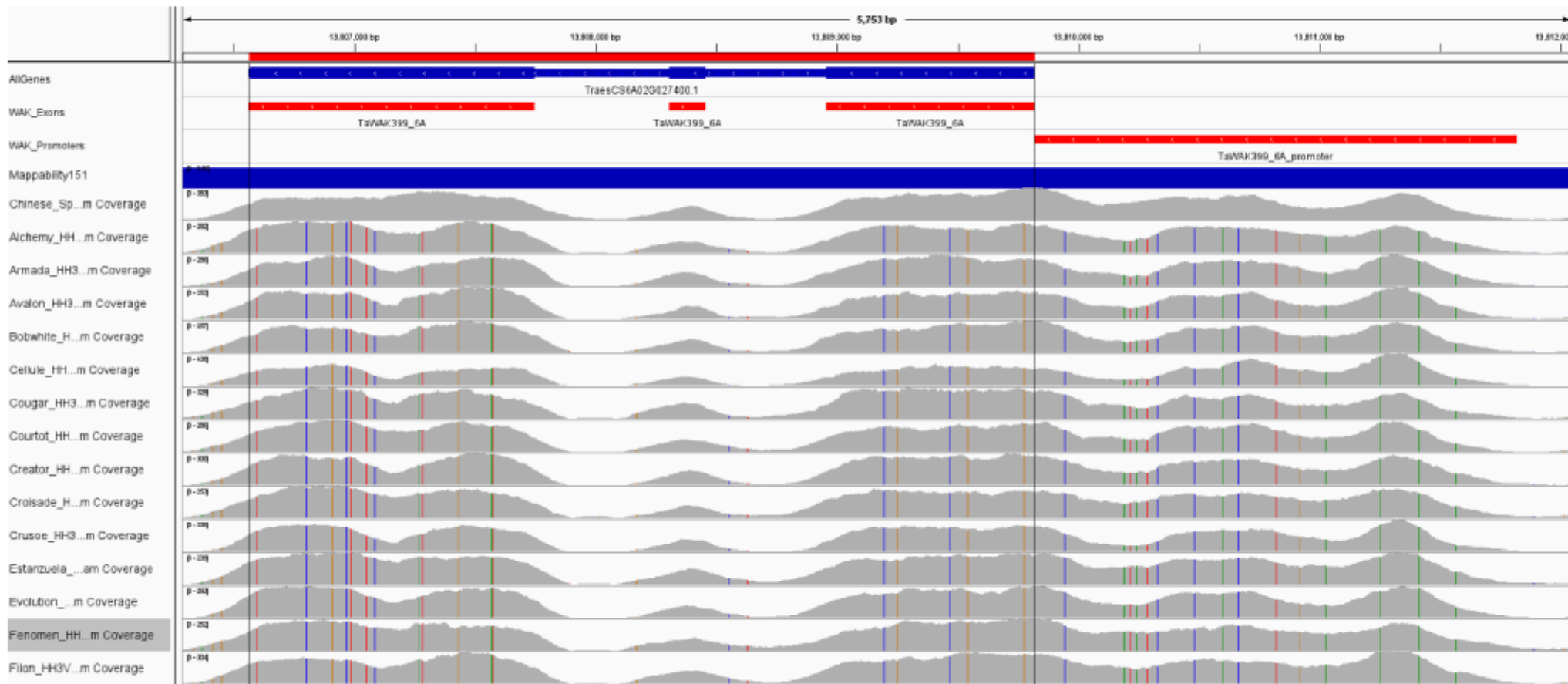
No SNPs at all



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Some WAKs show high level of sequence variation

TaWAK399



IGV
snapshot

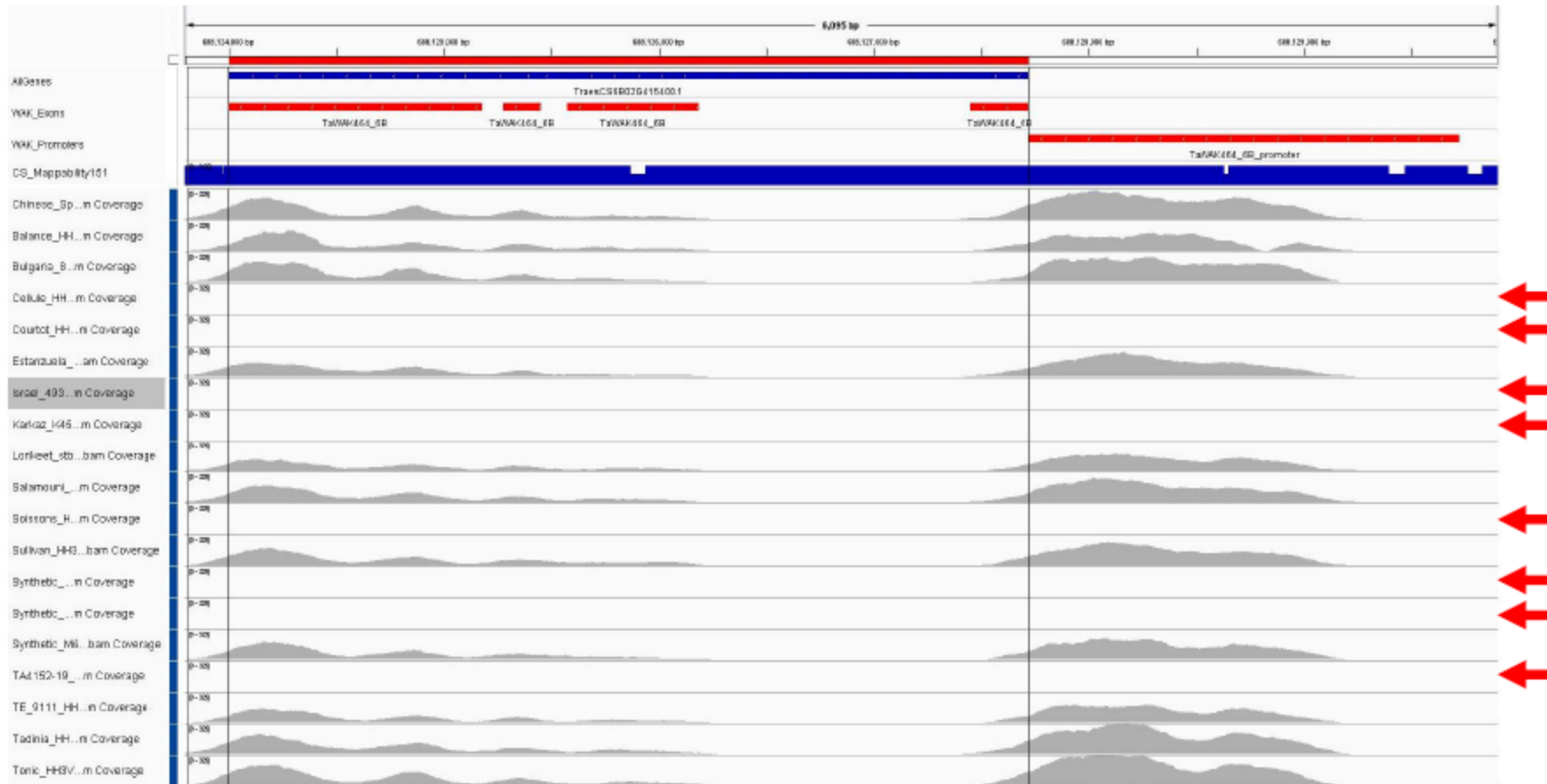
A total of 30 SNPs in this gene
Is this the same gene or a new gene?



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Some WAKs show presence/absence variation

TaWAK464



IGV
snapshot

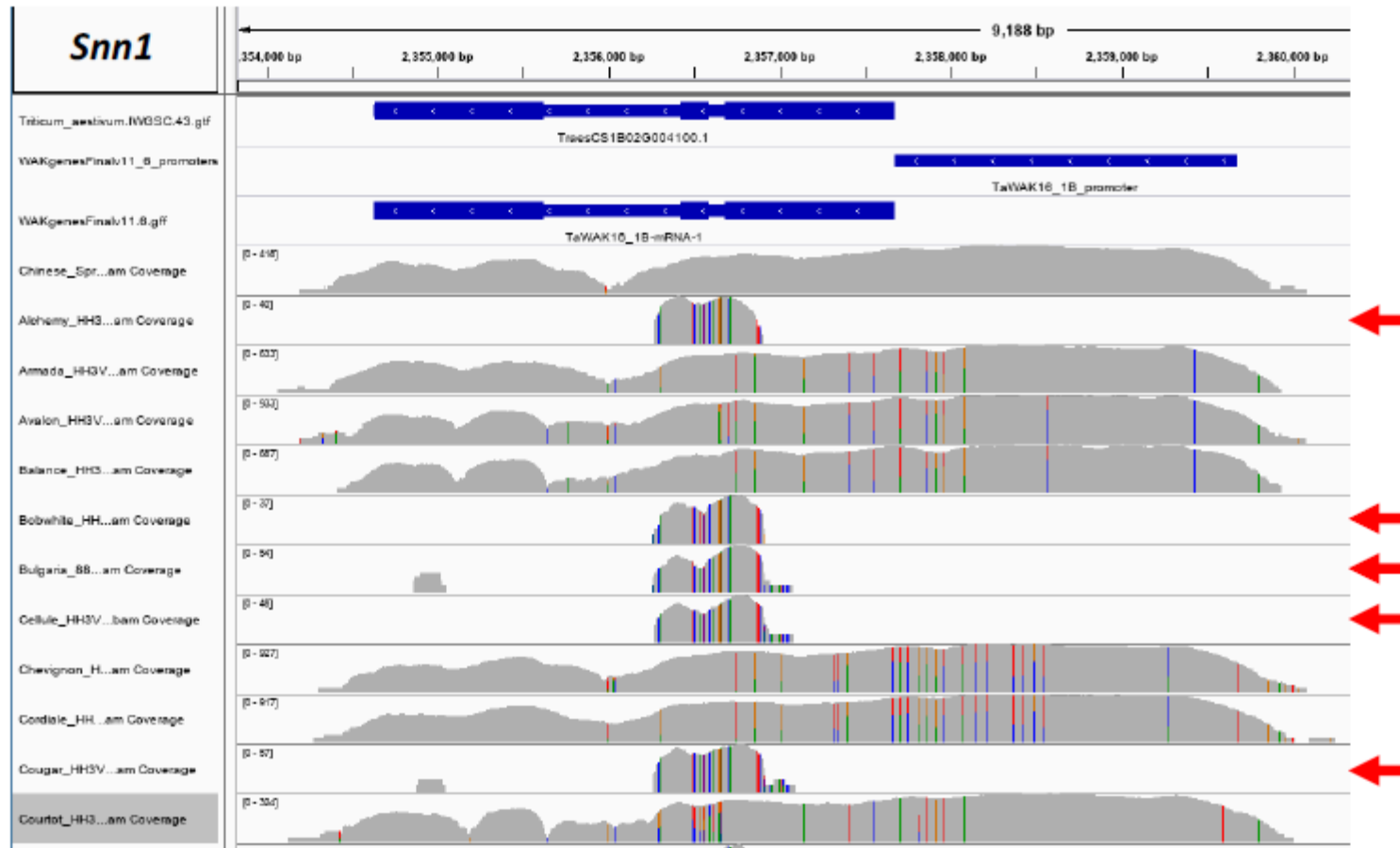
Gene is absent in 8/19 wheat varieties

Is this real or do we have some mapping issues?



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Snn1 also shows PAV in the investigated wheats



Snn1 confers susceptibility to strains of the fungus *Parastagonospora nodorum* that produce effector **SnTox1**

Snn1 appears to be absent in 48/94 analysed bread wheat



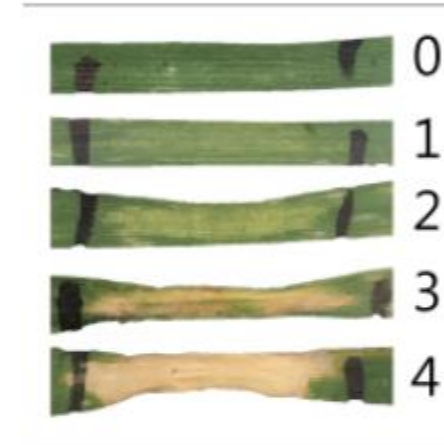
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Validation of PAV for *Snn1* in wheat

Snn1 confers sensitivity to the cognate *P. nodorum* “toxic” effector protein SnTox1

SnTox1 sensitivity data for the 48 varieties potentially missing *Snn1*:

<u>Varieties No.</u>	<u>Tox1 sensitivity score</u>
38	0
3	0.125
7	0.250

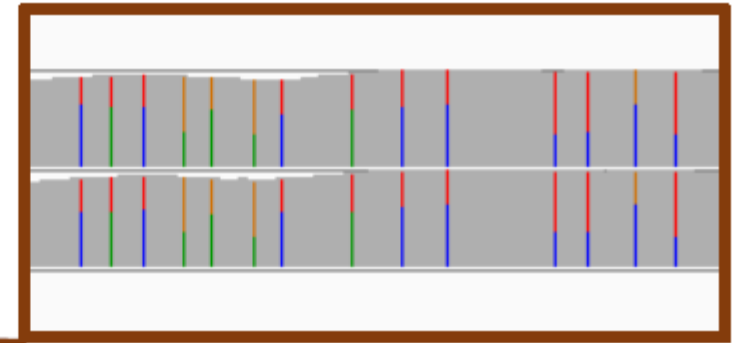
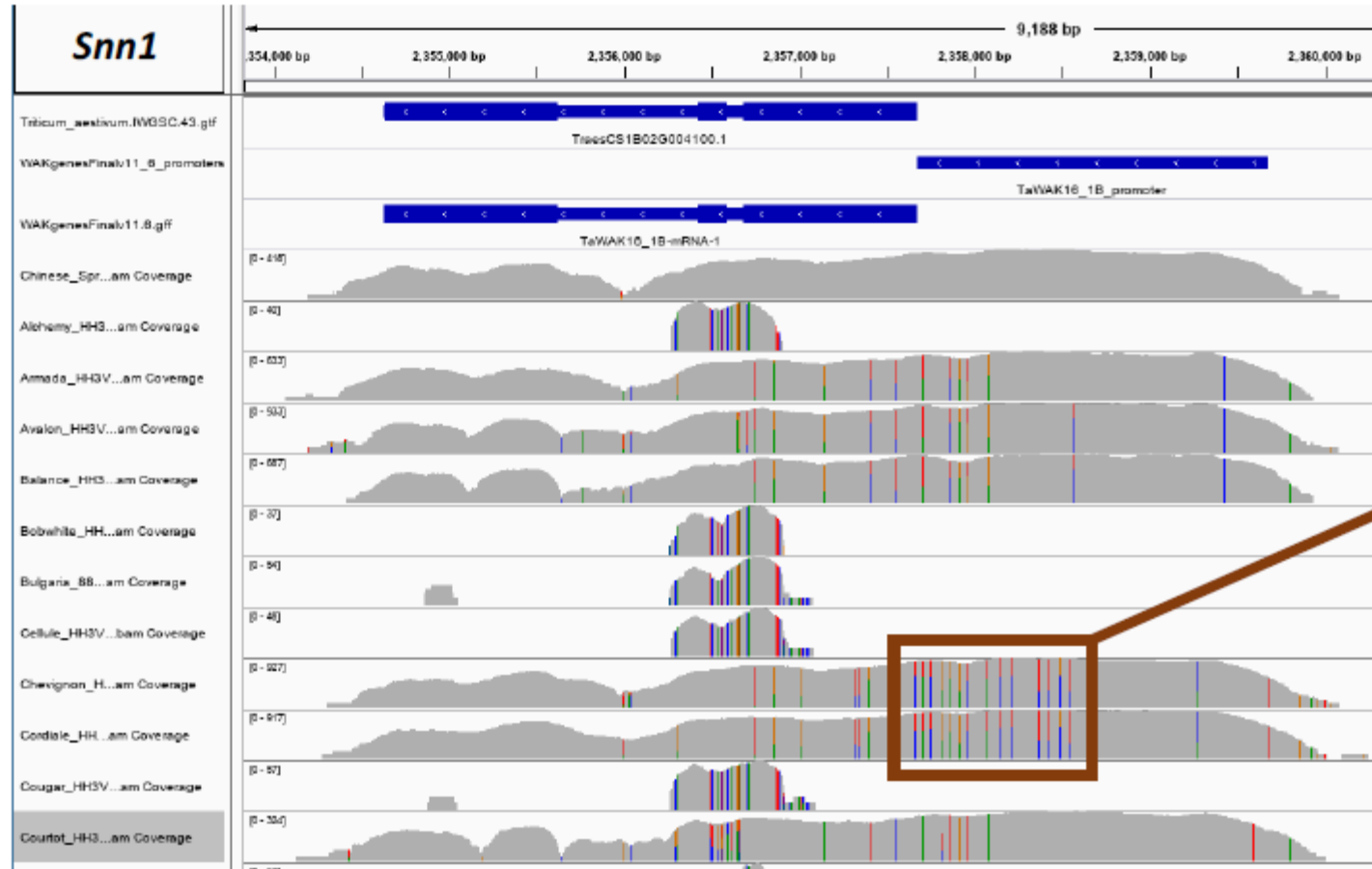


Conclusion: all wheats identified as missing *Snn1* through WAKs capture are insensitive to SnTox1, as expected



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Snn1 may also show copy number variation (CNV)



Heterozygous SNPs
(close to 50% frequency)

Some wheats appear to carry more than one non-identical *Snn1* copy



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Snn1 shows PAV and CNV in wheat germplasm



Chromosome level NRGene RefSeq genome assemblies for 9 bread wheats and 1 spelt wheat
Chromosome level W2RAP (EI) genome assemblies for 4 bread wheats and 1 durum wheat

Arina	absent
Claire	absent
Landmark	absent
Lancer	present
Kronos	present
Julius	absent
Cadenza	present
Jagger	present – 2 copies
Mace	absent
Norin 61	present – 2 copies
Paragon	absent
Robigus	absent
Spelt	present*
Stanley	present – 2 copies
SY Mattis	absent

Using our current WAKs capture dataset it may be impossible to resolve sequences of duplicated WAKs



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RESEARCH

Dan Smith
Rob King
Mike Hammond-Kosack
Kim Hammond-Kosack

INRAE



Cyrille Saintenac
David Lopez



James Cockram

Wheat Breeders

Ruth Bryant (RAGT)
Nick Bird (KWS)
Matt Kerton (DSV)
Finn Borum (Sejet)
Simon Berry (Limagrain)

Thank you!

International
Wheat Genome
Sequencing
Consortium

WGIN Scientific Outreach Jan – July 2020

Seedstor at the GRU – for access to all WGIN seedstocks

Joint GINs website – June 2020

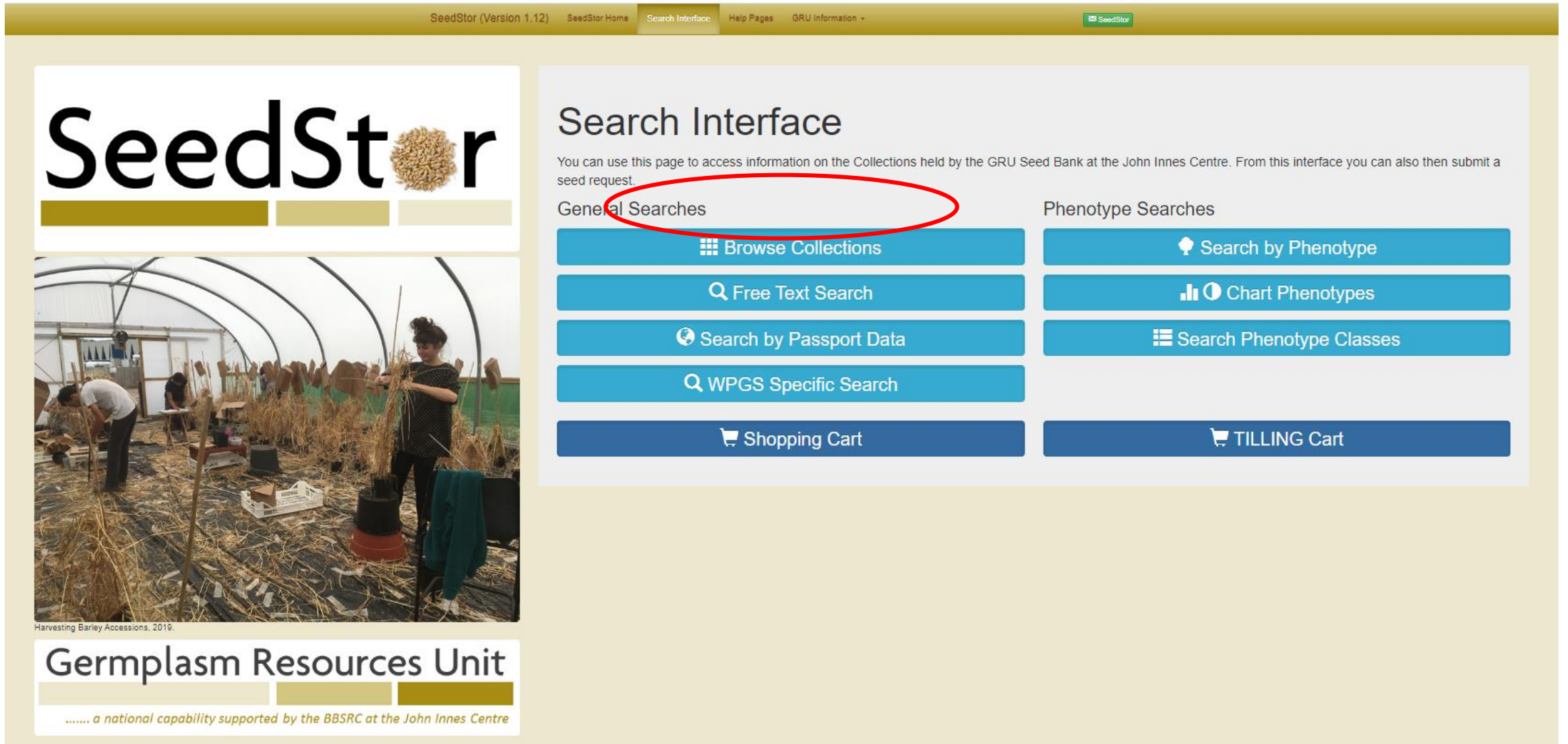
Virtual Cereals ppt – June 2020

Crop Production Magazine – July 2020 WGIN, PCGIN and OREGIN

**Open Access Government site – advertising the virtual Stakeholder meeting
11-12th Nov 2020**

All WGIN generated seed stocks available from Seedstor at the GRU

<https://www.seedstor.ac.uk/search-panel.php>



The screenshot shows the SeedStor website's search interface. At the top, there is a navigation bar with links for 'SeedStor (Version 1.12)', 'SeedStor Home', 'Search Interface', 'Help Pages', and 'GRU Information'. The main header features the 'SeedStor' logo, where the 'o' is replaced by a cluster of seeds. Below the logo is a photograph of a greenhouse with people working on barley plants, captioned 'Harvesting Barley Accessions, 2019'. The central section is titled 'Search Interface' and includes a brief description: 'You can use this page to access information on the Collections held by the GRU Seed Bank at the John Innes Centre. From this interface you can also then submit a seed request.' Below this, there are two columns of search options. The left column, titled 'General Searches', contains five buttons: 'Browse Collections', 'Free Text Search', 'Search by Passport Data', 'WPGS Specific Search', and 'Shopping Cart'. The right column, titled 'Phenotype Searches', contains three buttons: 'Search by Phenotype', 'Chart Phenotypes', and 'Search Phenotype Classes'. At the bottom, there is a 'TILLING Cart' button. The footer of the page reads 'Germplasm Resources Unit' and '..... a national capability supported by the BBSRC at the John Innes Centre'.

SeedStor (Version 1.12) SeedStor Home Search Interface Help Pages GRU Information - SeedStor

SeedStor

Harvesting Barley Accessions, 2019.

Germplasm Resources Unit

..... a national capability supported by the BBSRC at the John Innes Centre

Search Interface

You can use this page to access information on the Collections held by the GRU Seed Bank at the John Innes Centre. From this interface you can also then submit a seed request.


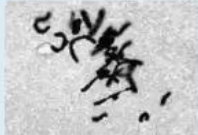
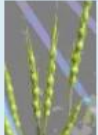



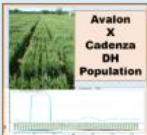













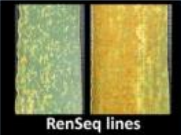

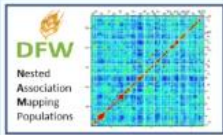

General Searches

- Browse Collections
- Free Text Search
- Search by Passport Data
- WPGS Specific Search
- Shopping Cart

Phenotype Searches

- Search by Phenotype
- Chart Phenotypes
- Search Phenotype Classes
- TILLING Cart

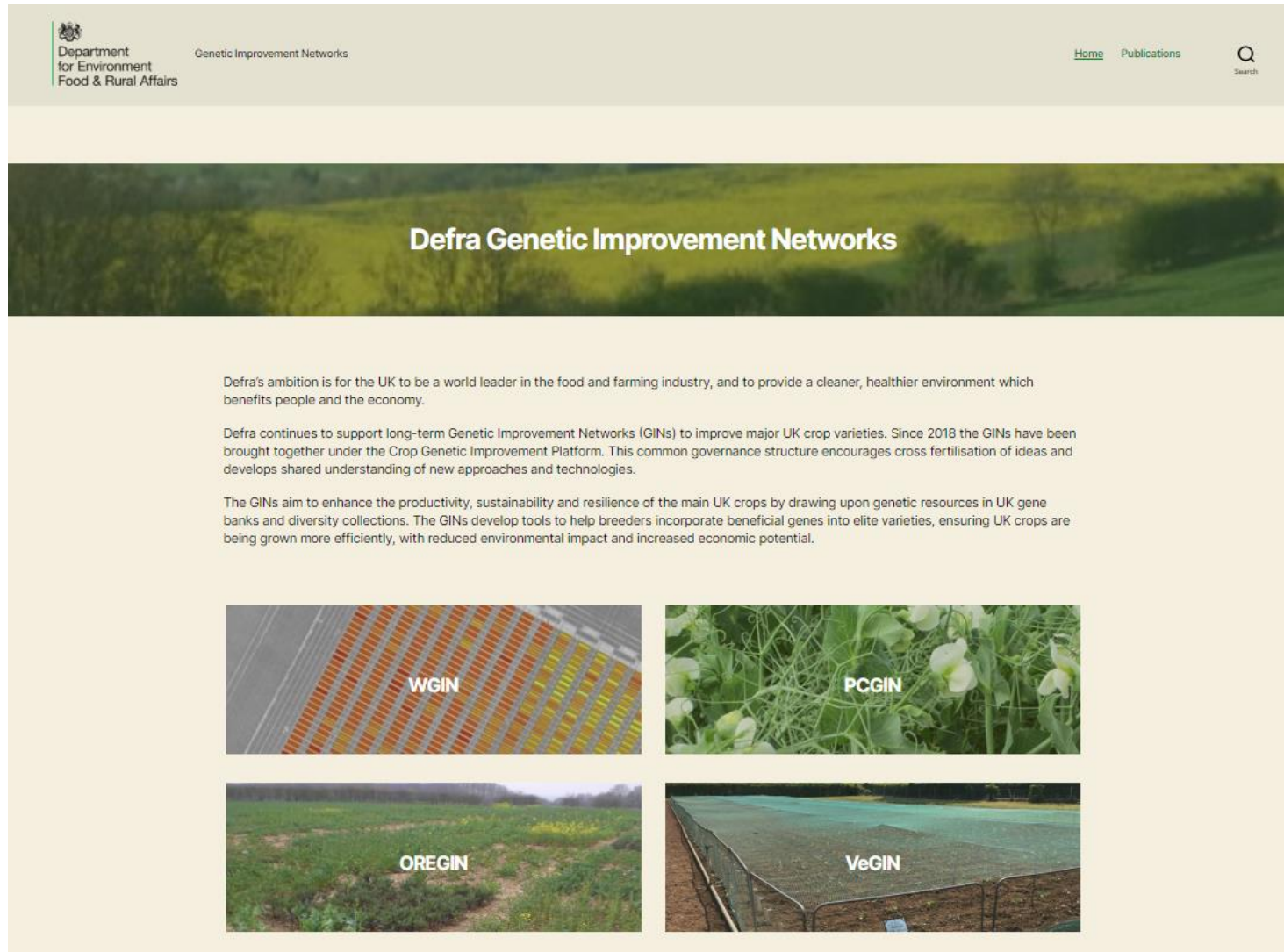
<https://www.seedstor.ac.uk/search-browsecollections.php>

 <p>BBSRC Small Grain Cereal Collections ⓘ</p>	 <p>Wheat Precise Genetic Stocks ⓘ</p>	 <p>Cereal Crop Wild Relatives (Triticeae) ⓘ</p>	 <p>Watkins Historic Collection of Landrace Wheats ⓘ</p>	 <p>Watkins Stabilised Collection of Hexaploid Landrace Wheats ⓘ</p>
 <p>JIC Pisum Collection ⓘ</p>	 <p>Avalon x Cadenza DH Population ⓘ</p>	 <p>RevGen TILLING population (Brassica rapa) ⓘ</p>	 <p>RevGen TILLING population (Brassica napus) ⓘ</p>	 <p>Bristol CerealsDB Stocks Collection Set of sequenced wheat lines from the Functional Genomics Group University of BRISTOL Bristol Wheat Genomics Group ⓘ</p>
 <p>Triticeae Genome Association panel ⓘ</p>	 <p>Wheat TILLING in silico wheat TILLING populations (Exome capture) ⓘ</p>	 <p>Vicia Faba ⓘ</p>	 <p>Wheat Pan Genome Pangenome Collection ⓘ</p>	 <p>Open Wild Wheat Consortium: Aegilops tauschii Diversity Panel ⓘ</p>
 <p>Designing Future Wheat Toolkit ⓘ</p>	 <p>BREEDERS TOOL KIT DFW ⓘ</p>	 <p>GEDIFLUX Collection 1945-2000 ⓘ</p>	 <p>Paragon x Chinese Spring SSD ⓘ</p>	 <p>Paragon γ Deletions ⓘ</p>
 <p>RenSeq lines Wheat Resistance gene enrichment (REN) sequencing collection ⓘ</p>	 <p>The Paragon Library Paragon Near Isogenic Line Library ⓘ</p>	 <p>DFW Nested Association Mapping Populations DFW Wheat Nested Association Mapping (DFW-NAM) panel ⓘ</p>	 <p>EMS induced Mutations Paragon defra Wheat Genetics Experiment Network Paragon EMS Mutants ⓘ</p>	

The new joint GINs website: <https://defracropgenetics.org>

Tested in May and went live in June 2020

QR for the site



News
Publications per GIN

Brief project descriptions
+ dates for stakeholder
meetings

Link-outs to the four
individual GIN websites

Scaleable
for use on any
mobile device
in portrait or
landscape modes

Developer : James Seager (RRes -BCP PHI-base team), software is WordPress

Virtual Cereals event – 11th – 12th June 2020

Webinar Schedule

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T. monococcum
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- Video

WGIN



11 Jun 2020

13:00 - 13:45

Plant Breeding Innovations

JOIN WEBINAR

Chaired by Anthony John, Department of International Trade

This session explores the opportunity that plant breeding techniques such as gene editing and sequencing, alongside increasing collaboration between researchers and industry, offer in creating crops and varieties that are much fitter for a future that aims to be low in carbon and pesticide usage.

- **Kim Hammond-Kosack, Rothamsted Research** reveals a bold new resilient world in which breeding technologies will deliver resistance to aphids, take-all, septoria and slugs in the future
- **James Brosnan, chair of the International Barley Hub**, which is galvanising the research community and supply chain to address the big issues of resilience and climate change, talks about the innovations coming barley's way
- **Cristobal Uauy** gives an insight into CRISPR gene editing technology and how it can be used to produce new varieties with benefits to farming and the environment.
- **Rob Hiles, Syngenta** looks at the potential benefits of hybrid wheats, which are getting closer to becoming a commercial reality.

BASIS POINT AVAILABLE

<https://www.cerealsevent.co.uk/cereals-2020-live-webinar-timetable>

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WGIN4 Core Project
March 2018 – March 2023

www.WGIN.org.uk



333 in the audience on the day
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Kim Hammond-Kosack



Department
for Environment
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Cereals LIVE 2020 VIRTUAL EVENT

11th June 2020

CPM magazine special issue on Crop Genetics – July 2020



The global reach of plant science

Innovation Genetics special

Could the UK's "extraordinary" plant-science sector be limbering up for an integral role in the genetics revolution that will deliver the farming of the future to communities the world over? *CPM* explores the opportunities.

By Tom Allen-Stevens

As the Government faced criticism for appearing to slam shut one door on the path to prosperity for UK Agriculture, it may just have opened another.

At Cereals Live last month, farming minister Victoria Prentis explained why Government ruled out measures in the Agriculture Bill to prevent farming standards being undermined through imports (see full report on p34). But she struck a different note on gene-editing, highlighting that Defra doesn't agree with EU laws that treat the new plant-breeding technology (NPBT) as genetic modification.

"We've pushed for many years for the EU to come to the place we're in," she said.

"We're committed to taking a more scientific approach and we recognise the potential for

Agriculture Bill, this is definitely an important area for Defra to be engaging with over the course of the next 12 months."

This follows the tabling of an amendment to the Agriculture Bill in the House of Lords by former CLA president and Countryside Agency chair Lord Cameron. The amendment on agricultural research would allow the Defra secretary of state to change the way the Environmental Protection Act treats breeding techniques "where nucleic acid changes could have occurred naturally or through traditional breeding methods."

If the amendment's carried, any changes would only be made following public consultation and would be restricted to England.

Research programmes

Lord Cameron said he wanted the Bill to put forward a "clear message" that the Government will move forward to allow gene-editing in research programmes. "This is a way of speeding up the natural methods of farm breeding to ensure that we can improve the environmental and nutritional outcomes of feeding our ever-expanding human population, both at home and — more particularly, as far as I am concerned — in the developing world," he told the House during the Bill's second reading last month.

So just what is the prospect for UK plant-science research and what role could enable farmers have? Moreover, with a

This *CPM* genetics special explores the prospects for UK-based plant breeding over the next 11 pages. Since 2003, four Genetic Improvement Networks (GINs) have formed the focus of Defra's activity in this area, for wheat, oilseeds, pulses and vegetables. The departments awarded them a total of £5.5M for a five-year programme of activity up to 2023.

The wheat network, WGIN, for example, has £1.7M of this, with its main aim being to improve the resilience of the UK wheat crop through genetics. About 70% of its effort goes towards trait discovery while the rest is spent on developing genetic and genomic resources, available licence-free to commercial breeders to introduce into their elite lines.

One new aspect of the 17-year-old programme is that there's now an alliance with AHDB to strengthen direct links with farmers. Traits being explored include nitrogen use efficiency, resistance to lodging, stugs and BYDV, as well as resistance to septoria and yellow rust. Work on quality traits includes research on specific weight undertaken at John Innes Centre, for example, with novel lines showing up to 20% improvement.

Drones with high-performance cameras are being developed for faster phenotyping, while one of the jewels in WGIN's crown is the Walkins collection — a unique set of 1200 lines from 31 countries never previously used in modern breeding.

WGIN



AHDB
from theory to field

Collaborative research has long been the backbone of a Defra-funded breeding programme that has responded to the challenges facing oilseed rape growers. *CPM* explores the programme's current focus.
By Tom Allen-Stevens

Five crops will take you on the emotional rollercoaster in quite the same way as oilseed rape. There's the dazzling display of a crop in full flower, followed by the thick mat of pods with its promise of harvest bounty. And there's the straggling seedlings mercilessly sprayed by cabbage stem flea beetle as they sit in subservient surrender in a dry September soil.

Could something be done with the genetics to smoothen out the ride? This is one of the key aims of the Oilseed Rape Genetic Improvement Network (OREGIN). Set up in 2003 as one of four Defra-funded genetic networks, it brings together researchers and breeders in a collaborative approach to crop-breeding work and resources. Priority plant characteristics being investigated include resistance to insects, viruses and diseases, including stem canker, light leaf spot and clubroot, and improved tiller/seed efficiency.

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“Without the GINs there's some cutting-edge genetic research that simply wouldn't be carried out in the UK.”

The OREGIN of resilience?

But it's the loss of chemistry, the weather and market pressures that are commonly cited as cutting increasing strain on the oilseed sector, and these factors haven't gone unnoticed. "Everyone is acutely aware of how much of a priority cabbage stem flea beetle is," says AHDB research and knowledge exchange manager Dean Thwaites.

AHDB doesn't contribute to funding, he explains, but does get involved in the many spin-off research projects that have come about through OREGIN, and sits on the stakeholder group. "Who decided to have the opportunity to influence the programme, although the targets OREGIN has identified and the direction taken we fully endorse. It demonstrates good industry involvement," notes Dean.

Alternative approaches (usually, the decision taken is to seek out alternative approaches to crop management, with emphasis on those that integrate genetics with sound agronomic techniques and methods to mitigate biotic and abiotic stresses. "Previous research had implicated specific genes as being detrimental to important characteristics of rapeseed, so the current phase of OREGIN includes peer-reviewing activities to test predicted impacts of the loss of those genes," he explains.

This involves the development of new winter OREGIN lines with benchmarking relative to a panel of around 30 reference varieties, along with the development of molecular markers to assist future breeding.

A characteristic of all GINs, and a unique feature of the wheat programme, is that information has always been made publicly available. "Licence-free, to guide breeders' choices," Dean adds.

"They're not starting from scratch — breeders have been incorporating these improvements since the programme began. What's different now are the advances in breeding technology. Breeders target genes of interest or areas of the genome associated with a trait. Markers help them quickly identify if this gene or set of genes has come through in a new cross, and this can reduce the time it takes to bring a new variety to market. OREGIN gives the breeders not only the genepool that has the interesting trait, but the markers to help identify it," says Dean.



Plant breeders and geneticists are acutely aware of how much of a priority cabbage stem flea beetle is, says Dean Thwaites.

PCGIN



Innovation Pulse genetics

Massive demand for plant-based proteins puts the spotlight on peas and beans to deliver for the UK market. *CPM* delves into the research aimed at putting varieties on farms that will meet the challenge.
By Tom Allen-Stevens

A crop that fixes its own nitrogen from the air, is nutrient-rich, with properties that offer a wide range of established health benefits and one that can have a carbon-positive impact in many of its applications: such a crop should surely be heralded and championed?

"Peas come with built-in public good, so present a dual prospect for society and farmers alike," he notes. The EU currently imports around 90% of its protein requirement, with soybean and soya meal imports into the UK alone between 2.5-3M tonnes. "EU policy for the past 40 years has driven quite a significant overcapacity of energy-cereal grains and that's created a massive deficit of home-grown protein," Jack maintains.

"Soymeal is very competitively priced and

it's a good product for monogastric animals, but there is the opportunity in dairy and pigs to substitute around the edges of the market. With changing consumer habits, protein for human consumption is a growing market we risk not capitalising on."

Fundamental problem Jack would like to see "right alliances" between state and livestock producers, underpinned by a "decentralisation" of farm-to-farm trading. But he recognises there's a fundamental problem with pulses: it's the fact it's being addressed through improving crop performance and reliability, by establishing the genetic basis for agronomic traits such as standing ability, yield and disease. "Genetic resistance markers have been defined for powdery mildew in peas, for example, but not for downy mildew, an oomycete that has a large impact in diminishing yield of both peas and beans," he continues.

The difficulty here is that downy mildew has many different races, so just one source of genetic resistance would be quickly overcome — three or preferably four genes would be more robust, but there's now a pressing need, he notes. "Most of the seed treatments for this disease have been withdrawn or are restricted temporarily in their application, making the discovery of disease

The opportunity for protein substitution is to source output linked by availability. Steve points out — pulses will be best only ever to be included one year in five in the standard UK rotation. "This is an area that gets a lot of rhetoric, but not a lot of action, however."

Details response is to fund the Pulse Crop Genetic Improvement Network (PCGIN). One of four networks, it's a platform that sets out to serve the process of crop improvement for legumes in the UK. PCGIN is currently running on a five-year programme, with

standing channelled into four work packages designed to meet current and future industry requirements.

"We hope the programme produces more resilience in pulse crops to make them more attractive to farmers, and to increase the market value of their product. These two

requirements are linked to the major strands of PCGIN activity," explains Steve.

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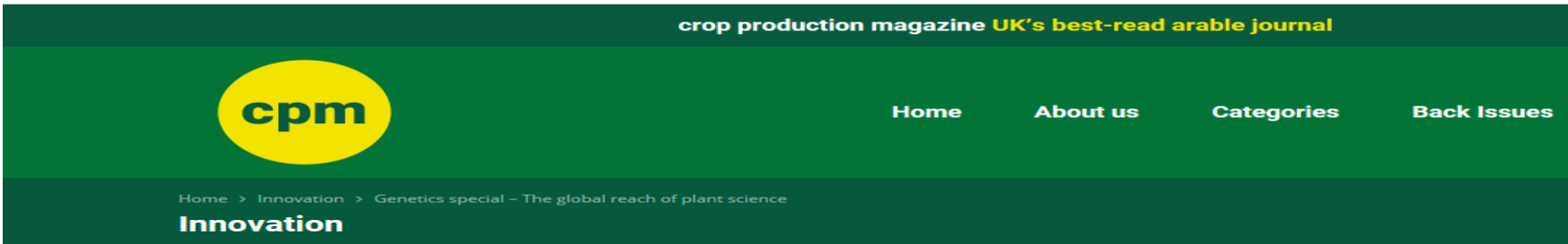
PCGIN's Steve Walker agrees that year-on-year variation in yields is a problem, keeping pulse crops out of the rotation for many. "Particularly in spring sown crops, there's a correlation yields are variable and unreliable, although there's also evidence this is no more the case in pulses than for other spring sown crops," he notes.

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July 2020

Genetics special – The global reach of plant science

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1) 'Genetics special – The global reach of plant science'

<http://www.cpm-magazine.co.uk/2020/07/05/genetics-special-the-global-reach-of-plant-science/>

So just what is the prospect for UK plant-science research and what role could arable farmers have? Moreover, with a US/UK trade agreement being discussed, how will UK plant science fit into the new world order, and what support can we expect from government?

This *CPM* genetics special explores the prospects for UK-based plant breeding. Since 2003, four Genetic Improvement Networks (GINs) have formed the focus of Defra's activity in this area, for wheat, oilseeds, pulses and vegetables. The department's awarded them a total of £5.5M for a five-year programme of activity up to 2023.



WGIN aims to improve the resilience of the UK wheat crop through genetics. For full details see GINs provide shot in the arm

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Drones with high-performance cameras are being developed for faster phenotyping, while one of the jewels in WGIN's crown is the Watkins collection – a unique set of 1200 lines from 31 countries never previously used in modern breeding. A range of novel traits is also available through 323 lines of *Triticum monococcum*, a diploid

wheat rarely used in modern breeding – resistance to take all, septoria, yellow and brown rust, mildew and aphids have all been identified.

Similar achievements have been made with OREGIN and PCGIN. But is it enough? "We see an opportunity for a step change in the way we do plant science," says Prof Dale Sanders, director of the John Innes Centre.

2) 'Theory to Field – The OREGIN of resilience?'

<http://www.cpm-magazine.co.uk/2020/07/06/theory-to-field-the-oregin-of-resilience/>

3) 'Pulse Genetics – Reach for the GIN'

<http://www.cpm-magazine.co.uk/2020/07/09/pulse-genetics-reach-for-the-gin/>



Agricultural Sciences section

The Defra funded UK Wheat Genetic Improvement Network, in its 16th year of funding and still going strong.

This year's virtual WGIN Stakeholders' Meeting will take place on Wednesday and Thursday November 11th and 12th 2020.

This event is open for registration from September onwards via Eventbrite by visiting the WGIN website (www.wgin.org.uk/) where a copy of the full programme can also be downloaded. This is an opportunity to 'meet' and discuss current and emerging topics in wheat research, genetic improvement through breeding and the latest production methods with wheat scientists based in academia and industry, commercial plant breeders, crop consultant, farmers and farm managers.

Ongoing since May 2019

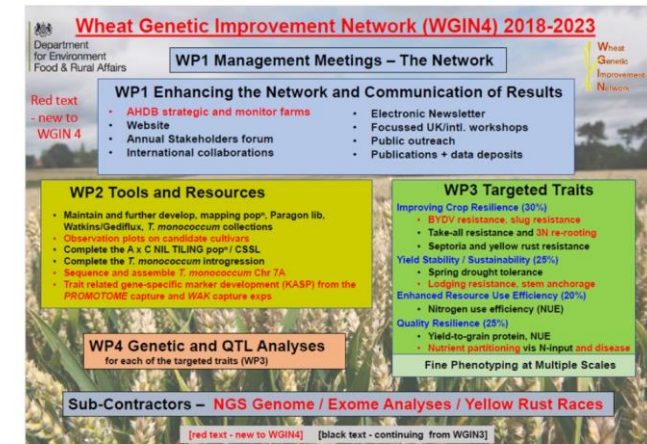


Figure 1 The organisational schematic of WGIN4. All red text highlights new additions compared to WGIN3

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