

WGIN 3

Resistance to multiple foliar fungal pathogens and take-all root disease in wheat

Vanessa McMillan



Department
for Environment
Food & Rural Affairs

Major foliar wheat pathogens in UK



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Wheat yellow rust
Puccinia striiformis f.sp. *tritici*



Septoria leaf blotch
Zymoseptoria tritici



Wheat brown rust
Puccinia triticina



Powdery mildew
Blumeria graminis f.sp. *tritici*

Exploiting the Watkins landrace collection



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- 2008 - Watkins landrace collection (n = 740 genotypes) phenotyped for resistance against foliar fungal pathogens and take-all root disease



- High foliar disease pressure – brown rust, yellow rust, septoria and powdery mildew assessments carried out

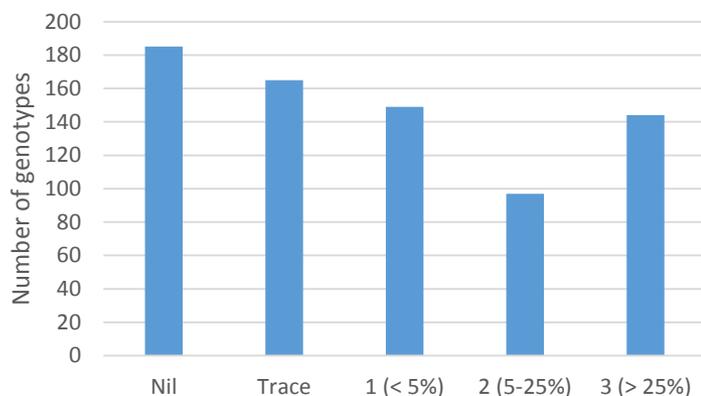


Exploiting the Watkins landrace collection

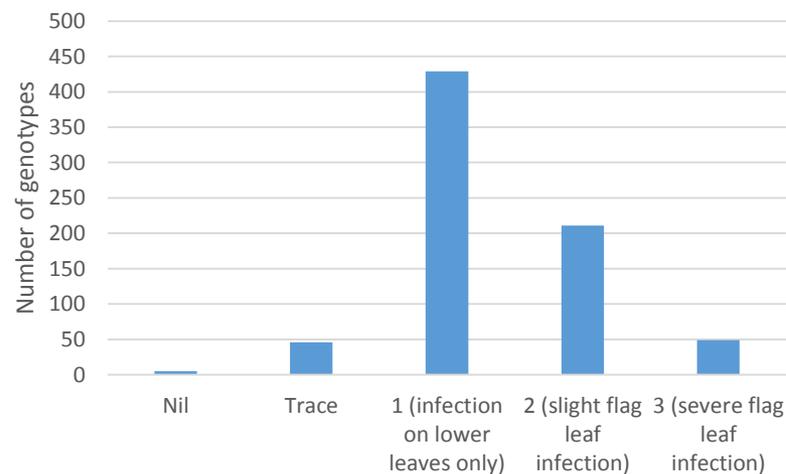


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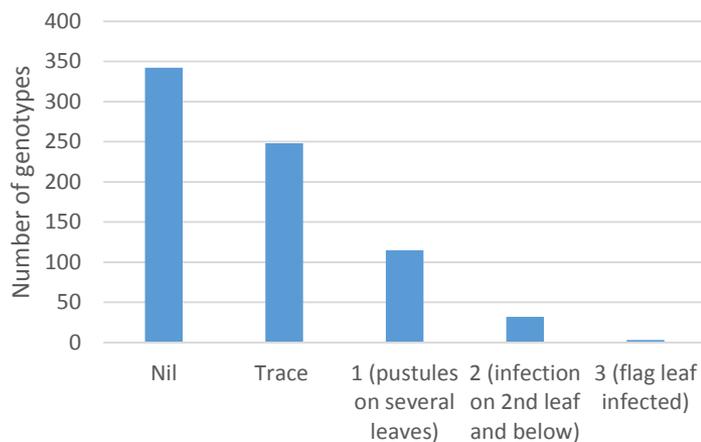
Yellow Rust on flag leaf
(% flag leaf area infected)



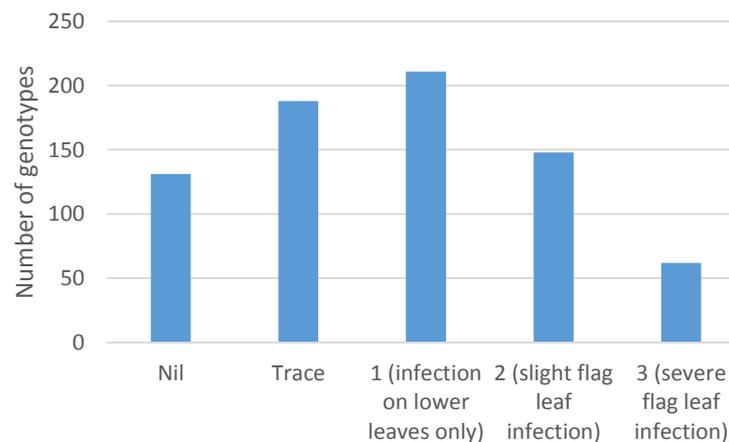
Septoria assessment



Brown Rust assessment



Powdery Mildew assessment



Exploiting the Watkins landrace collection



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10 Watkins genotypes with a high degree of resistance to all 4 foliar pathogens

Also a high take-all disease year with root infection early in the season

Was the foliar disease resistance an induced plant response?

Accession	Growth habit	Country of Origin	2008 Disease assessments			
			Yellow rust	Brown rust	Septoria	Mildew
18	Spring	India	0	0	T	T
137	Spring	Australia	T	T	0	T
203	Winter	India	0	0	0	T
231	Spring	Hungary	0	0	T	0
262	Spring	Canary Islands	0	0	0	0
399	Spring	China	T	0	T	0
495	Spring	Morocco	0	0	T	0
610	Spring	Yugoslavia	0	0	T	T
733	Spring	Iran	T	T	T	T
786	Spring	USSR	0	T	T	0

0 – no disease , T = trace

WGIN 3 Watkins foliar disease experiments



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- 10 Watkins genotypes sown in both **1st wheat (no take-all)** and **3rd wheat (high take-all)** field trials in autumn 2014, 2015 and 2016
- No fungicides applied to allow natural disease to develop
- Score for foliar diseases + take-all

Watkins foliar disease field trial 2015



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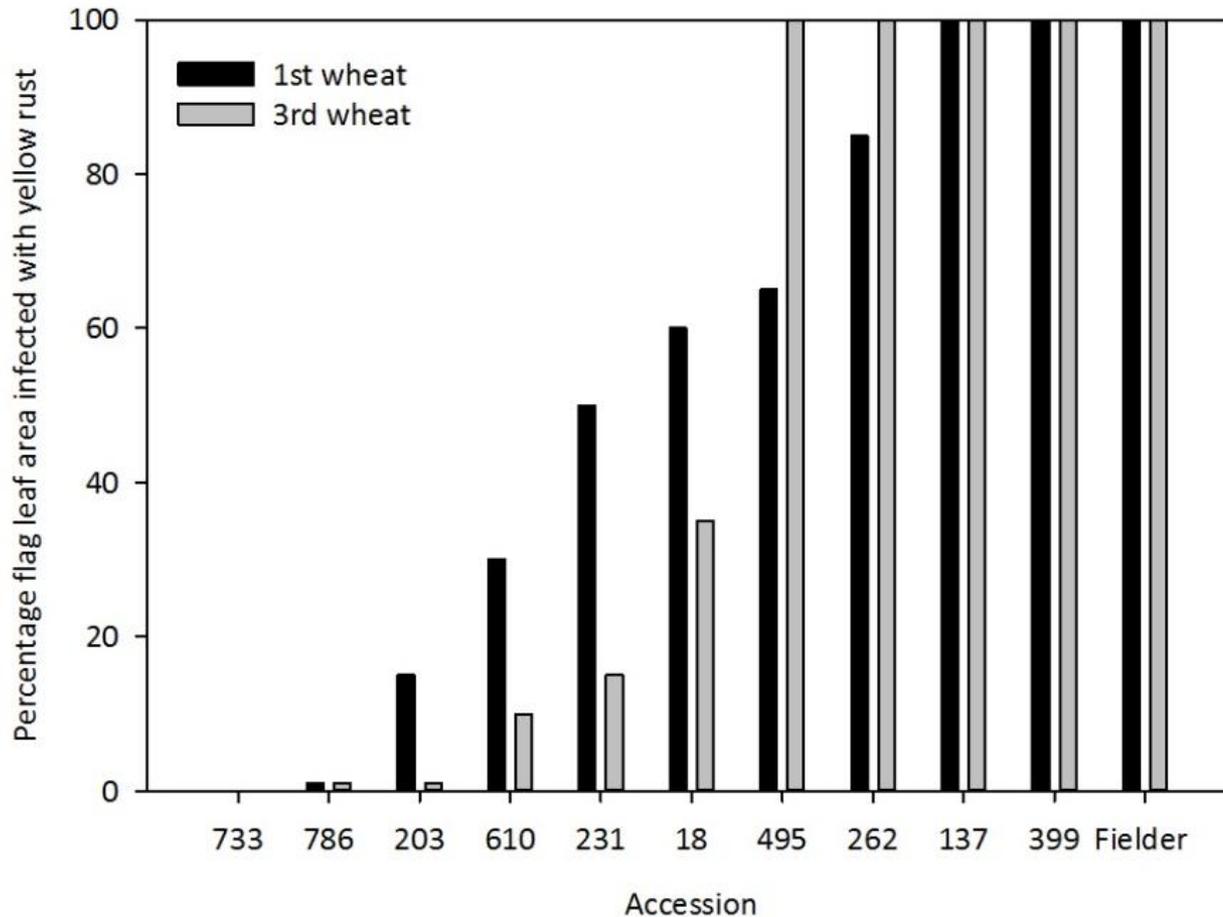
26th June 2015 1st wheat Long Hoos 4

Yellow rust dominant disease that developed across 2015 field trials

Evidence of resistance to yellow rust



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- Evidence of induced response due to take-all?
- Did varieties escape YR in 2008 or different YR races?

Evidence of resistance to yellow rust



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Watkins 203

Low levels of yellow rust sporulation



Watkins 733

No sporulation

Watkins foliar disease trial 2016



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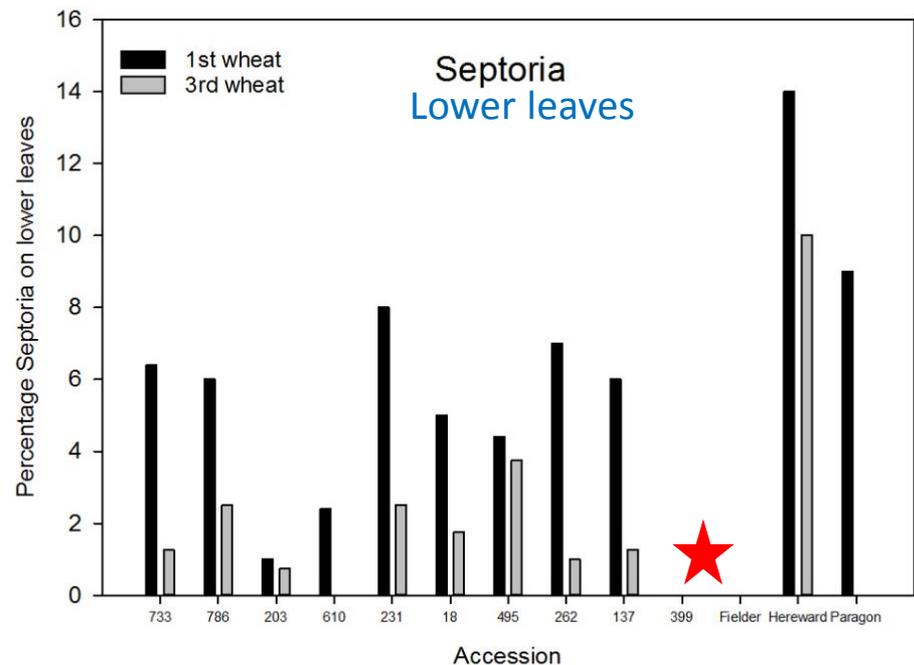
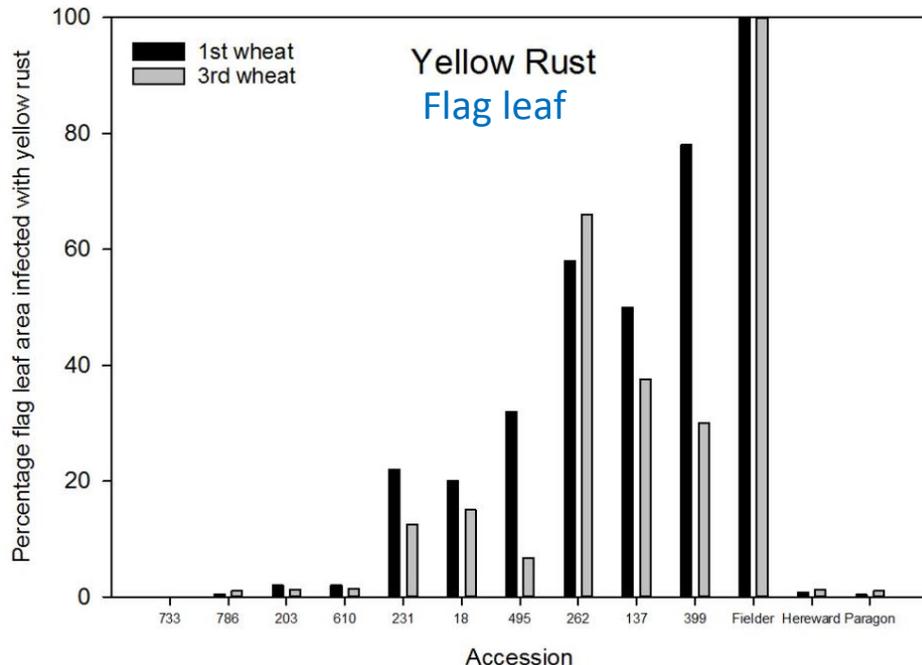
- Repeat field trial with 5 replicates of each genotype sown in autumn 2015 in Long Hoos 5 (1st wheat) and Long Hoos 6/7 (3rd wheat)
- Yellow rust, septoria and brown rust developed

6th June 2016 – Yellow rust and Septoria



SCOTT WATSON

4



- Yellow Rust shows similar pattern to 2015

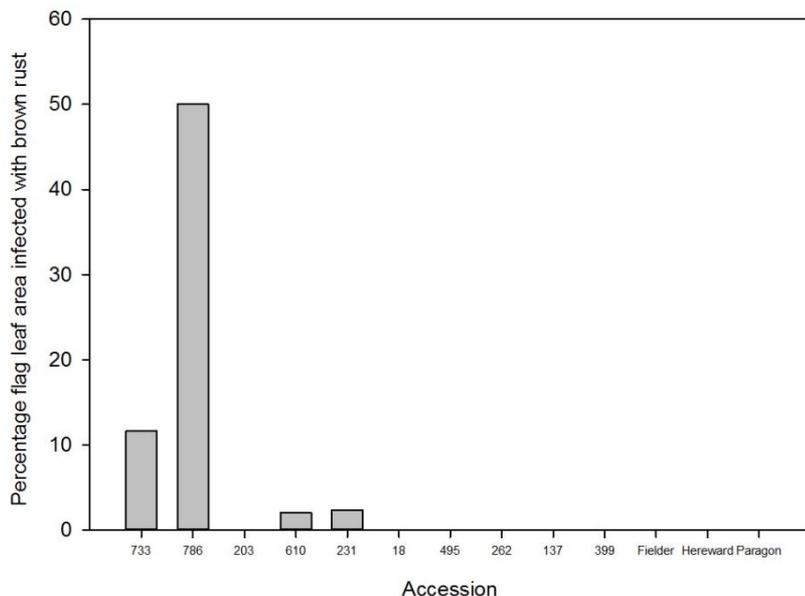
★ Low levels of Septoria on all genotypes except 399 and Fielder where high levels of yellow rust are found, therefore impossible to assess Septoria infections

- All genotypes at GS 57-61, except 610 at GS 47

22nd June 2016 – Brown rust developed across the 1st wheat trial site



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Watkins 733



Watkins 786

- Watkins 733 and 786 were most resistant to yellow rust but are very susceptible to brown rust – do not possess multi disease resistance
- Watkins 203 most promising for showing high levels of resistance against both yellow rust, brown rust and septoria

Watkins mapping population development



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Summer 2015 Field crossing with cv. Fielder

Accession Number	Growth habit	Country of Origin	Ears crossed	F ₁ grains
203	Winter	India	8	31
231	Spring	Hungary	8	54
610	Spring	Yugoslavia	6	33
733	Spring	Iran	6	49
786	Spring	USSR	N/A	N/A

Summer 2016

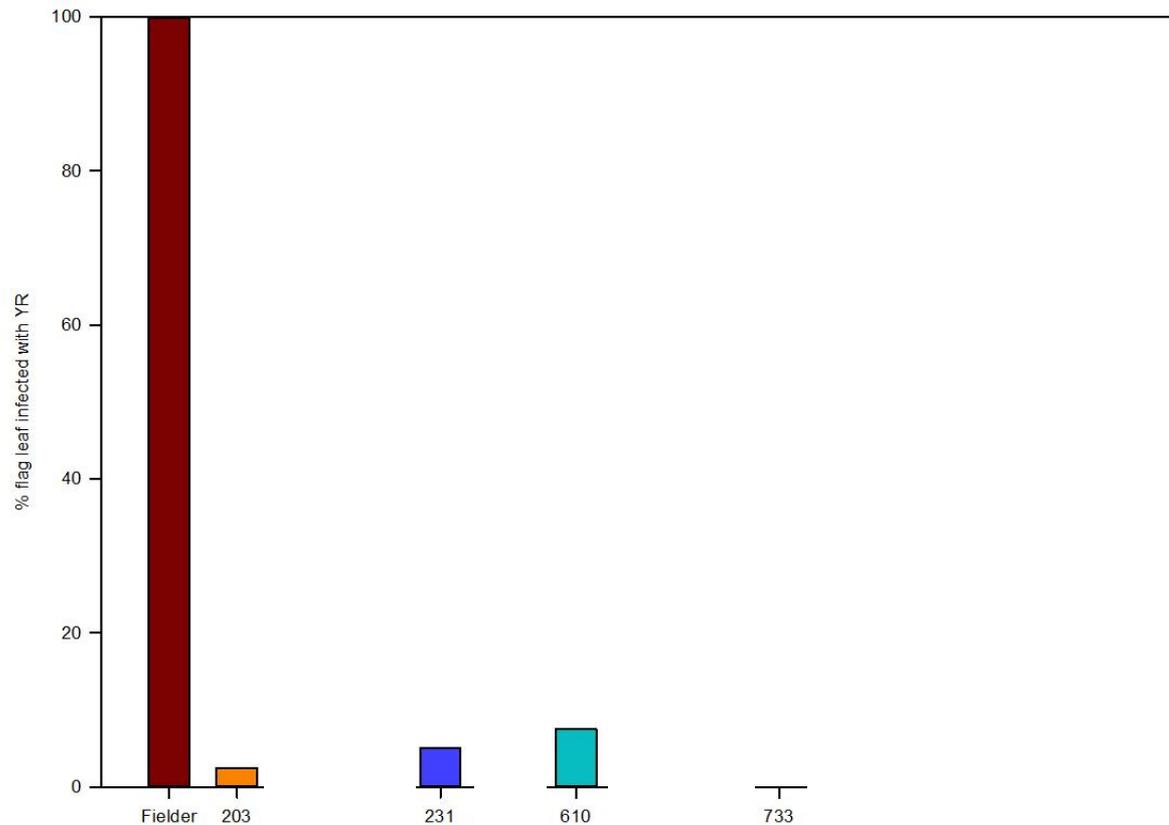
- F₁ grain sown in glasshouse to generate F₂ and for backcrossing to cv. Fielder
- Watkins 786 x Fielder crossing carried out in glasshouse
- F₁ grain included in a spring field trial 2016 to study inheritance

F₁ plants – spring field trial



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- Six F₁ grain from each of the 4 crosses sown
- Two replicate plots of parent genotypes (40 seeds per plot)
- Yellow Rust assessments on 30th June 2016

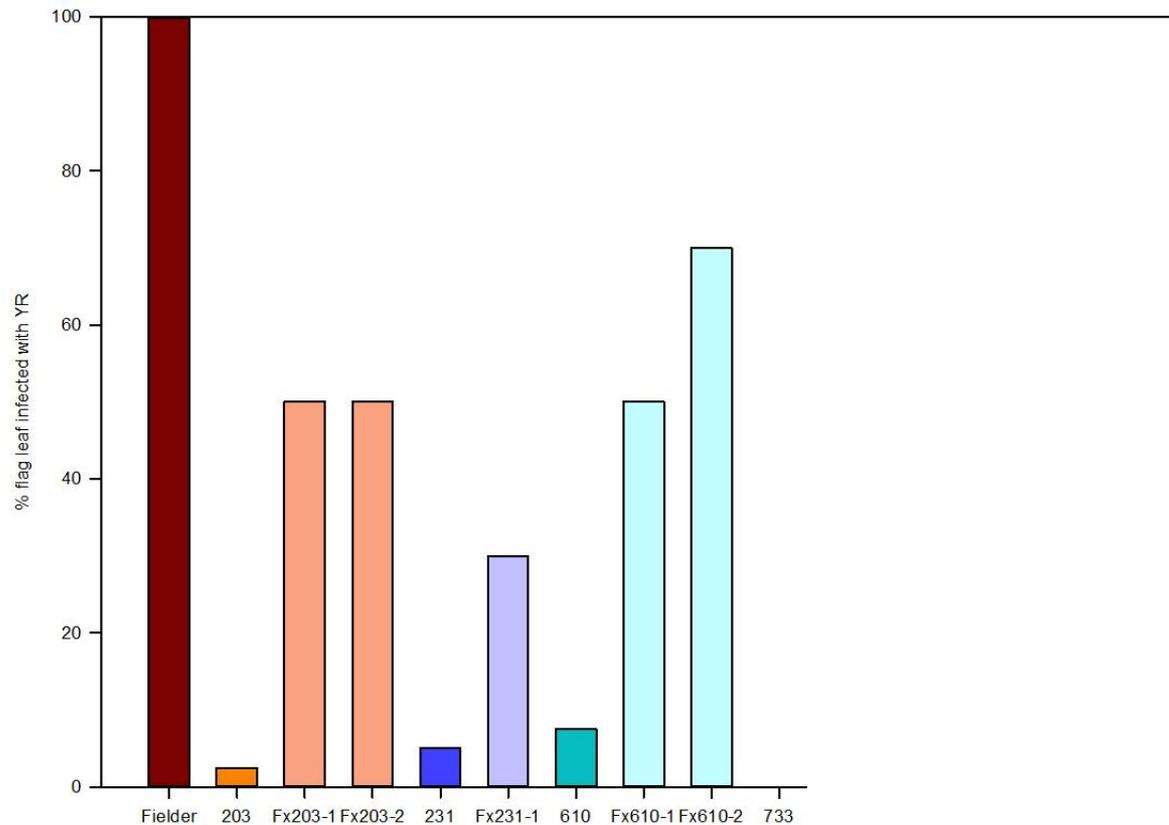


F₁ plants – spring field trial



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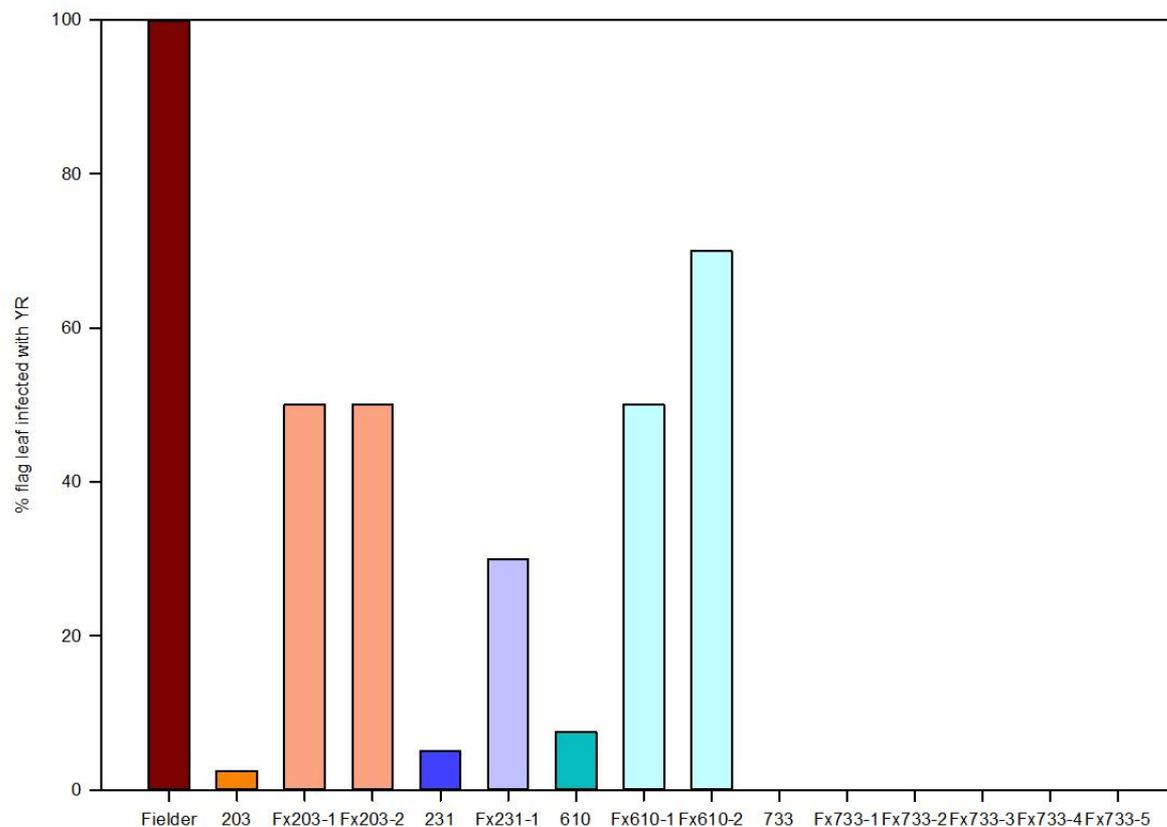


F₁ plants – spring field trial



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- Six F₁ grain from each of the 4 crosses sown
- Two replicate plots of parent genotypes (40 seeds per plot)
- Yellow Rust assessments on 30th June 2016



Summary



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- Five Watkins genotypes with evidence of moderate-high resistance against YR
- Watkins 203 most promising genotype for multi-disease resistance
- Trend towards less foliar disease in 3rd wheat (high take-all) field trial across both seasons – to be tested in controlled environment conditions

On-going work

- Repeat 1st and 3rd wheat multi-disease resistance trials drilled autumn 2016
- *Zymoseptoria* field trial drilled autumn 2016
- F₂ inheritance trial drilled autumn 2016
- Check for known Yr and multi-disease resistance genes
- Seedling race tests

Exploiting *Triticum monococcum* as a novel source of genetic diversity for improvement of hexaploid wheat



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T. monococcum
wheat ear

- The diploid wheat, *T. monococcum* ($A^m A^m$) was widely cultivated during early cereal farming on poorer soils
- After the Bronze Age *T. monococcum* cultivation diminished
- A^m genome not directly involved in the generation of
 - modern durum wheat (tetraploid)
 - common bread wheat (hexaploid)

RRes *Triticum monococcum* collection



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Total number	323 (Vavilov, USDA, IPK)
Country of origin	35
Spring habit	229
Winter habit	86

WGIN phenotyping

- Yellow rust
- Take-all root disease
- Eyespot
- Septoria (Kostya Kanyuka)
- Aphid resistance (Lesley Smart and Gia Aradottir)
- Root penetration (Yaoxiang Ge and Richard Whalley)

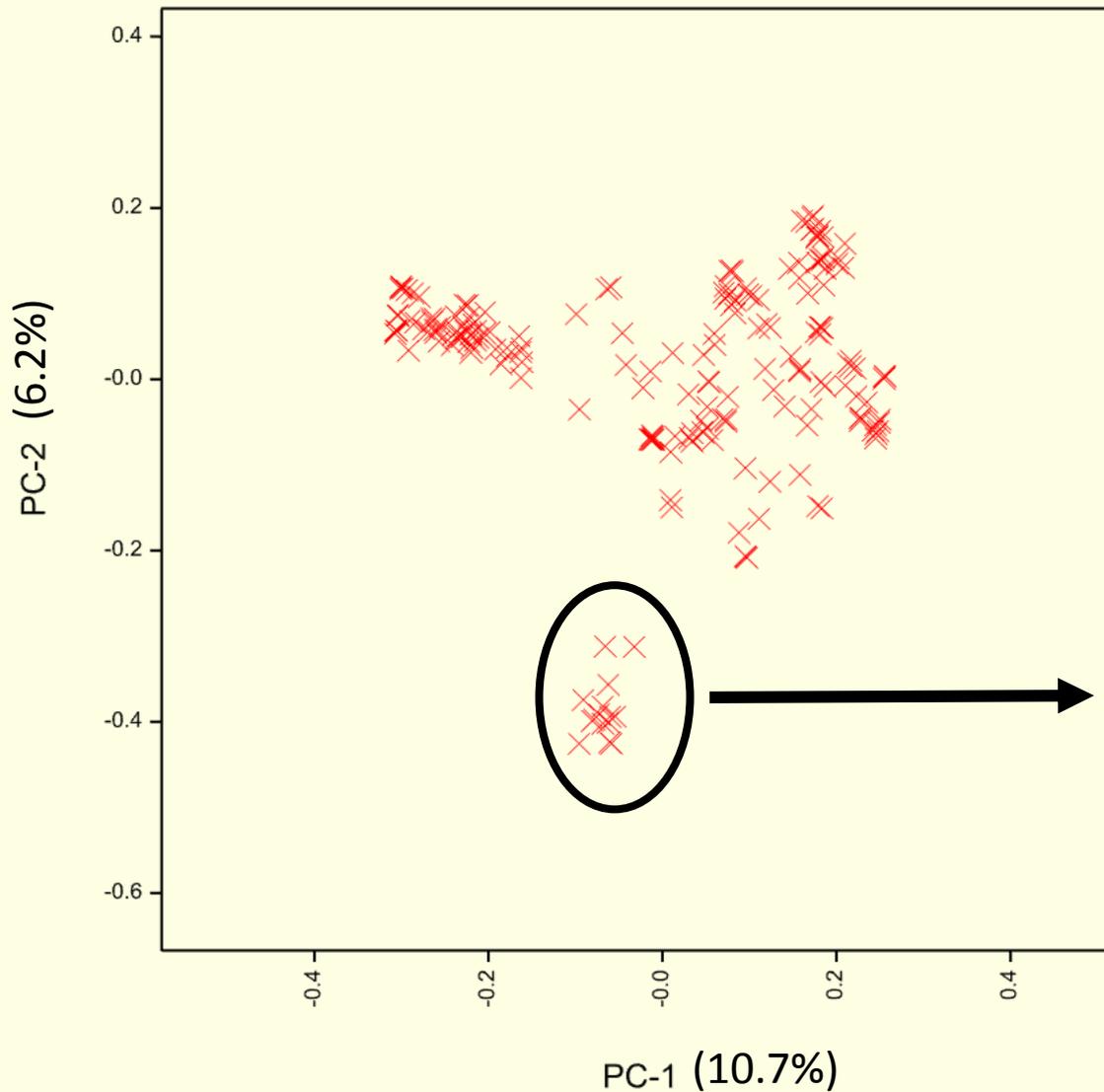
- Recently genotyped 203 viable genotypes using 35K array at Bristol University

Triticum monococcum collection

Principal Coordinates Analysis



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T. boeoticum = wild
einkorn wheat

T. monococcum =
domesticated einkorn
wheat

Hairy leaves, possibly
T. boeoticum
Country of origin = Turkey

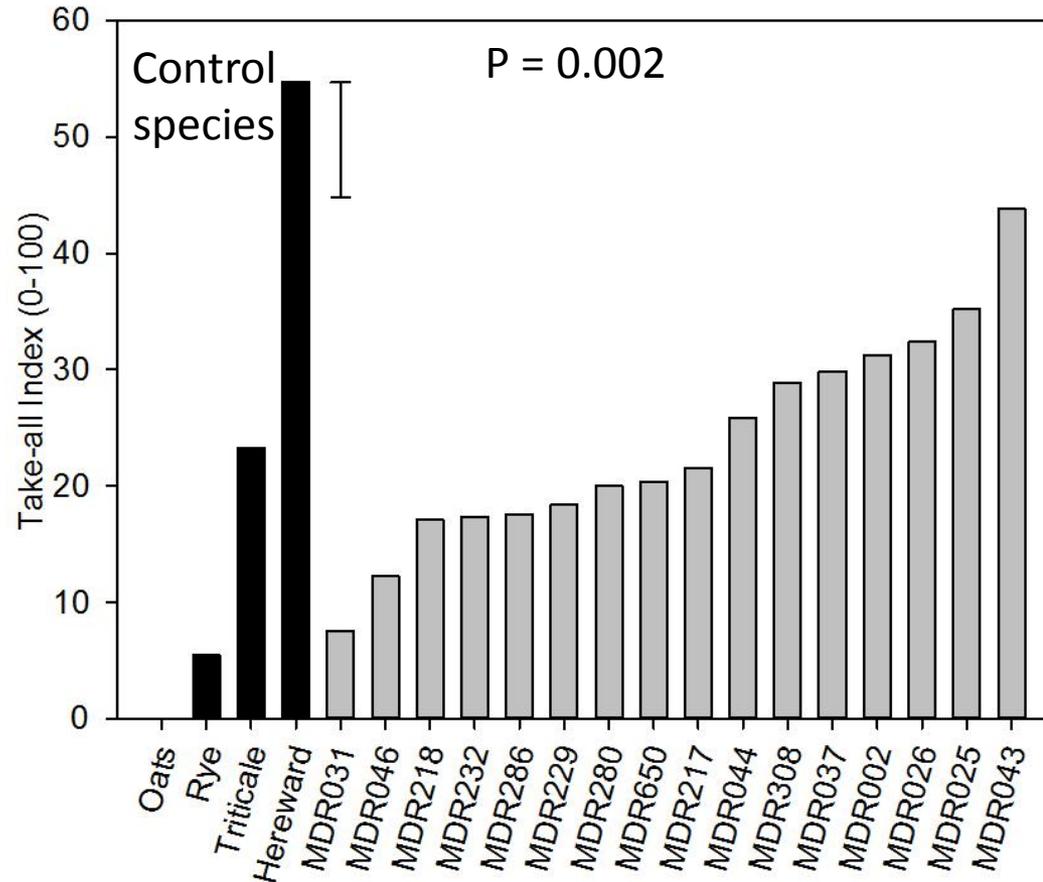
203 *Tm* genotypes, 1026 markers

Take-all root disease - highly resistant genotypes identified within *T. monococcum*



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- 3rd wheat field trials 2006-2011 (WGIN 1 and 2)
- **34 *T. monococcum* genotypes (AA diploid genome)** tested over 5 years



Take-all *Triticum monococcum* mapping populations



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F₂ *Tm* cross progeny numbers:

Parentage		Estimated F ₃ progeny number
MDR031 (R) x MDR043 (vS)	31 ears from 3 plants	450 ←
MDR031 x MDR229	16 ears from 1 plant	320
MDR031 x MDR650	48 ears from 3 plants	900
MDR043 (vS) x MDR031 (R)	48 ears from 3 plants	960
MDR043 (vS) x MDR046 (R)	36 ears from 3 plants	750 ←
MDR229 x MDR031	94 ears from 6 plants	2000

Populations advanced by SSD in 2015/16 from F₄ to F₆ for future field phenotyping ←

Triticum monococcum take-all root resistance MDR031(R) x MDR043 (S) mapping population



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- 516 F₂ seeds → 380 F₆ lines
- 0.5 – 33.5 g of each line available
- **129 lines** > 18 g seed selected for field trial + parents + Hereward control plots
- Plot size 4 rows x 0.6 m length, 80 seeds per plot
- Randomised block design (3-5 reps/genotype)
- **3rd wheat field trial** drilled in Claycroft 6th Oct 2016

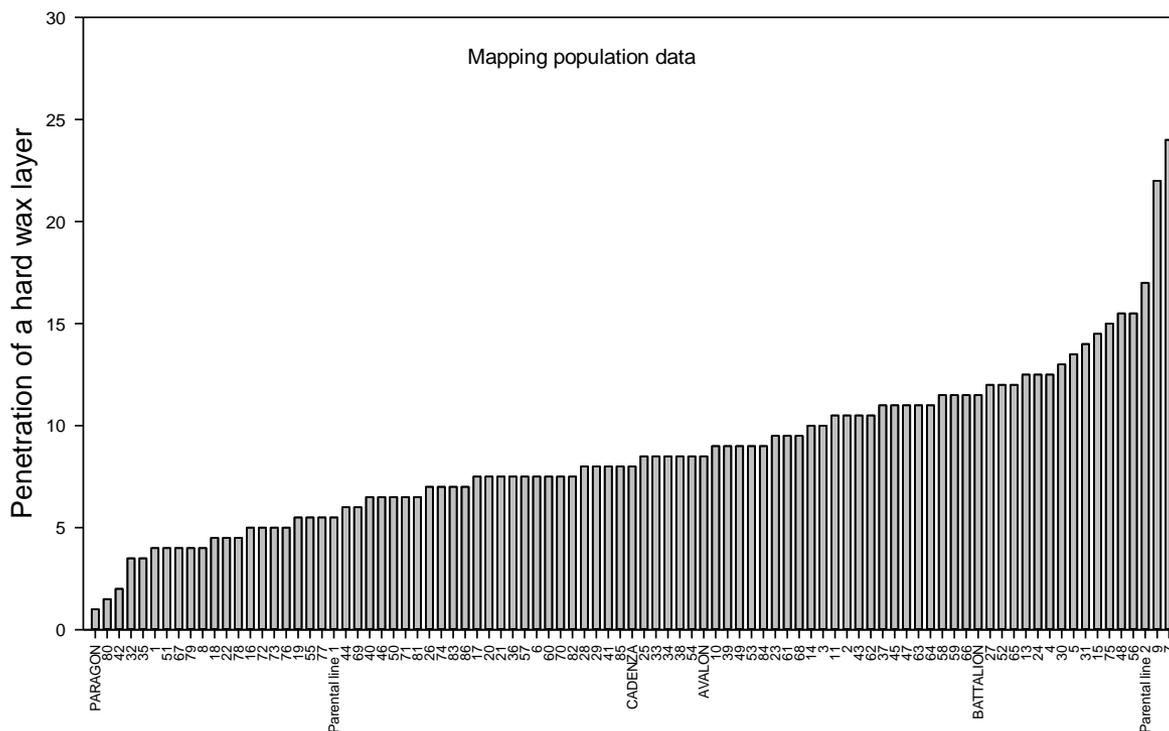


Penetration of strong layers by roots



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MDR037 (poor root penetration) x MDR229 (strong root penetration) mapping population

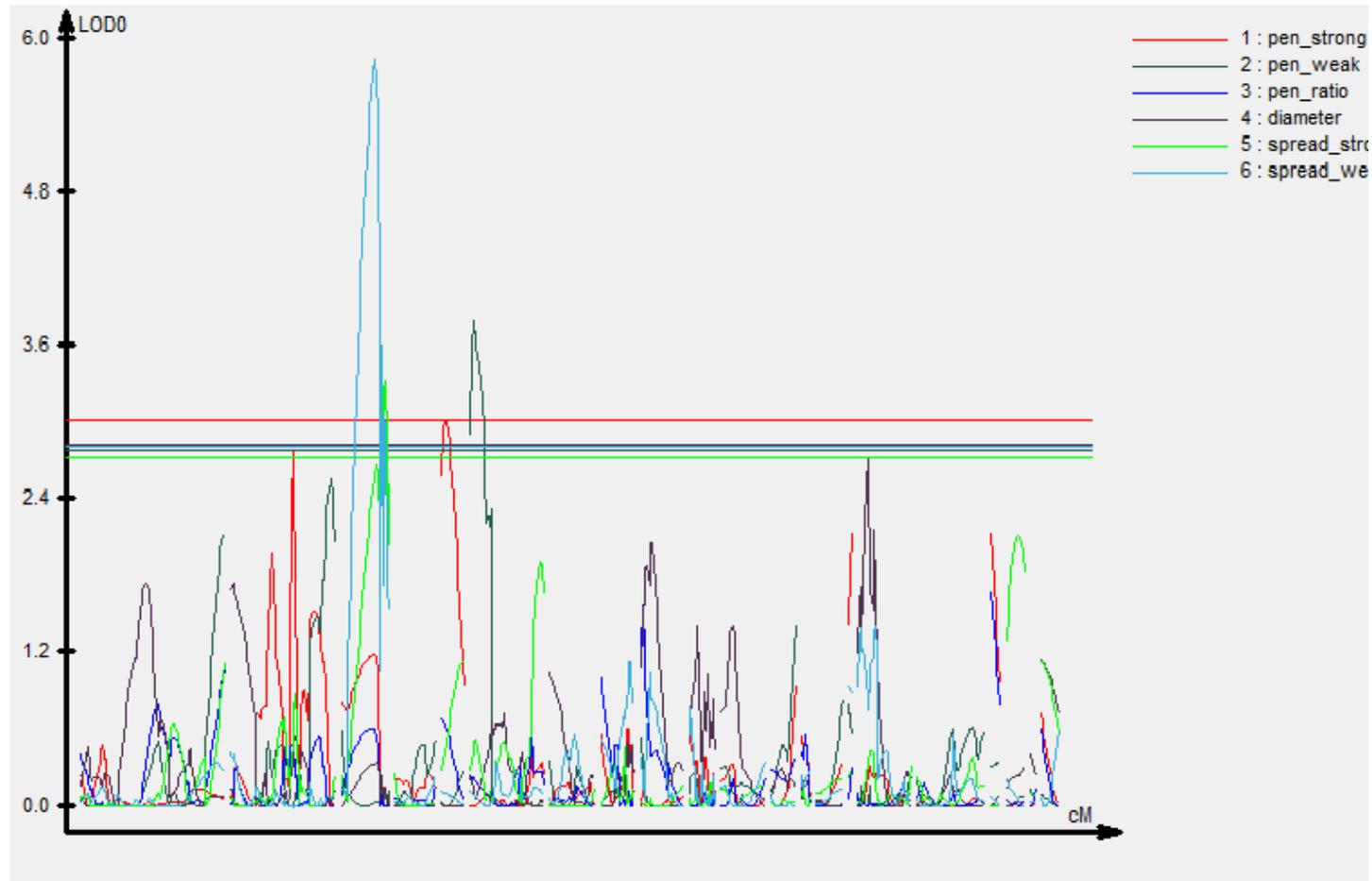


Penetration of strong layers by roots



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MDR037 (poor root penetration) x MDR229 (strong root penetration) mapping population



Summary



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- Novel resistance traits identified within *T. monococcum*
- Preliminary evidence of different groupings based on genotyping of *T. monococcum* collection
- MDR031 (R) x MDR043 (S) F₆ take-all phenotyping trial drilled autumn 2016
- MDR037 (poor penetration) x MDR229 (strong penetration) – root strength – preliminary analyses reveal multiple QTLs
- Strategies for introgression into hexaploid wheat being tested

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T. monococcum source genotypes

MDR 308 (DV92) - *TmStb1* locus mediated resistance to *Zymoseptoria tritici*

MDR 031 - Seedling and adult plant root resistance to the take-all fungus
(*Gaeumannomyces graminis* var. *tritici*)

MDR 049 - Seedling and adult plant resistance to two aphid species

- o Bird cherry-oat aphid *Rhopalosiphum padi*
- o Grain aphid *Sitobion avenae*

Towards introgressing *TmStb1* into bread wheat



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Current strategy (so far not very successful)

cross *T. monococcum* (*Tm*) to *T. aestivum* cv. Paragon *ph-1*
embryo rescue in F₁
backcross the hybrid to *T. aestivum* cv. Paragon

Trying two alternative strategies

Strategy #1

colchicin treat *Tm* to produce autotetraploid
cross *Tm* autotetraploid directly to wild-type hexaploid and
durum wheat

Strategy #2

use tetraploid durum wheat as a bridging species
cross *Tm* with durum wheat
backcross this hybrid to hexaploid wheat