

# MAGIC wheat in the UK: not just for mapping

Agricultural context

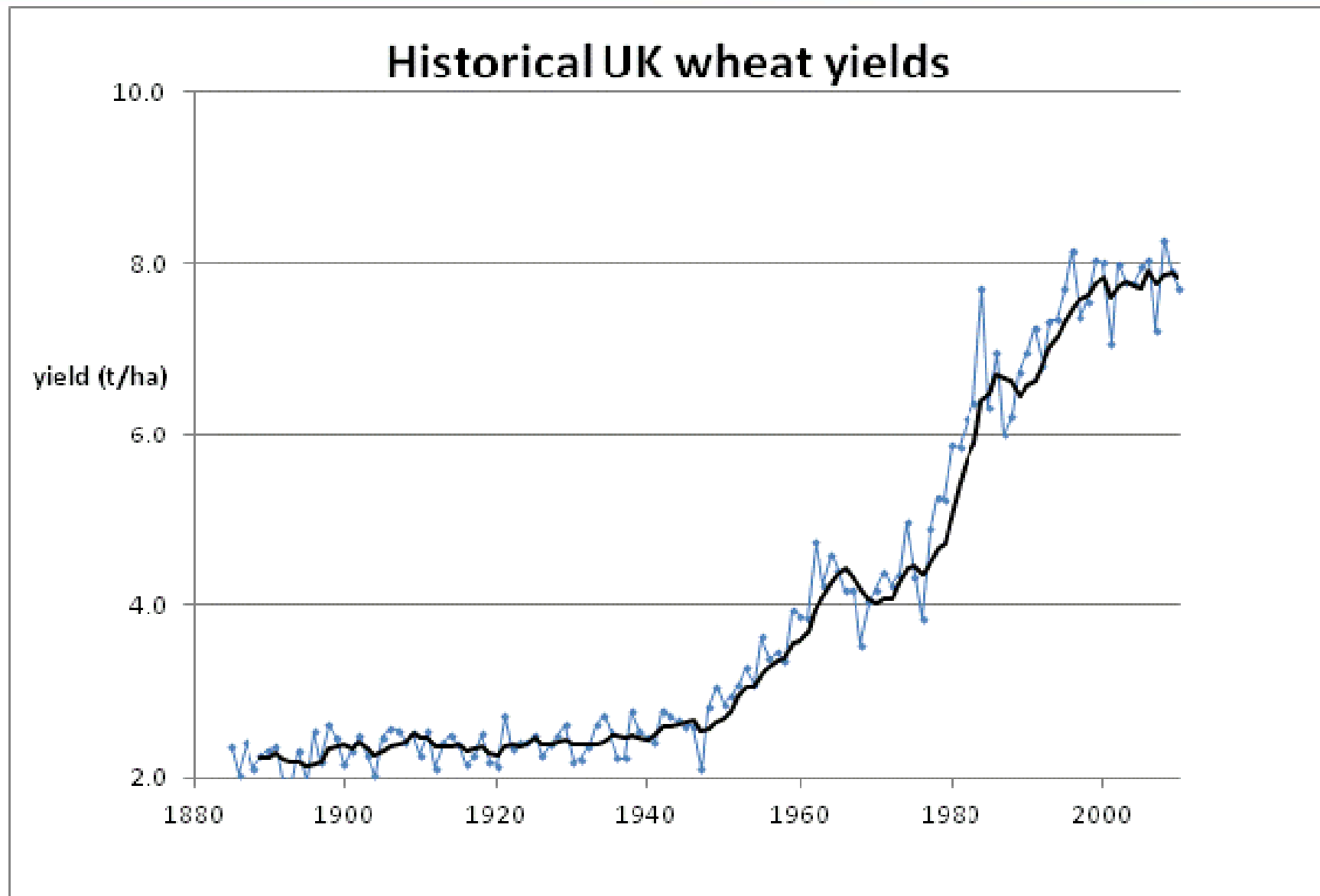
Construction

Derivation of inbred lines

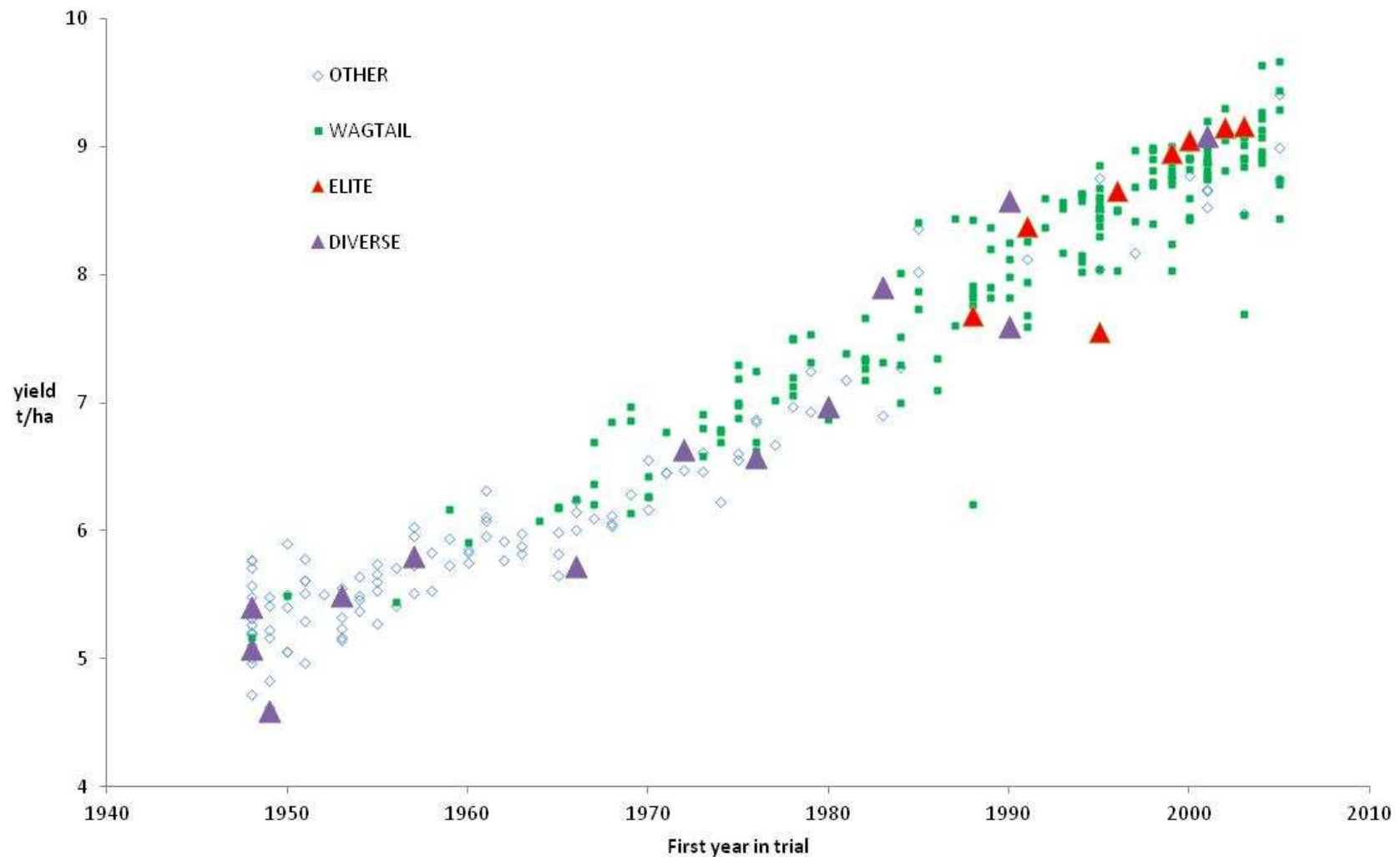
Genetic diversity and LD

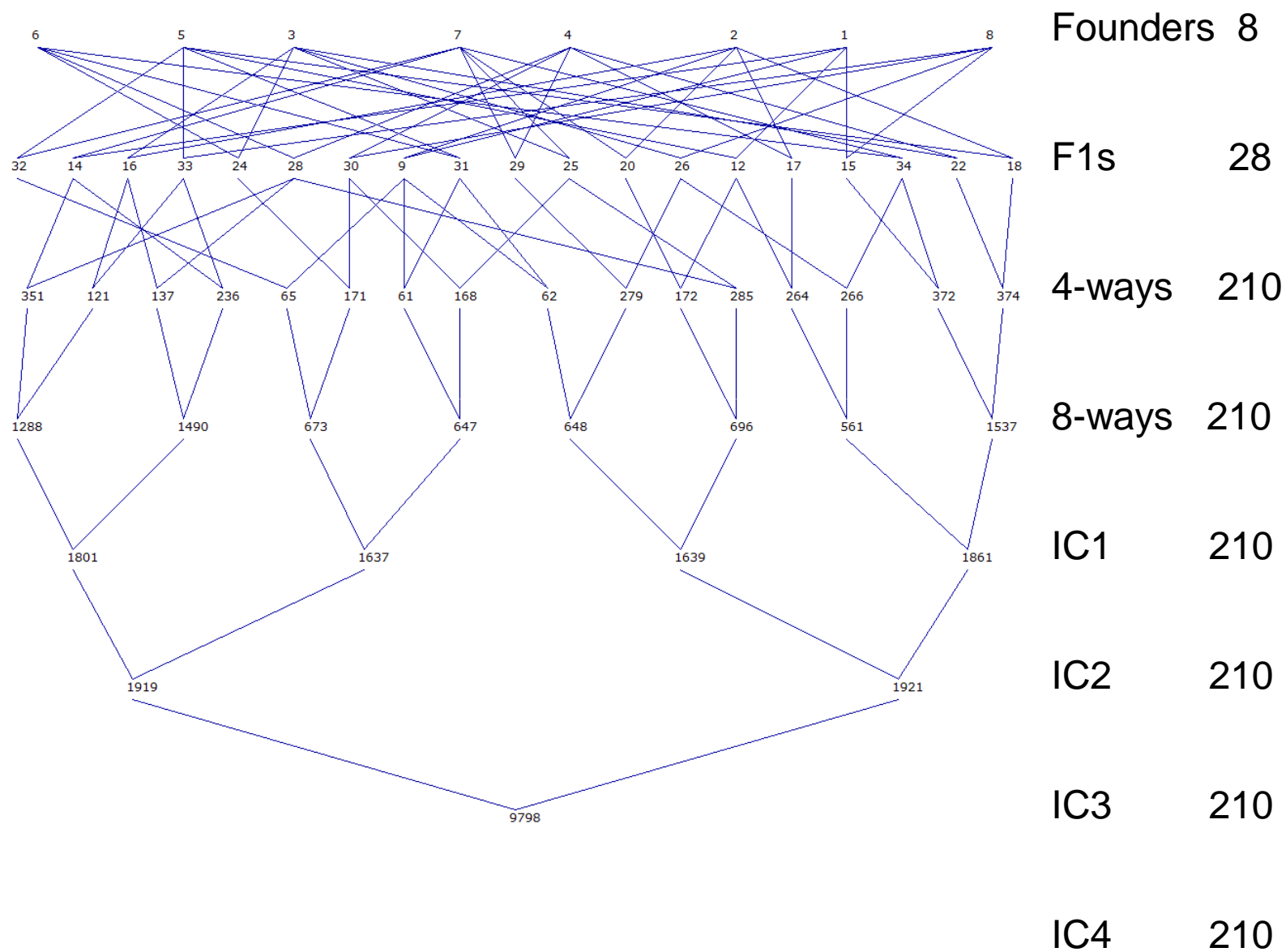
Novel phenotypic variation

Selection and breeding



WAGTAIL and MAGIC: yield and year of introduction





# Production of inbred lines by RABID

Doubled haploids                      too expensive

Bulk breeding                          uncontrolled relationships

Single seed descent                  current best

Rabid Bulk Inbreeding (RABID)

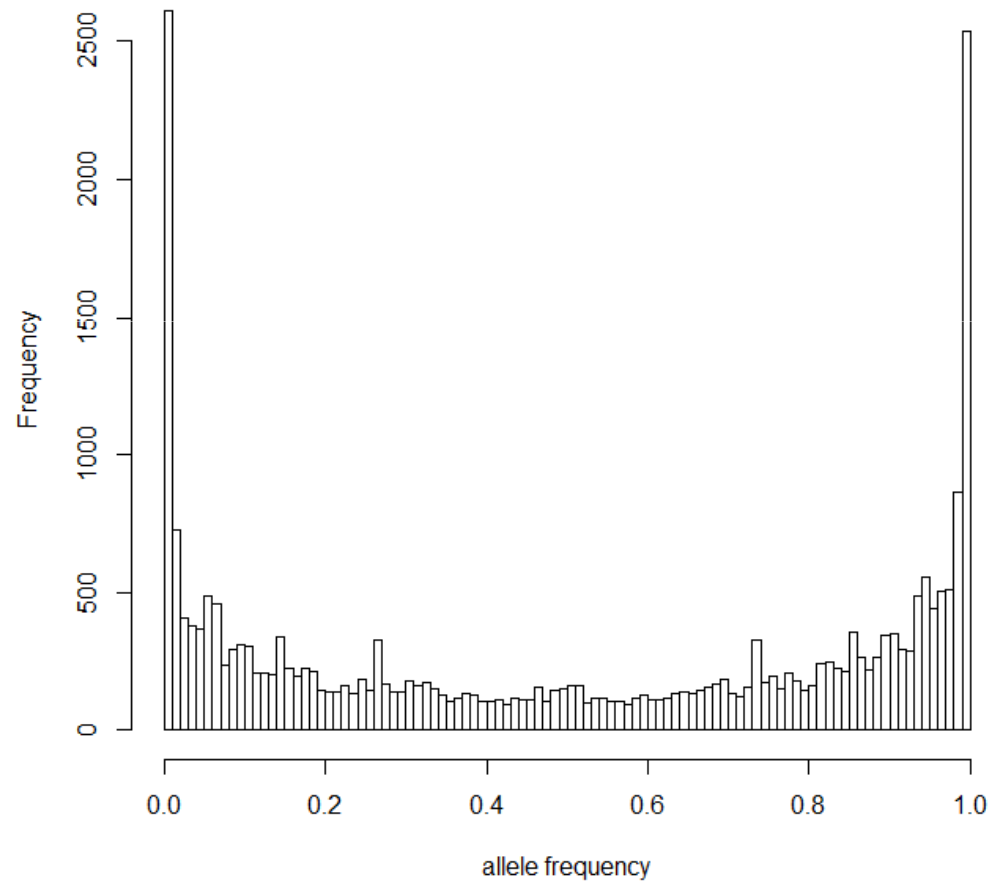
bulk breeding + markers  
as quick as SSD  
can automate

Is being used for second cycle inbreds

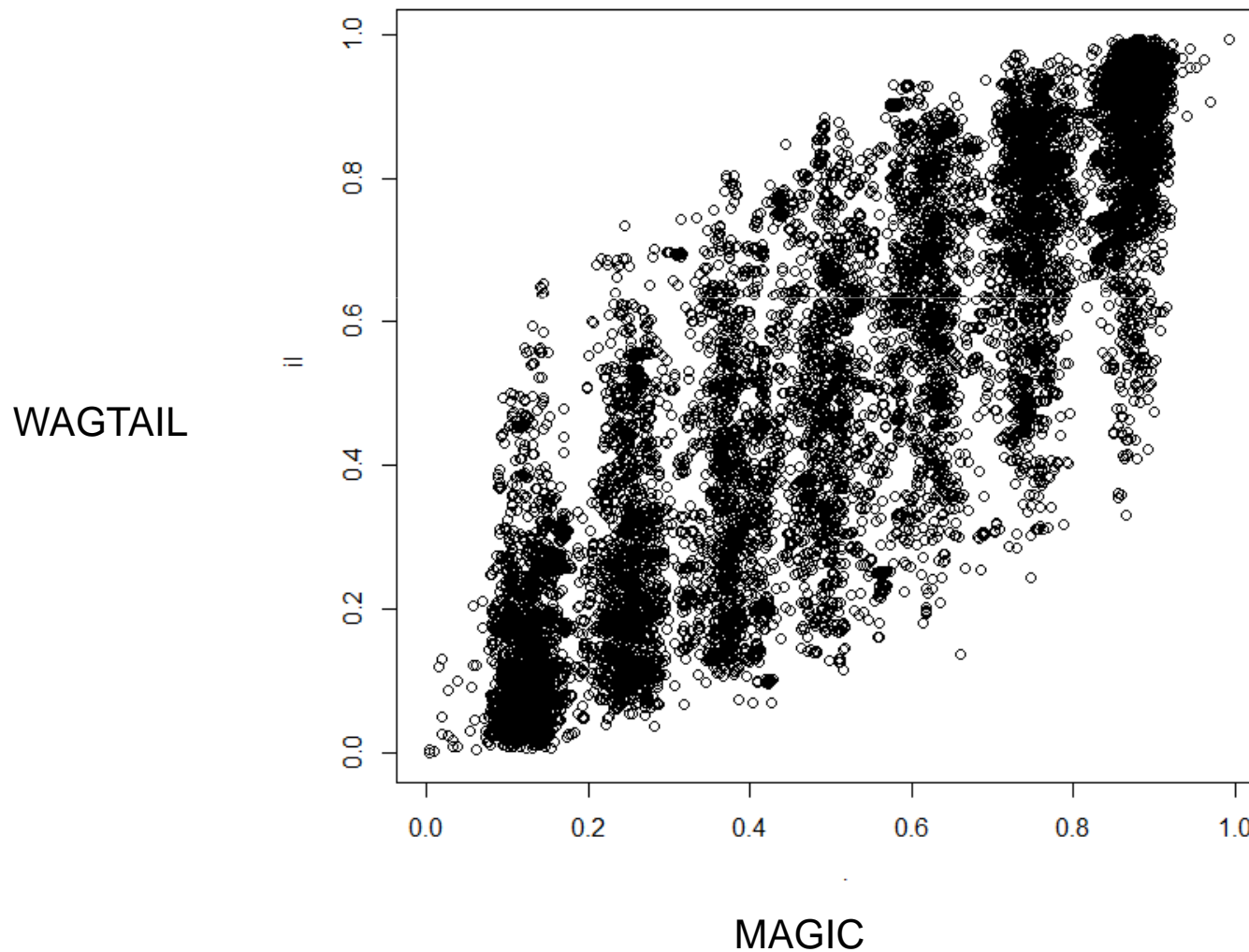
See poster.

## 26512 markers segregating in WAGTAIL

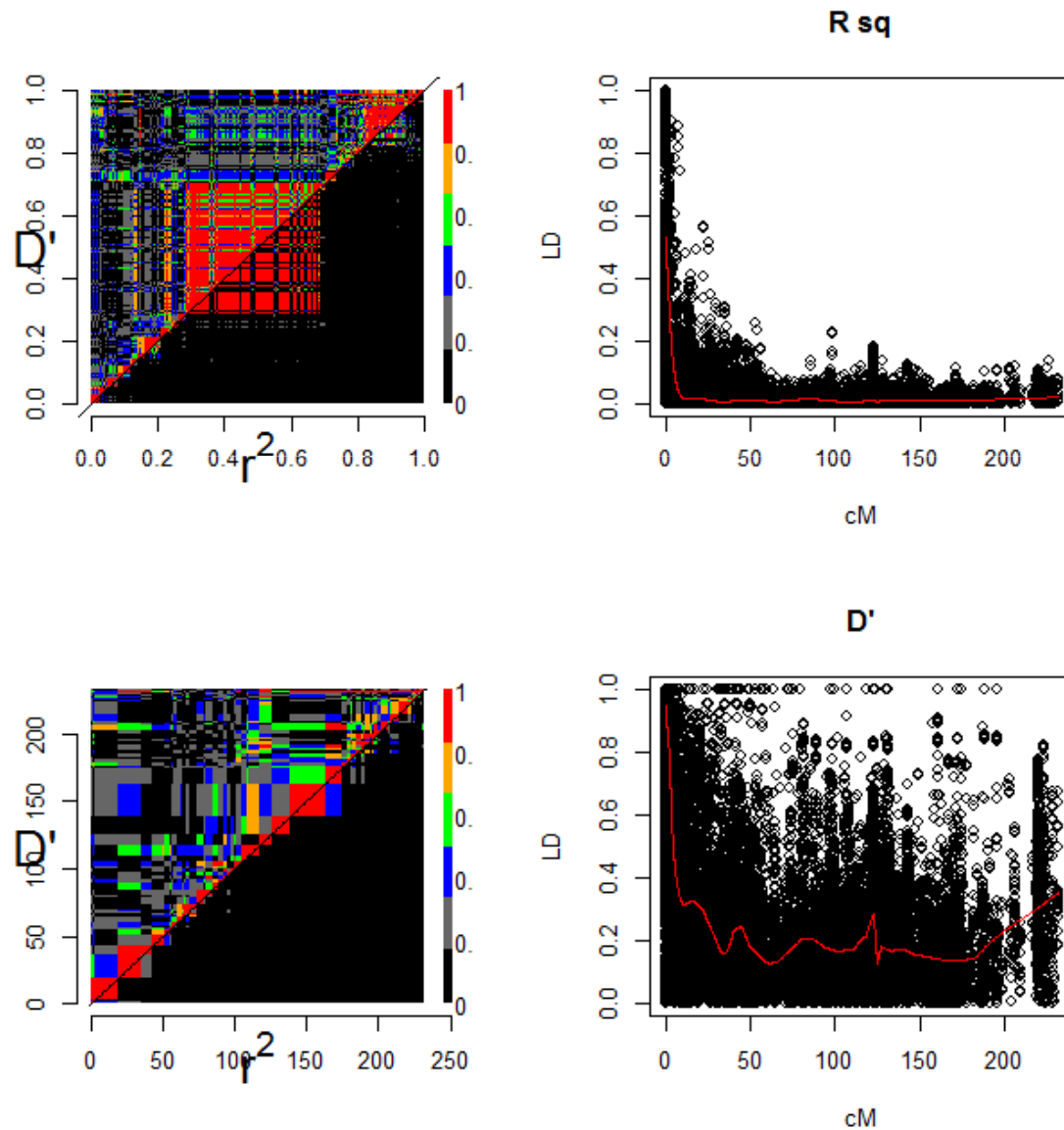
allele freq 26512 SNPs



## 15968 markers segregating in MAGIC

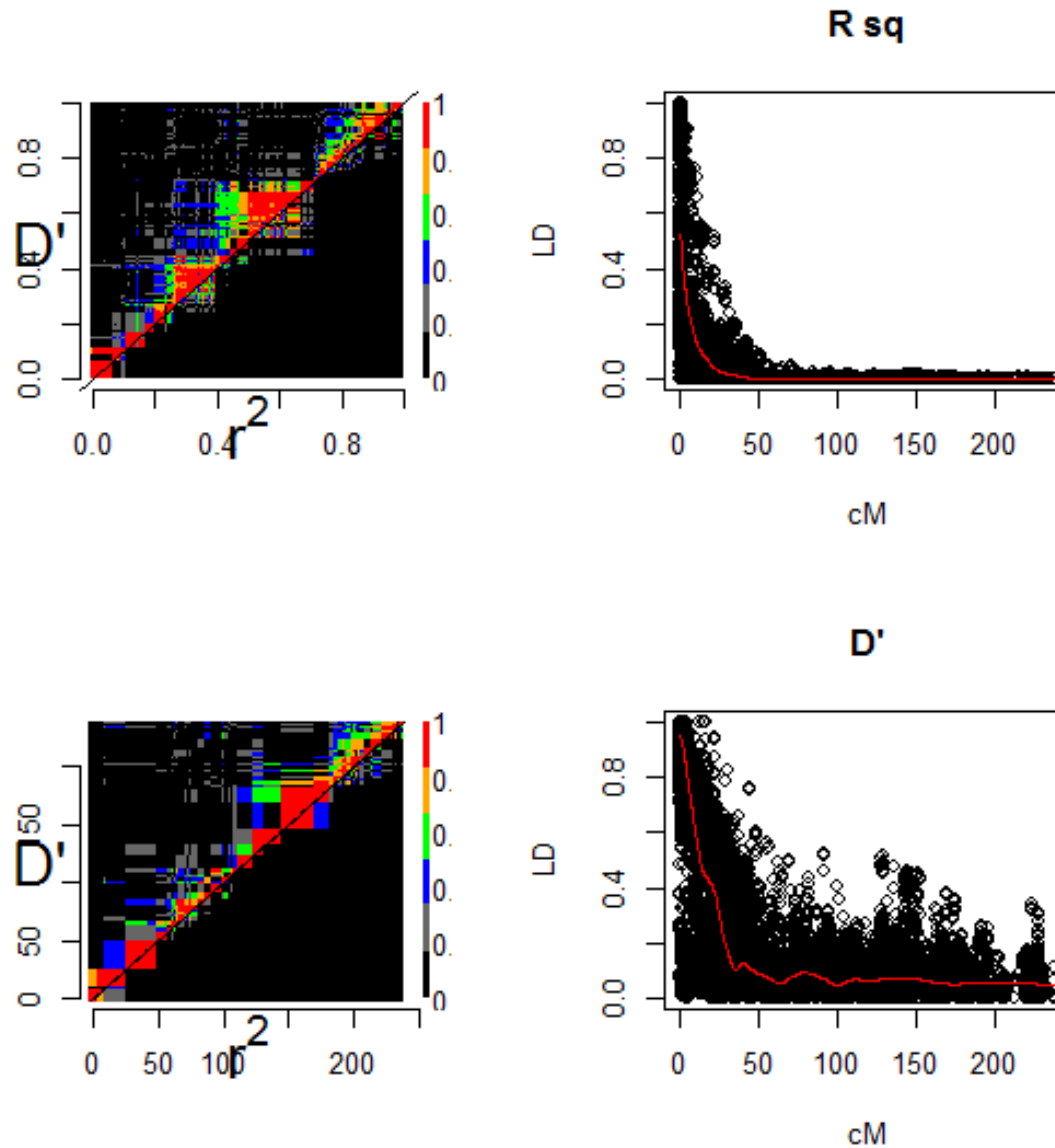


## WAGTAIL LD pattern: 2A





## MAGIC LD pattern: 2A





22<sup>nd</sup> August 2011

## New wheat yellow rust race confirmed

Mike Abram

Monday 22 August 2011 16:00



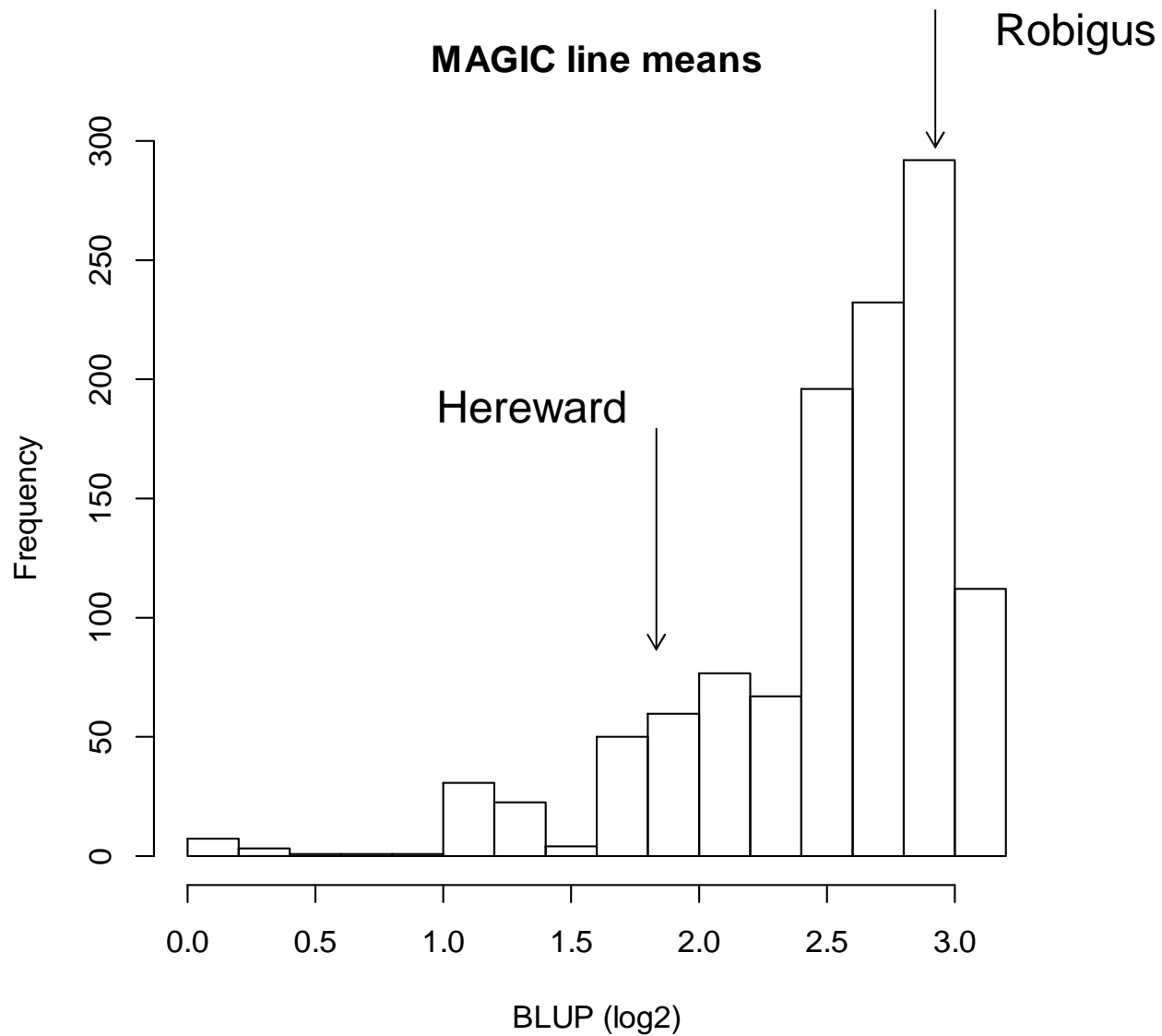
**A new race of yellow rust in winter wheat has been confirmed by the UK Cereal Pathogen Virulence Survey (UKCPVS).**

Yellow rust samples collected from three farm crops of Warrior winter wheat earlier this summer have re-infected the variety in the first round of testing by NIAB TAG.

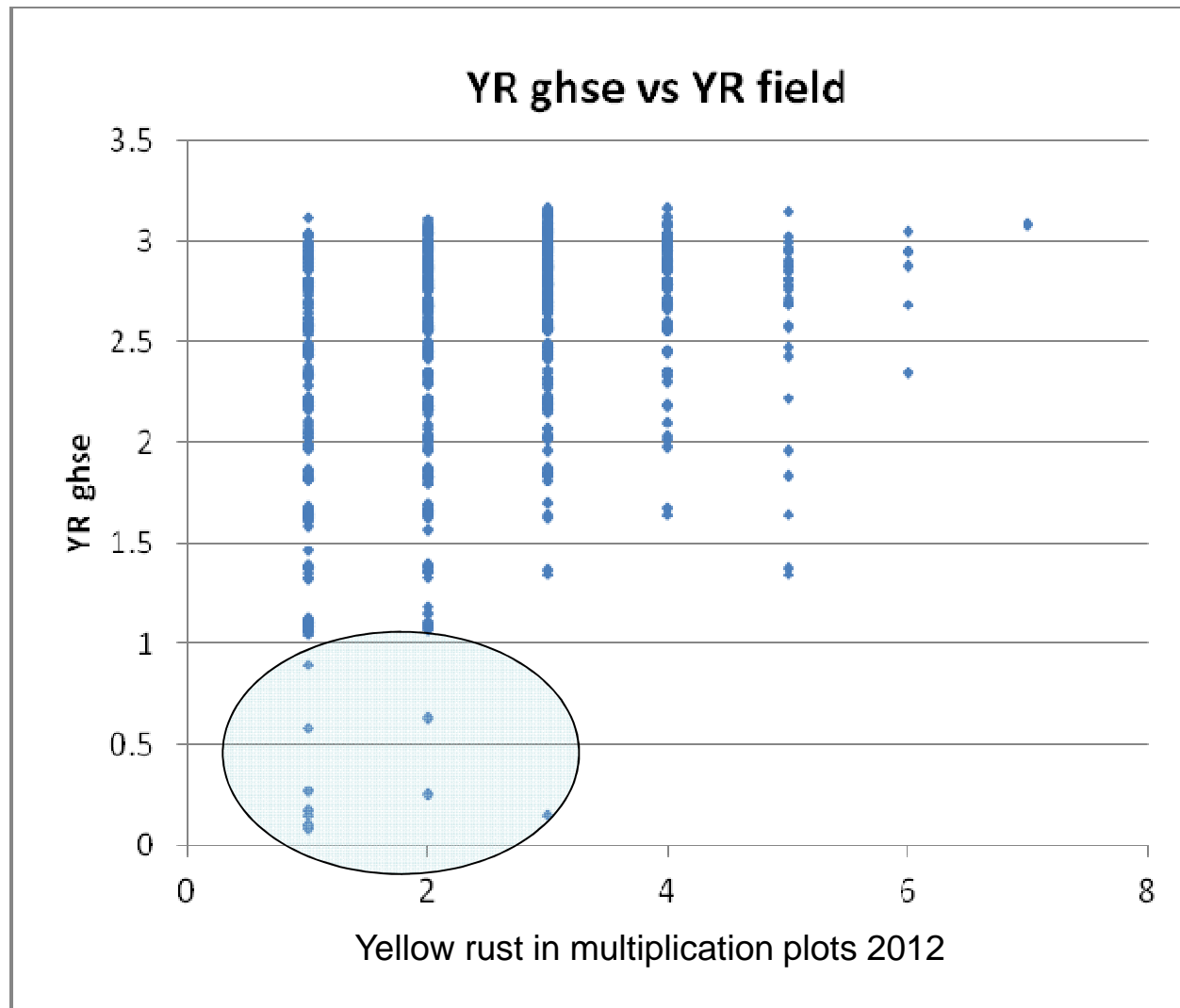


"Warrior had been previously resistant to all yellow rust disease isolates at seedling and adult plant stages. The new isolates have been shown to infect the seedlings of the variety, which is evidence that we are dealing with a new race," explains Rosemary Bayles, principal cereal pathologist at NIAB

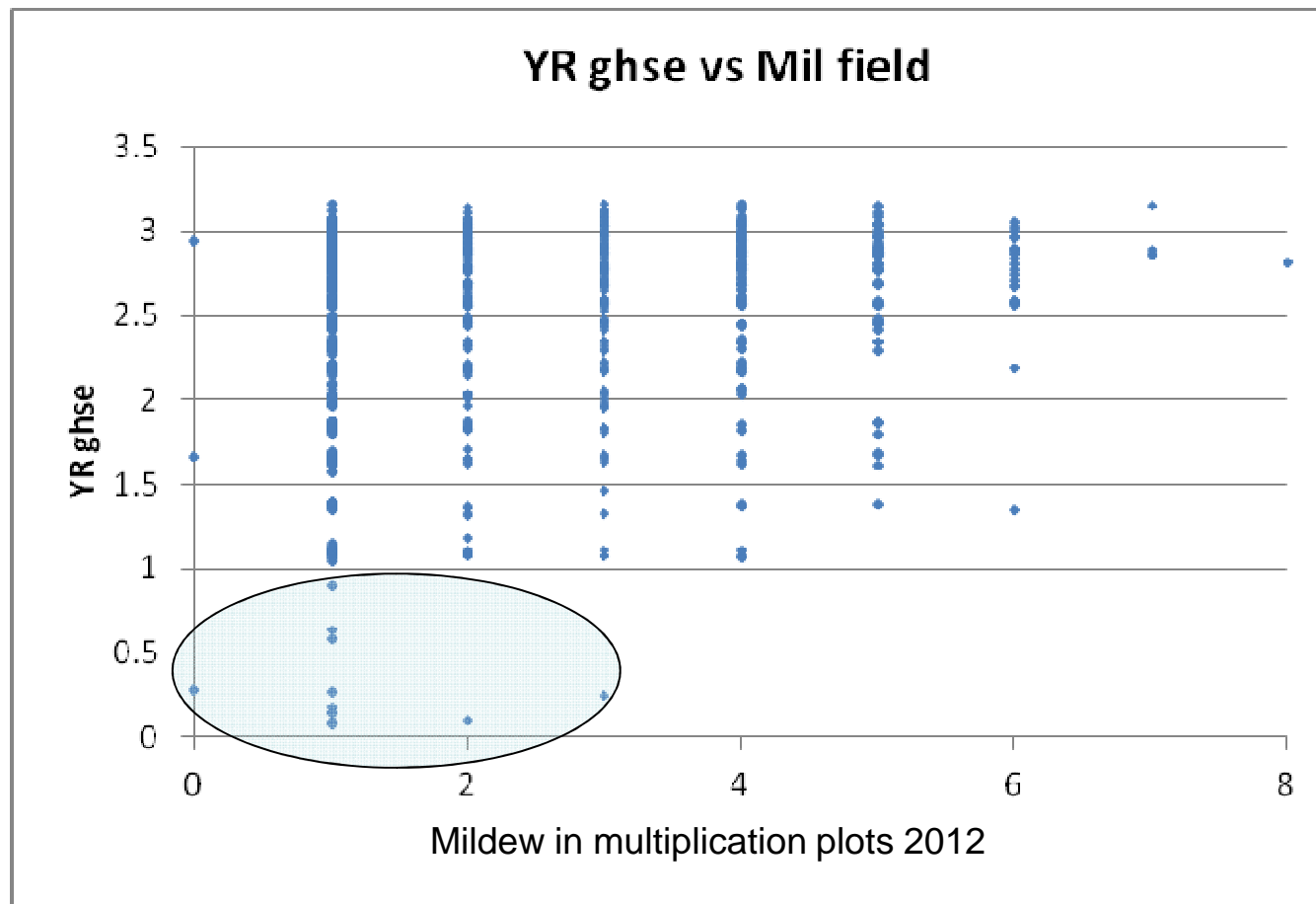
## Distribution of disease scores



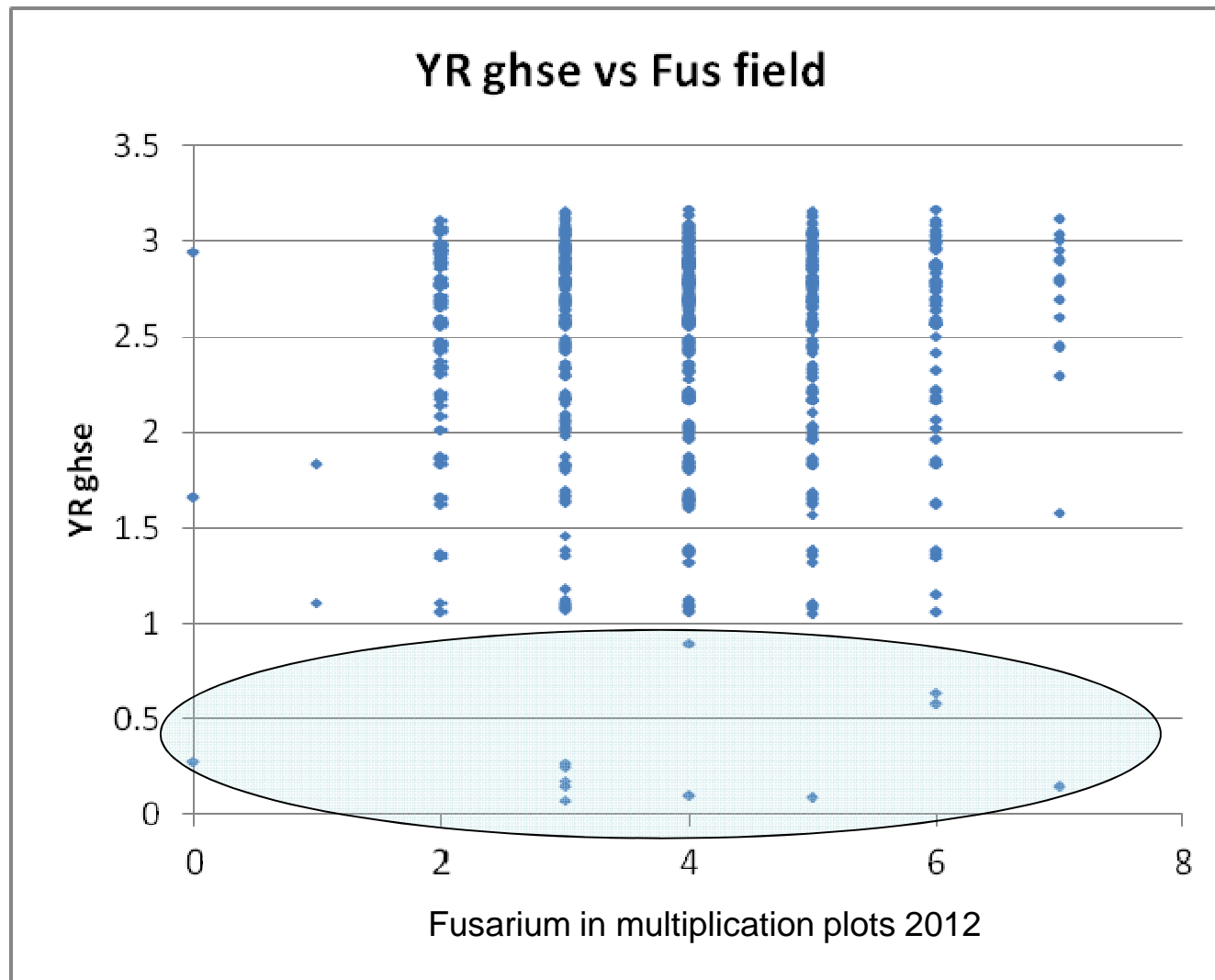
## Correlations with 2012 multiplication plots: yellow rust



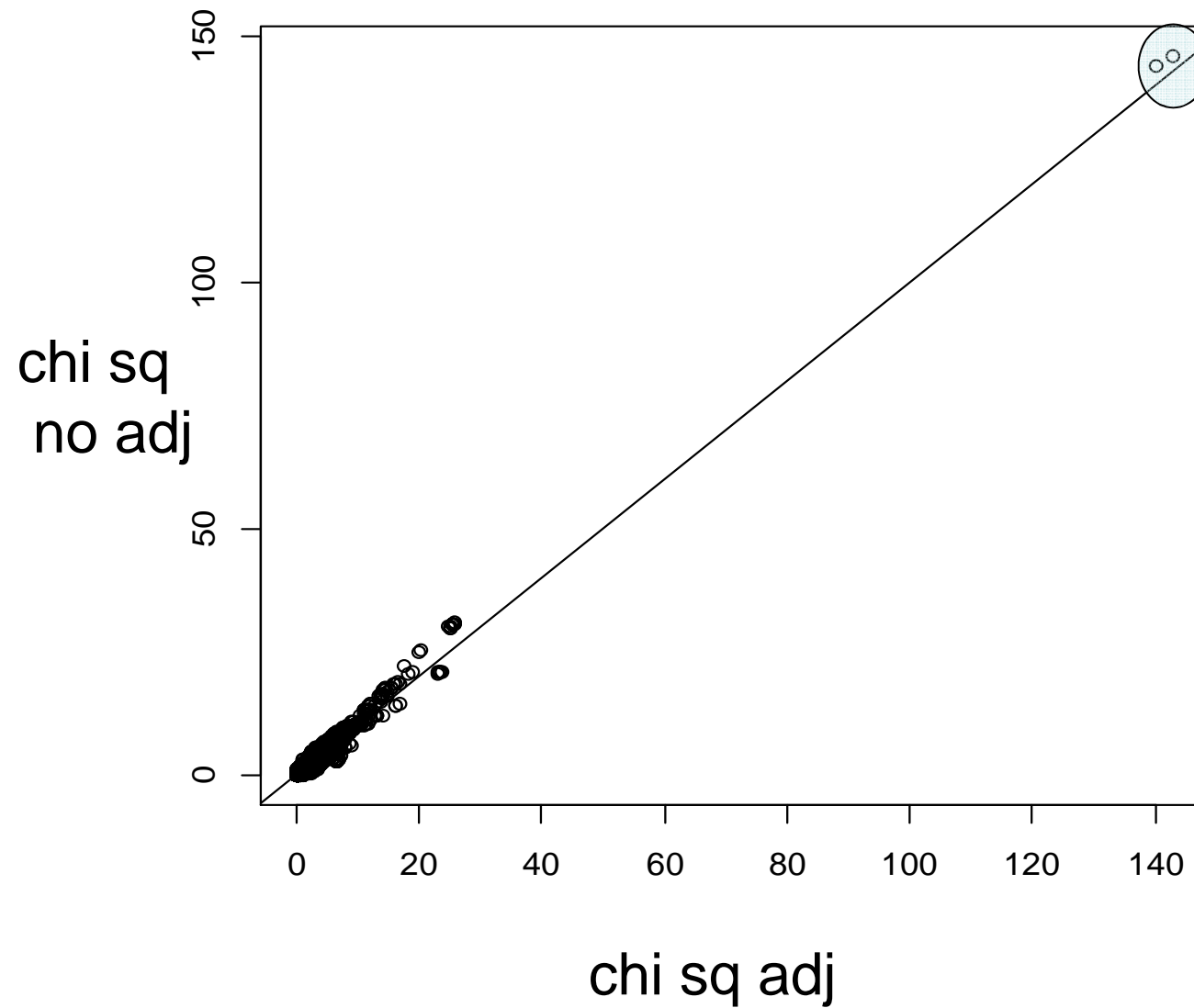
## Correlations with 2012 multiplication plots: mildew



## Correlations with 2012 field scores: fusarium



### Scan for YR seedling resistance





## 2012 yield trial: state of the art phenomics

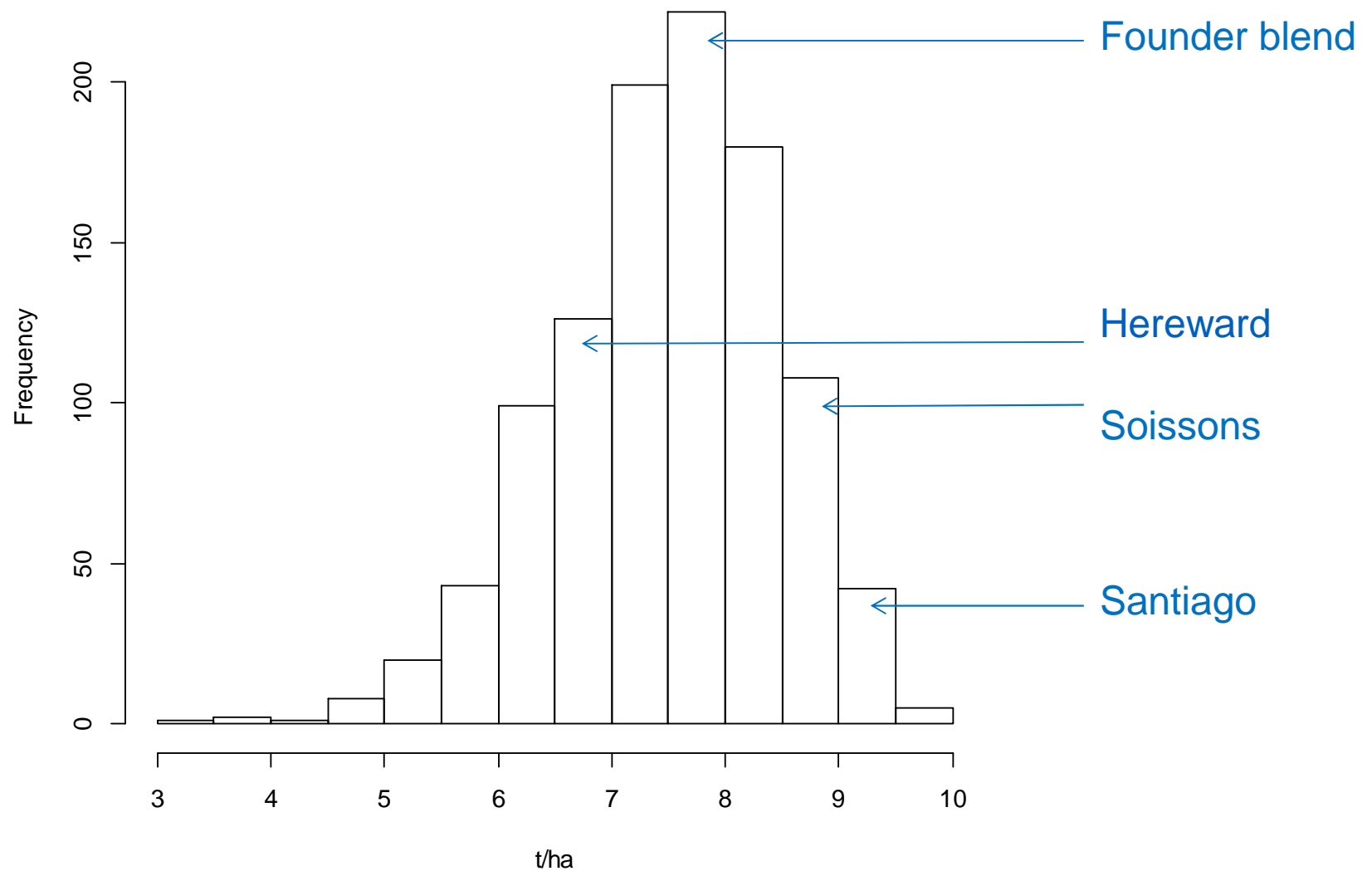
1068 entries, 2156 plots, 2.6 ha (65 cricket squares)

High throughput phenotyping with two genome wide yield-potential assessment instruments.





## Distribution of line means for yield



## Breeders: how good are they?

### Breeder's selections made on 2011 multiplication plots

Mean of population	7.45	t/ha
Mean of lines tagged in 2011	7.81	t/ha
Proportion of lines tagged	0.09	
Realised heritability	0.35	
Heritability per plot in 2012	0.67	

# Sublime



MEL 172-4



# Ridiculous



MEL 133-2  
chlorotic



MEL 005-3  
wheat on the cob



MEL 054-1  
OWBM queuing up

## Genomic prediction

Cross validation correlations with WAGTAIL and MAGIC

Ridge regression

Trait	FT	HT	FHB	FHB.adj	Av
all data	0.38	0.31	0.32	0.29	0.3
M → M	0.20	0.20	0.18	0.19	0.2
W → W	0.59	0.59	0.54	0.42	0.5
M → W	0.09	-0.01	0.00	-0.02	0.0
W → M	0.06	-0.01	0.02	-0.02	0.0

## Genomic prediction

Cross validation correlations with WAGTAIL and MAGIC

LASSO

Trait	FT	HT	FHB	FHB.adj	Av
all data	0.39	0.52	0.38	0.48	0.4
M $\rightarrow$ M	0.31	0.56	0.32	0.50	0.4
W $\rightarrow$ W	0.46	0.56	0.53	0.32	0.5
M $\rightarrow$ W	0.16	0.25	0.22	0.21	0.2
W $\rightarrow$ M	0.08	0.01	0.02	-0.03	0.0

## Next steps

Publish.

Release data and seed.

Get more phenotypes.

Test recombinant Spring lines.

Test for bread-making quality.

Start work on the other generations and populations.

WAGTAIL - MAGIC as mutual validation sets in GWAS

# MAGIC wheat in the UK: not just for mapping

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