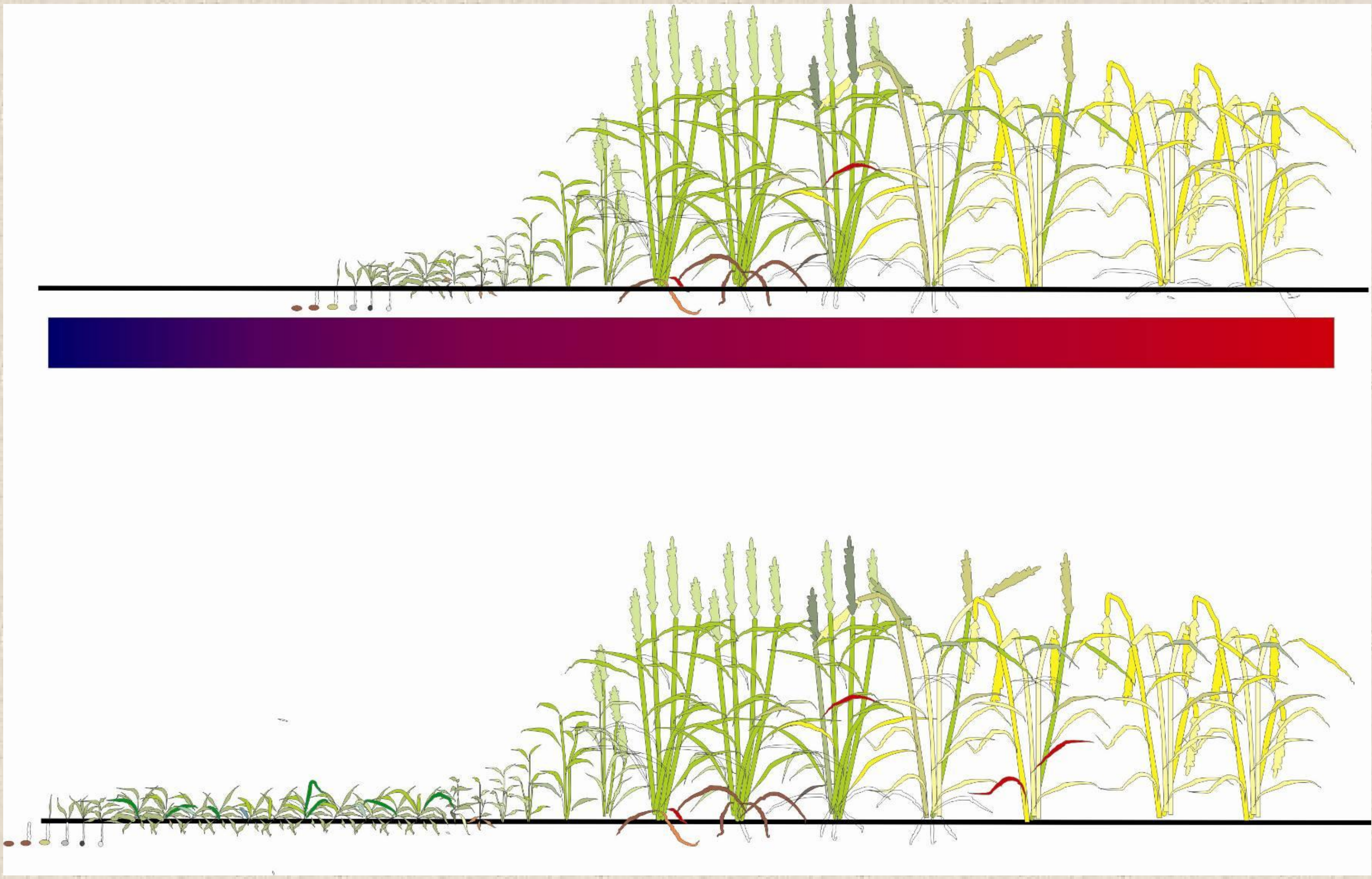
WGIN2 JIC Update
KWS 16th February 2011
Simon Griffiths

Development of Near Isogenic Lines

Fitting wheat to it's environment

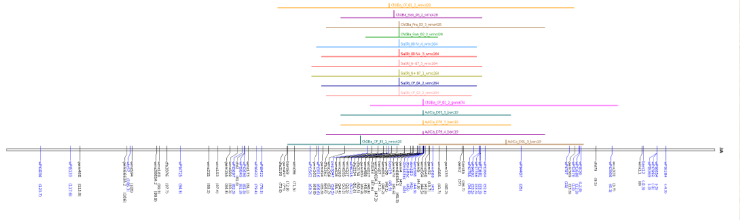
The genetic fine tuning of adaptation for high yield and efficient nutrient use

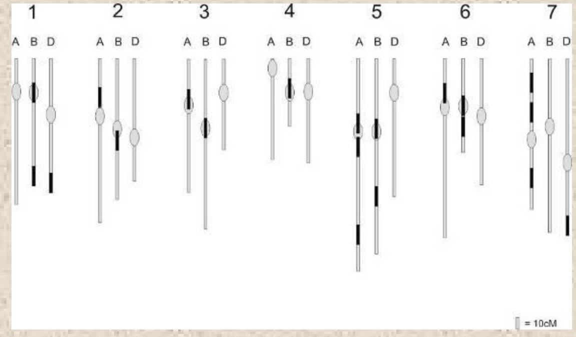


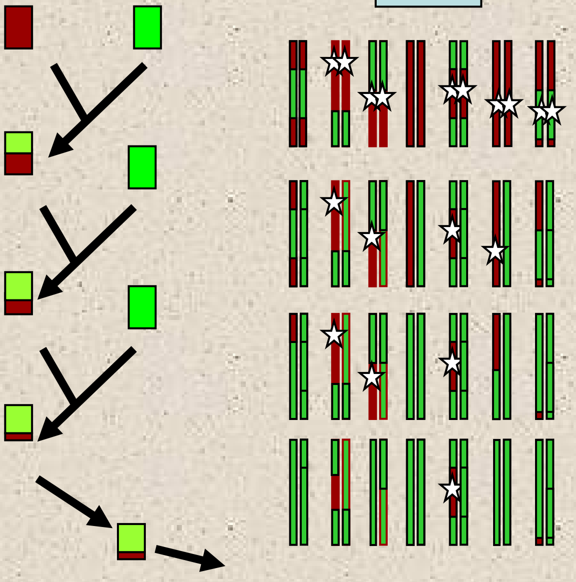
Dissection of genetic gain in UK winter wheat

- Spark x Rialto
- Avalon x Cadenza
- Buster x Charger
- Charger x Badger
- Savannah x Rialto
- Shango x Shamrock
- Malacca x Charger
- Savannah x Renesansa
- Lynx x Cadenza
- Beaver x Soissons
- Weebil x Bacanora
- Milan x Catbird

Clone genes and breed better wheat







Rht8 NIL in Paragon

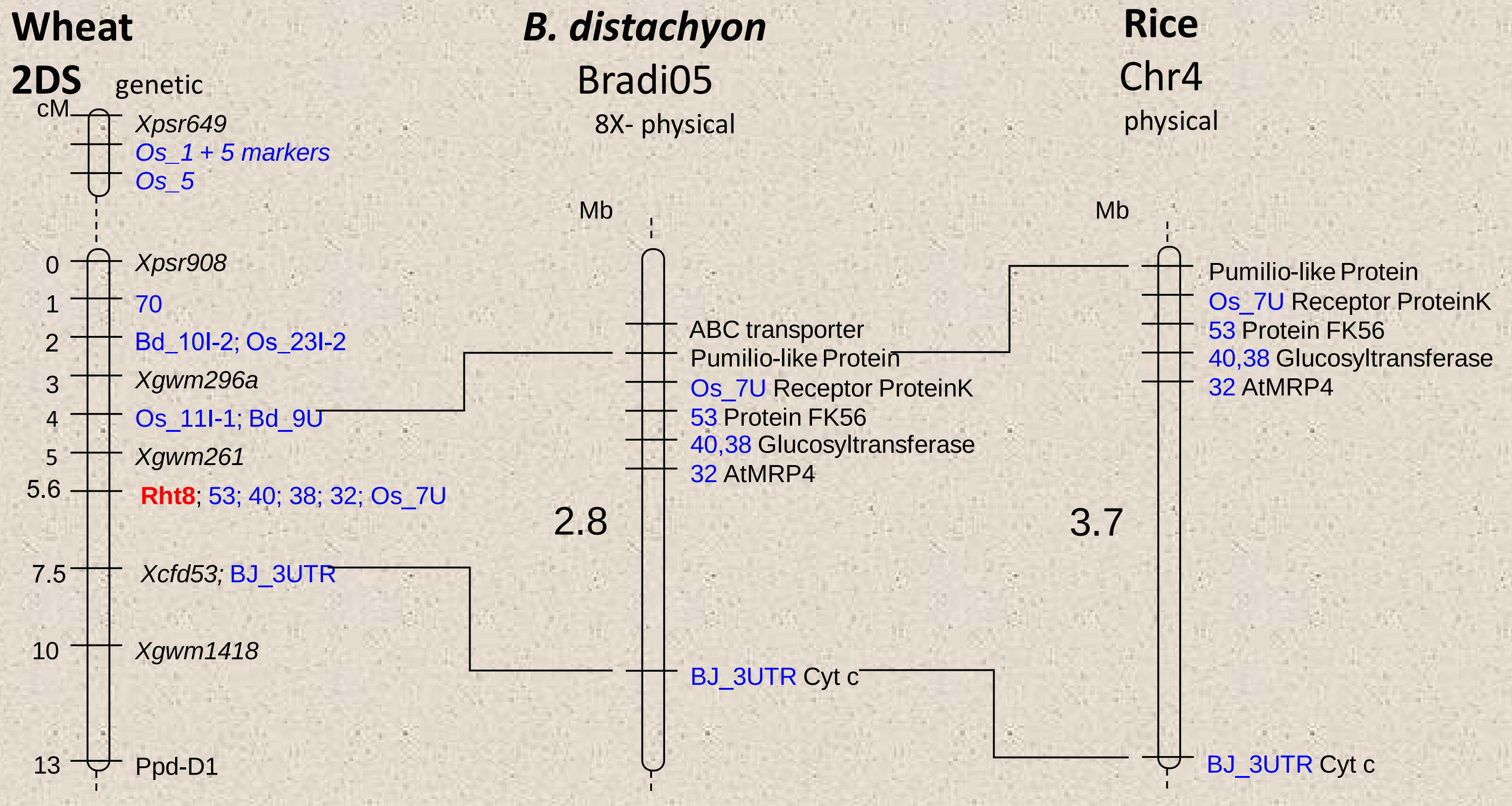
Rht8 BC_3

Paragon

Fine mapping *Rht8* on 2DS

Progress to date:

370 new Gene based markers allowed anchoring the syntenic region in model organisms



Wheat

2DS genetic

cM

Xpsr649

Os_1 + 5 markers

Os_5

0 *Xpsr908*

1 70

2 Bd_10I-2; Os_23I-2

3 *Xgwm296a*

4 Os_11I-1; Bd_9U

5 *Xgwm261*

5.6 **Rht8**; 53; 40; 38; 32; Os_7U

7.5 *Xcfd53;* BJ_3UTR

10 *Xgwm1418*

13 Ppd-D1

B. distachyon

Bradi05

8X- physical

Mb

2.8

ABC transporter

Pumilio-like Protein

Os_7U Receptor ProteinK

53 Protein FK56

40,38 Glucosyltransferase

32 AtMRP4

BJ_3UTR Cyt c

Rice

Chr4

physical

Mb

3.7

Pumilio-like Protein

Os_7U Receptor ProteinK

53 Protein FK56

40,38 Glucosyltransferase

32 AtMRP4

BJ_3UTR Cyt c

Rht8 Fine mapping: Genotyping and phenotyping 152 F_3 families

	Marker Genotypes								Experiment1			Experiment2			Experiment3		
Recombinant class	*Xgwm 261*	53	OS_7U	38	32	*Rht8*	BJ_3UTR	*Xcfd 53*	Nr plants	Mean height	stdev	Nr plants	Mean height	stdev	Nr plants	Mean height	stdev
Cappelle-D	a	a	a	a	a	a	a	a	14	112.1	5.2	13	104	5.1	10	91.4	6
I	a	a	a	a	a	a	a	b	-	-	-	1	104	0	-	-	-
II	a	a	a	a	a	a	b	b	16	109.8	2.9	8	101	5	10	93	3
III	a	a	a	a	a	b	b	b	19	100.1	5.3	31	94.6	6.1	17	86	8.7
IV	a	a	a	a	b	b	b	b	4	100.3	5.4	6	85	12.2	3	85.7	4
V	a	a	a	b	b	b	b	b	8	103.9	3.2	11	93.4	6.7	-	-	-
VI	a	a	b	b	b	b	b	b	-	-	-	3	93.7	3.5	4	87.5	4.2
VII	a	b	b	b	b	b	b	b	16	102	6.5	26	93	7.2	5	89.2	2.9
Rht8 donor1	b	b	b	b	b	b	b	b	6	103.2	5.7	15	91.1	6.7	12	85.9	3.3
VIII	b	a	a	a	a	a	a	a	14	109.1	6.3	29	101	5.7	12	101	4.9
IX	b	b	a	a	a	a	a	a	2	108.5	6.4	-	-	-	-	-	-
X	b	b	b	a	a	a	a	a	1	108	0	-	-	-	6	92.3	4.7
XI	b	b	b	b	a	a	a	a	1	108	0	5	101	3.1	3	97.3	2.1
XII	b	b	b	b	b	a	a	a	14	111.4	3.8	21	104	4.5	16	94.8	5.1
XIII	b	b	b	b	b	b	a	a	1	96	0	40	94.6	7.8	3	84.3	6.8
XIV	b	b	b	b	b	b	b	a	-	-	-	3	97.3	7	-	-	-
Rht8 donor2	b	b	b	b	b	b	b	b	6	98.7	3.8	-	-	-	-	-	-

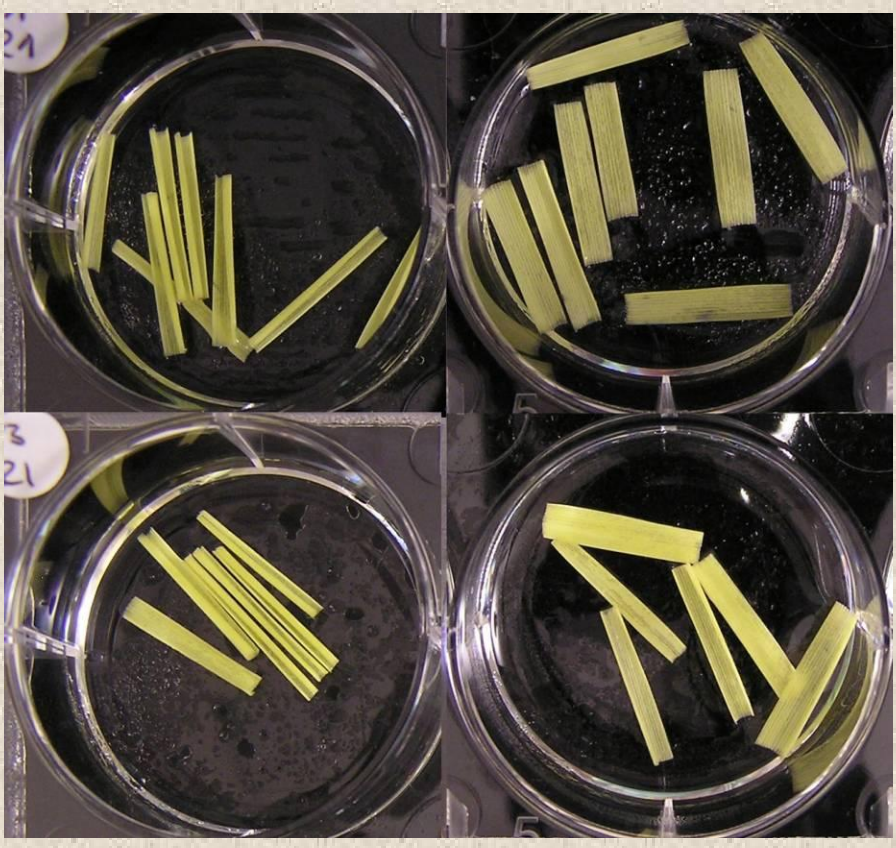
Wheat Leaf Unrolling Assay

control

1 ppm
Brassinolide

wt

Rht8



48h incubation

WGIN2 Avalon x Cadenza NIL development

Crop height

QTL	F$_1$	BC$_1$	BC$_2$	Hom
2A	■	■	■	■
2D	■	■	■	■
3A	■	■	■	■
3B	■	■	■	■
6A	■	■	■	■
6B	■	■	■	■

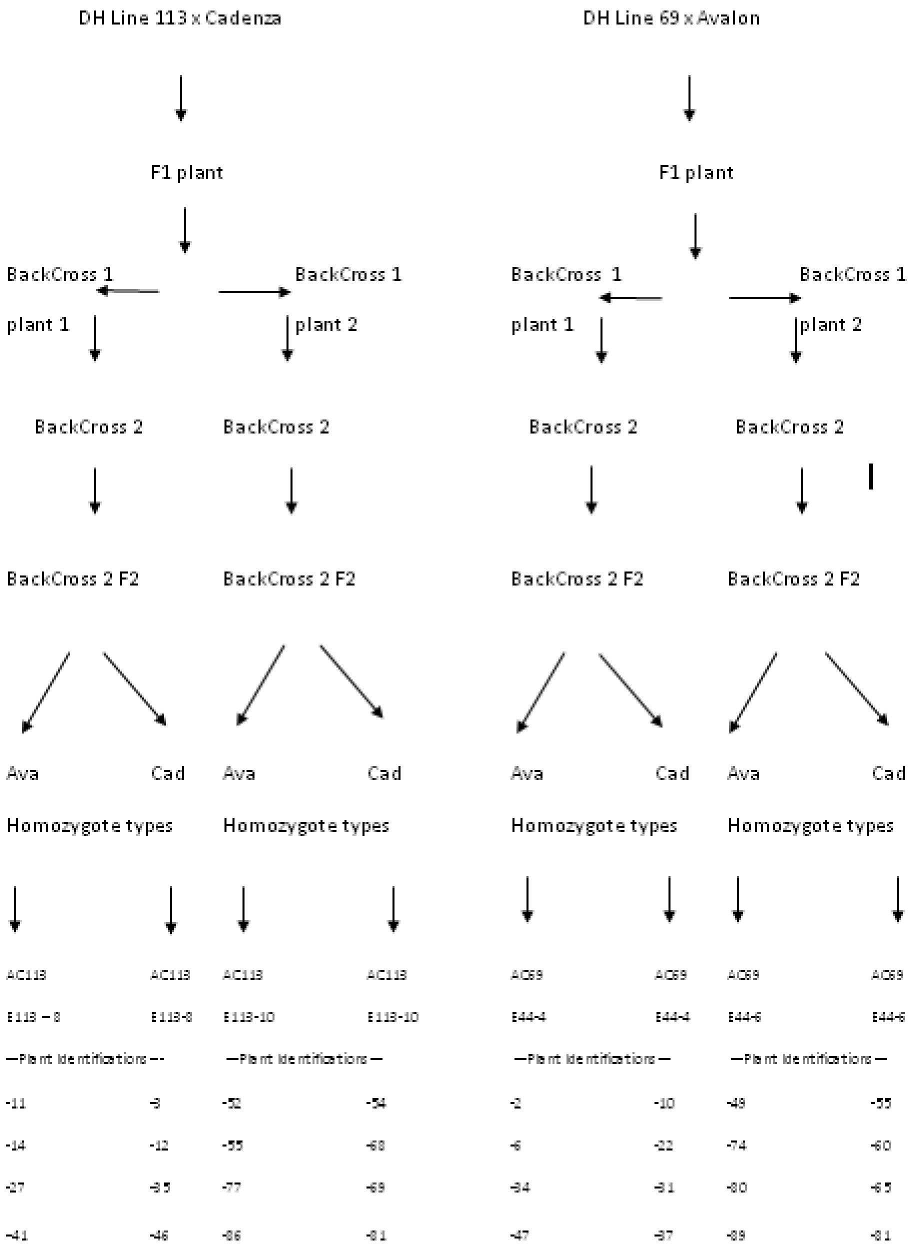
Ear emergence

QTL	F$_1$	BC$_1$	BC$_2$	Hom
1B	■	■	■	■
1D	■	■	■	■
6B	■	■	■	■

Yield

QTL	F$_1$	BC$_1$	BC$_2$	Hom
2D	■	■	■	■
3B	■	■	■	■
5A	■	■	■	■
7B	■	■	■	■
7D	■	■	■	■

Avalon x Cadenza 3A Near Isogenic Line (NIL) Material



DH Line 113 x Cadenza

F1 plant

BackCross 1 plant 1

BackCross 1 plant 2

DH Line 69 x Avalon

F1 plant

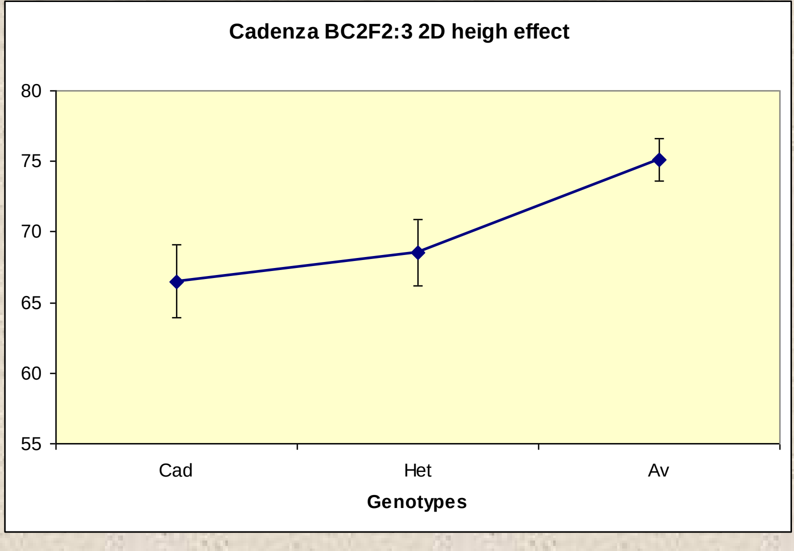
BackCross 1 plant 1

BackCross 1 plant 2

BackCross 2	BackCross 2	BackCross 2	BackCross 2
BackCross 2 F2	BackCross 2 F2	BackCross 2 F2	BackCross 2 F2
Ava Cad	Ava Cad	Ava Cad	Ava Cad
Homozygote types	Homozygote types	Homozygote types	Homozygote types

AC113	AC113	AC113	AC113	AC69	AC69	AC69	AC69
E113 – 8	E113-8	E113-10	E113-10	E44-4	E44-4	E44-6	E44-6
—Plant Identifications --		—Plant Identifications —		—Plant Identifications —		—Plant Identifications —	
-11	-3	-52	-54	-2	-10	-49	-55
-14	-12	-55	-68	-6	-22	-74	-60
-27	-35	-77	-69	-34	-31	-80	-65
-41	-46	-86	-81	-47	-37	-89	-81

Validation of QTL using WGIN NILs



Glasshouse validations look promising

All to be sown in 1m2 plots at Church farm this autumn

The non AxC WGIN NILs are still being developed- on target

- Lr19
- Wheat Functionality QTL

WGIN 2 exploiting new diversity

AE Watkins

- 10 SSD populations germinated well in $1m^2$ plots at Church Farm- grown for Landrace Pillar of Wheat Pre Breeding LOLA
- Luzie presented SSR genotyping and analysis at Stakeholder meeting- repeating nulls/fails at the moment for publication. Luzie presenting work at European Plant Genetic Resources Conference (Wageningen).

- Gediflux still needs work!

Populations

- Drought-Paragon x Garcia F_1 seed is dried off.
- Aim to screen large F2 (~1000) in Autumn to remove photoperiod insensitive and winter types, then progress with SSD.
- Paragon x Chinese Spring, and Paragon x Synthetic available for use.
- Avalon x Cadenza maintained and distributed

WGIN at JIC

Richard
Goram

Luzie
Wingen

Simon
Orford

Michelle
Leverington

John
Snape

Lesley
Fish

SEEDS OF DISCOVERY

A $70m/7 year Investment by the Mexican Government: 1/3 wheat, 1/3 maize, 1/3 bioinformatics

Exploitation of Global Genetic Resources in wheat and maize to address

- Food Security
- Climate change
- Resource Limitation

Mission Statement

Development of the genetic and associated technologies for the exploitation of genetic resources
to empower the global maize and wheat breeder
communities to address the challenges to global food
security including climate change and resource

Outcomes

Tools and/or genetic resources that can be deployed directly in any breeding program anywhere in the world

Whole Genome Selection

Facilitates selection for alleles across the whole genome

Provides more certainty of the allelic composition of potential parents

In silico selection is possible

Whole Genome Selection: SeeD

Developed for wheat (winter and spring)

Cost effective genotyping

Bioinformatics: Public domain

Dr Yann Manes (Leader)

CROPGEN
INTERNATIONAL

Exploiting Modern Gene Pools

Systematic

Winter * Spring

Identify gene pools unrelated to CIMMYT

European Winter Wheat

Synthetic Wheat

Systematic

More sampling of tetraploids

Systematic use of T. *tauschii*

Introgression into élite gene pools using WGS (?)

David Bonnett (CIMMYT)

Francis Ogbonnaya (ICARDA)

Targeted Exploitation of Global Genetic Resources to combat global climate change

There have been periods in the history of the earth when elevated CO2 and temperature were experienced

Target the genetic resources through FIGS

Growing Season Length

Need to understand the impact of alleles for photoperiodism, vernalization and photoperiod insensitivity

Quite a lot of work globally

Develop markers for alleles so that they can be moved into breeding material quickly

Drought Tolerance

Matthew Reynolds: phenotyping, land races

Amed Amir and David Bonnet: Synthetics

Wild relatives: FIGS

Target: Adaptation to dryland environments

Heat Stress

Terminal heat stress tolerance

Mexican wheat breeders (Pedro Figueroa) and CIMMYT assistance: Land races

Gene pools from regions that experience terminal heat stress

David Bonnet: Synthetics based on *T. turgidum*, India

FIGS: target genetic resources to be evaluated

Necrotrophic Diseases

Increasingly important: more dead tissue, conservation agriculture

Septoria tritici blotch
(*Mycosphaerella graminicola*)

Tan spot (*Pyrenophora tritici repentis*)

Necrotrophic Diseases (Cont.)

Crown rot (*Fusarium pseudograminearum*)

Spot blotch (*Bipolaris sorokiniana*)

Scab (*Fusarium graminearum*)

FIGS

Root Health

Assumes much greater importance

Crown rot (*Fusarium pseudograminearum*)

Pratylenchus sp. *(neglectus, thornei, penetrans)*

Julie Nicol

Insect Pests

Green bug (*Schizaphis graminum*)
Increasingly important: India
Hessian fly (*Mayetiola destructor*)
Sunn Pest
Cereal leaf beetle

Dr *Mustapha* El-*Bouhssini*
Dr Ravi Singh
FIGS

Phosphorous Use Efficiency

Genetic variation for VAM development
Implications for P nutrition?
Variation for PUE with and without VAM development

Ivan Ortiz Monasterio (?)

Nitrogen Use Efficiency

Genetic variation identified

Ivan Ortiz Monasterio (?)

FIGS

Processing Quality

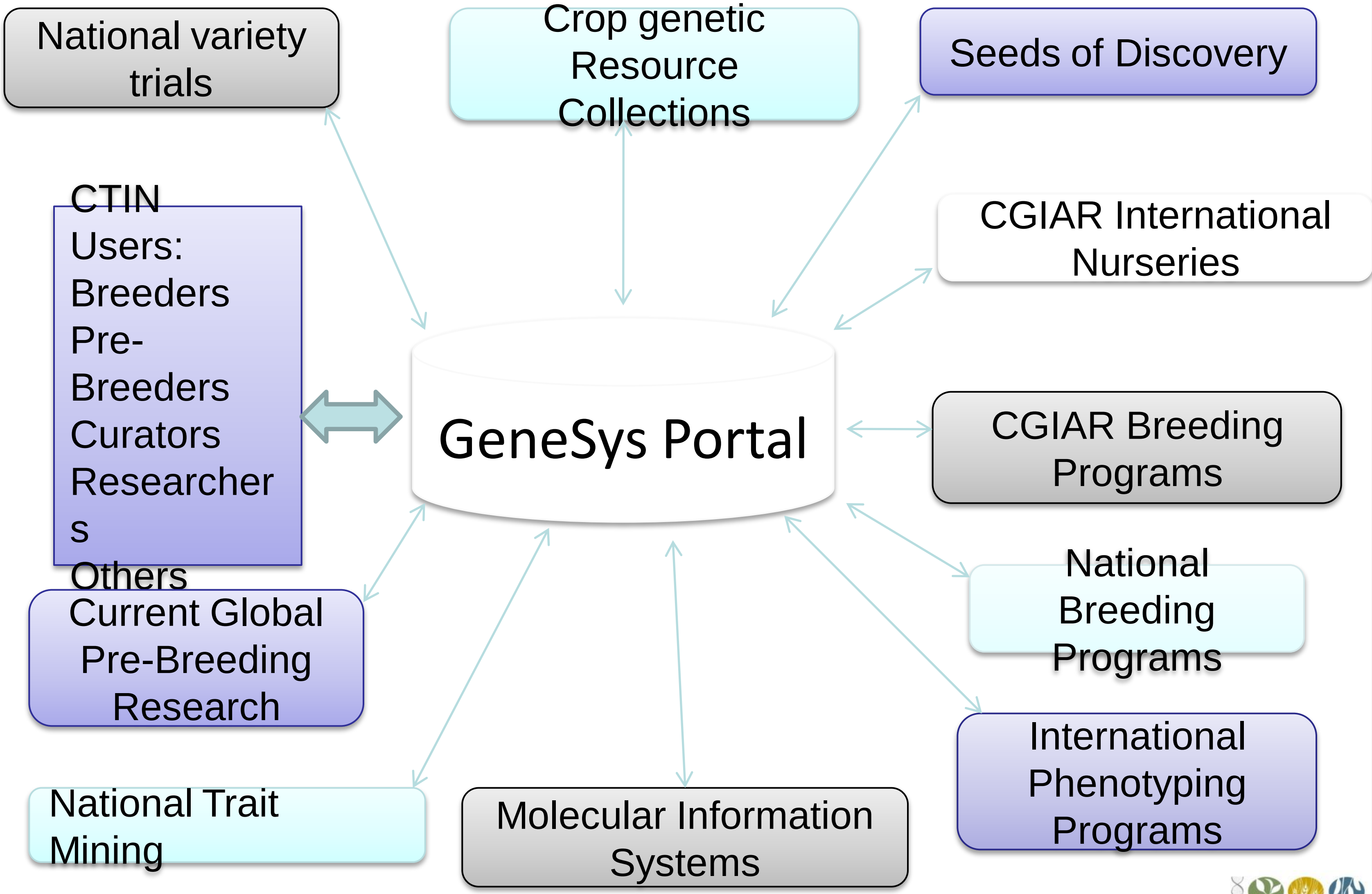
Human nutrition: Fe and Zn concentration in the grain

Milling Quality

Translocation of carbohydrates into the grain in late grain filling

Proteins and heat stress tolerance

Crop Trait Information Network



GeneSys Portal

National variety trials

Crop genetic Resource Collections

Seeds of Discovery

CGIAR International Nurseries

CGIAR Breeding Programs

National Breeding Programs

International Phenotyping Programs

Molecular Information Systems

National Trait Mining

Current Global Pre-Breeding Research

CTIN Users:
Breeders
Pre-Breeders
Curators
Researchers
Others

Insect resistance in wheat: Cereal aphids (RRes)

Lesley Smart, Janet Martin and Ruth Gordon-Weeks

Objective 7. To explore whether the differential response of hexaploid wheats to two different cereal aphid species has a genetic basis.

Milestone 1. Determine the differential susceptibility to two cereal aphid species of targeted lines from the Spark x Rialto mapping population.

Family

Aphididae

Sub-family

Aphidinae

Tribe

Macrosiphini

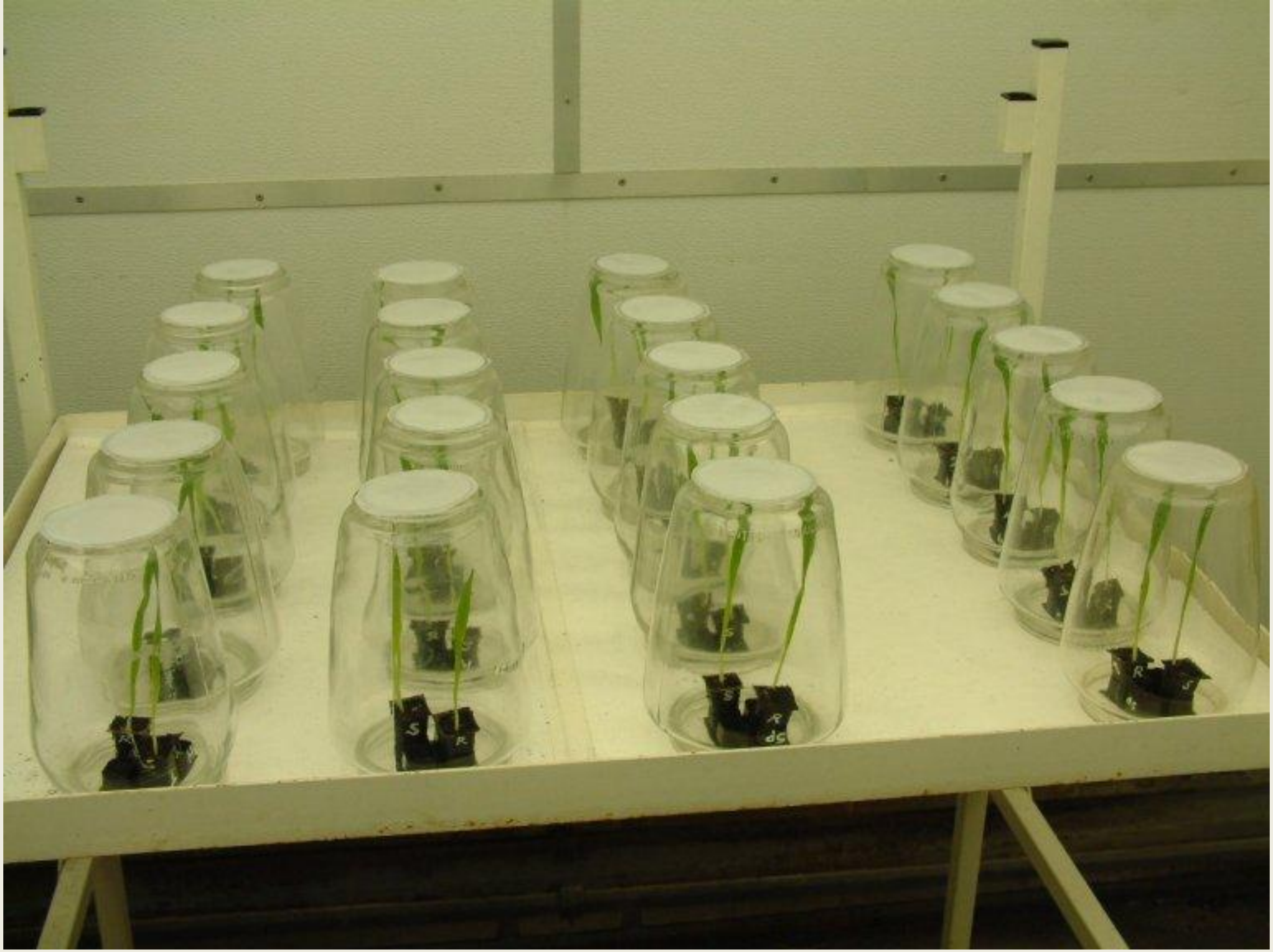
Diuraphis noxia
Russian Wheat aphid

Sitobion avenae
Grain aphid

Aphidini

Schizaphis graminum
Greenbug

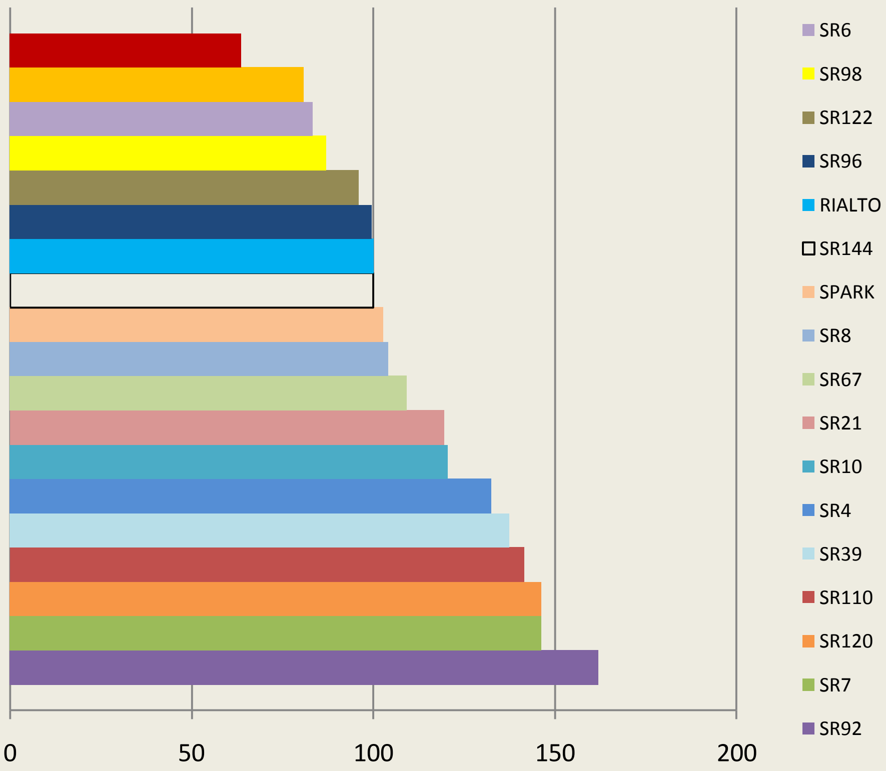
Rhopalosiphum padi
Bird-cherry oat aphid



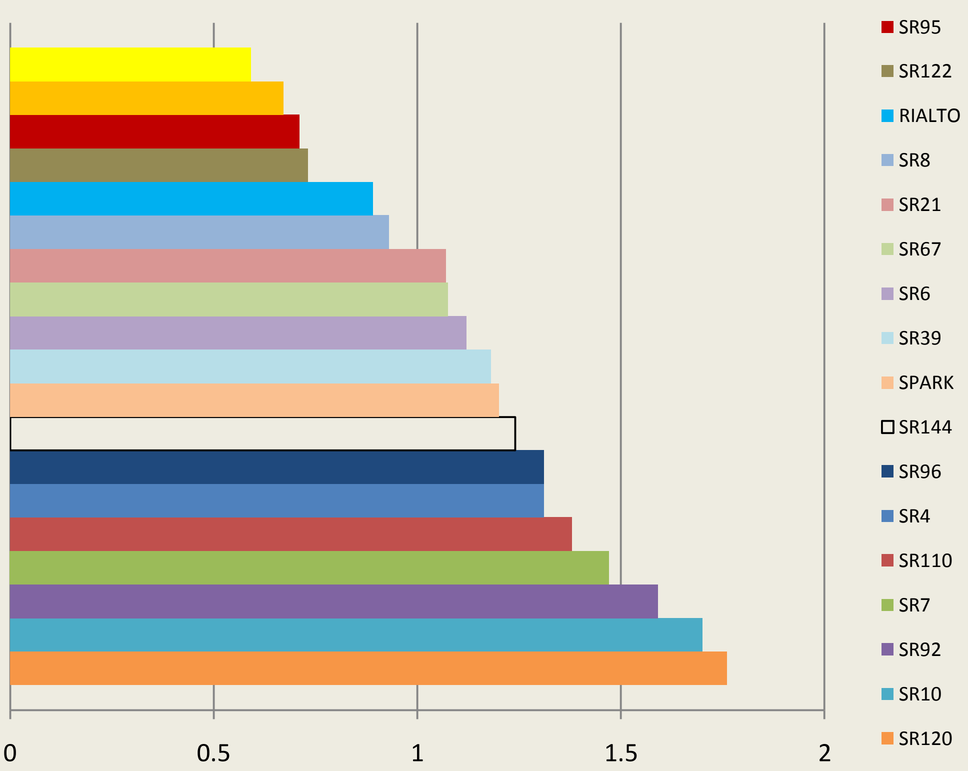
17 Genotypes plus the parental lines tested in choice tests, with cv. Solstice as the standard variety, against *Sitobion avenae* and *Rhopalosiphum padi.*

Preference Index *Sitobion avenae*

***Sitobion avenae* choice tests with Spark x Rialto mapping lines. Alates settled at 24h as a proportion of alates settled on Solstice = 100**

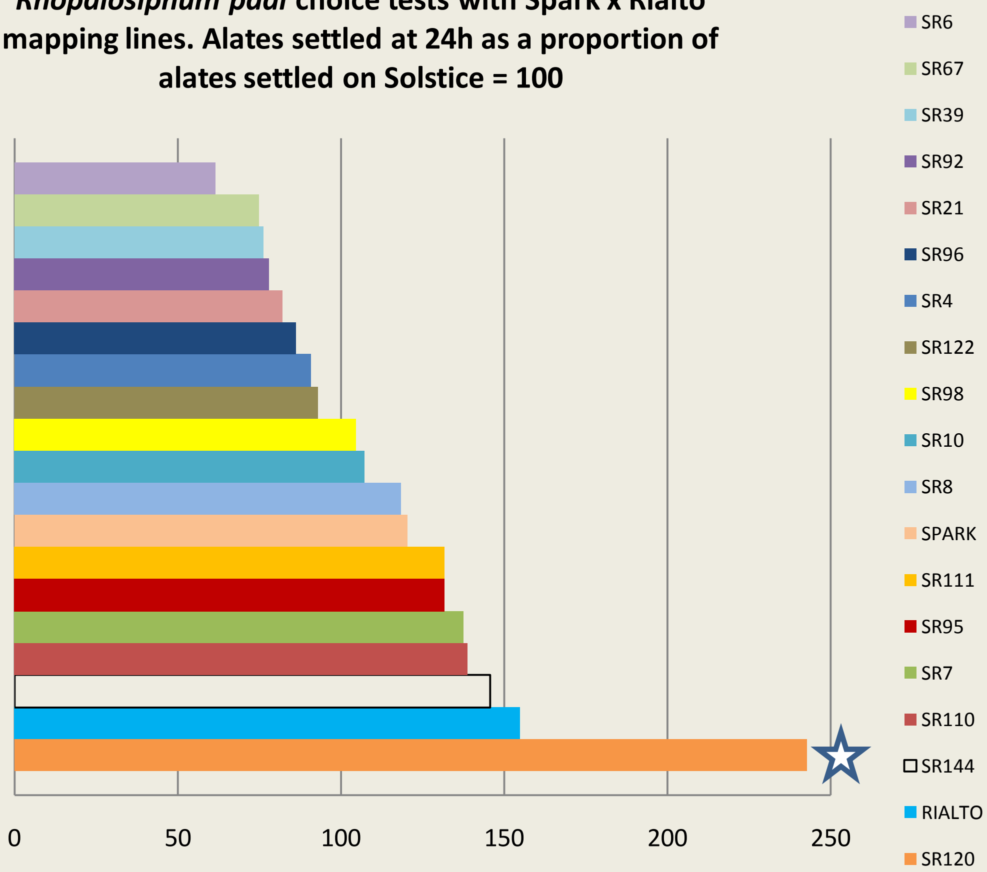


***Sitobion avenae* choice tests with Spark x Rialto mapping lines. Nymphs produced at 24h as a proportion of nymphs produced on Solstice = 1**

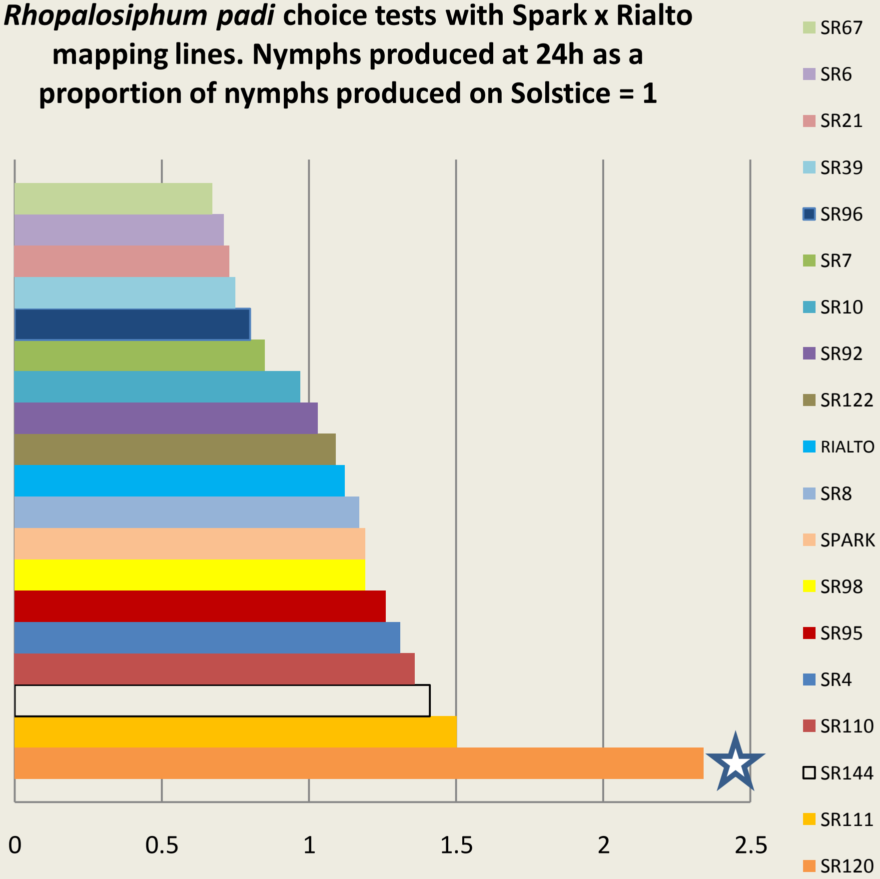


Preference Index *Rhopalosiphum padi*

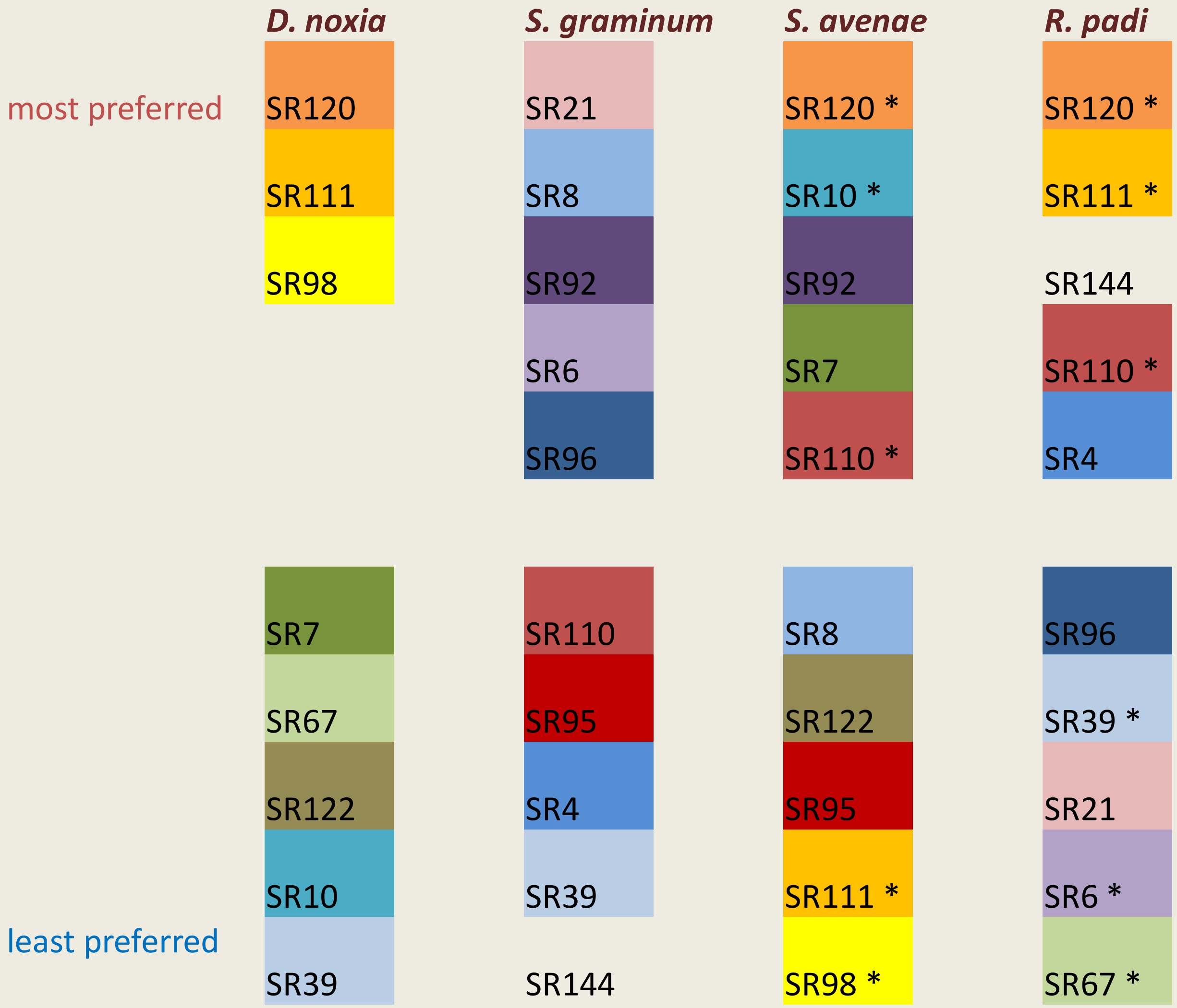
Rhopalosiphum padi **choice tests with Spark x Rialto mapping lines. Alates settled at 24h as a proportion of alates settled on Solstice = 100**



Rhopalosiphum padi **choice tests with Spark x Rialto mapping lines. Nymphs produced at 24h as a proportion of nymphs produced on Solstice = 1**



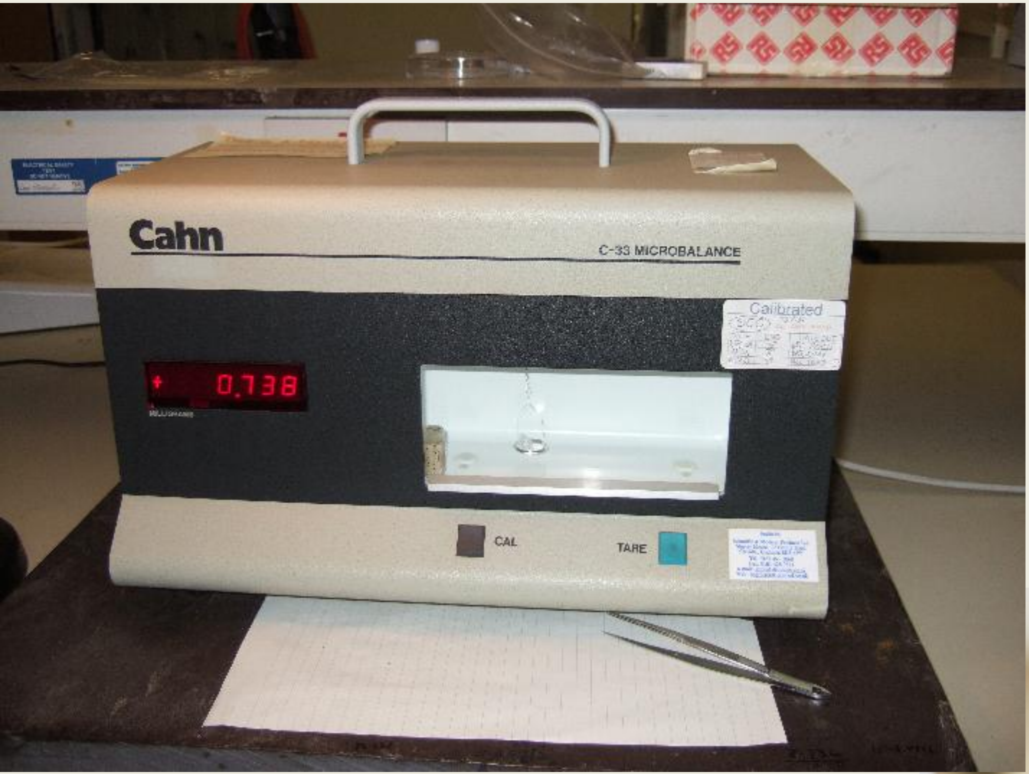
Spark x Rialto antixenosis responses



	D. noxia	*S. graminum*	*S. avenae*	*R. padi*
most preferred	SR120	SR21	SR120 *	SR120 *
	SR111	SR8	SR10 *	SR111 *
	SR98	SR92	SR92	SR144
		SR6	SR7	SR110 *
		SR96	SR110 *	SR4
	SR7	SR110	SR8	SR96
	SR67	SR95	SR122	SR39 *
	SR122	SR4	SR95	SR21
	SR10	SR39	SR111 *	SR6 *
least preferred	SR39	SR144	SR98 *	SR67 *

* Lines chosen for aphid development assays plus parental lines

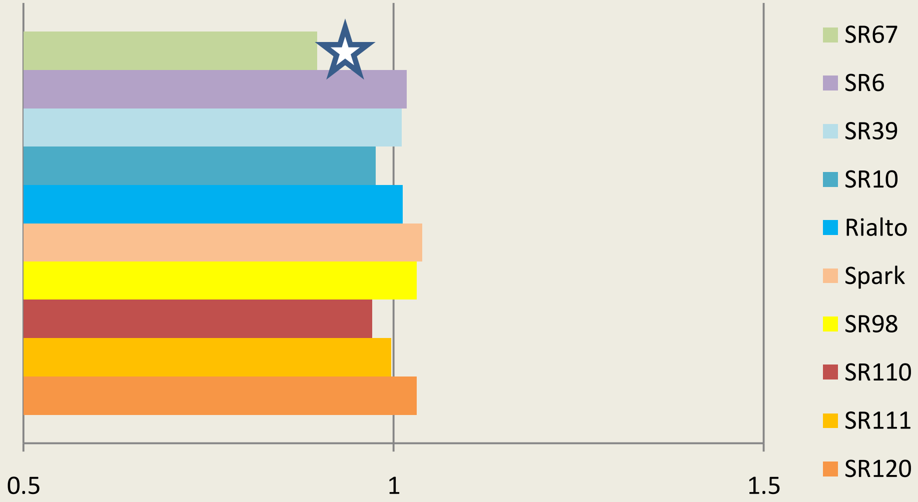
Mean Relative Growth Rate Assay



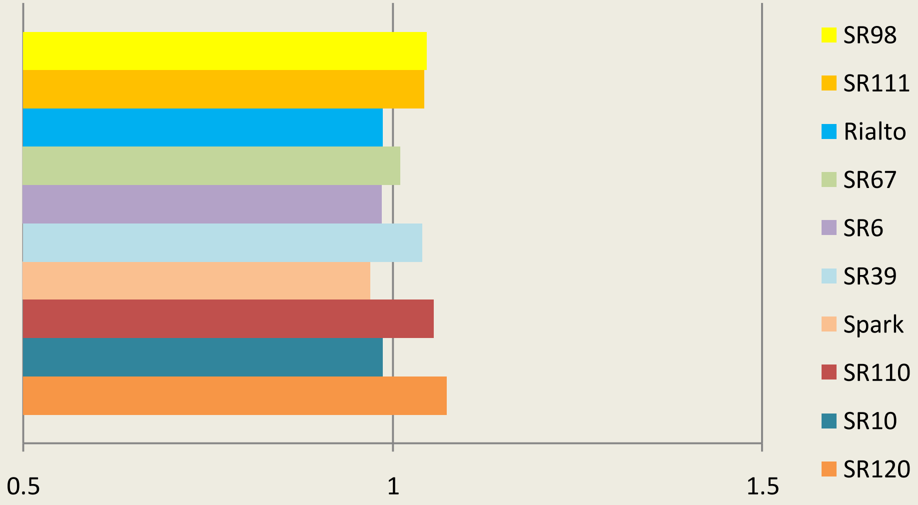
Neonate nymphs weighed in batches on day 1, returned to plant and survivors weighed again after 7days.

MRGR = (ln(7 day wt) - ln(birth wt)) /days

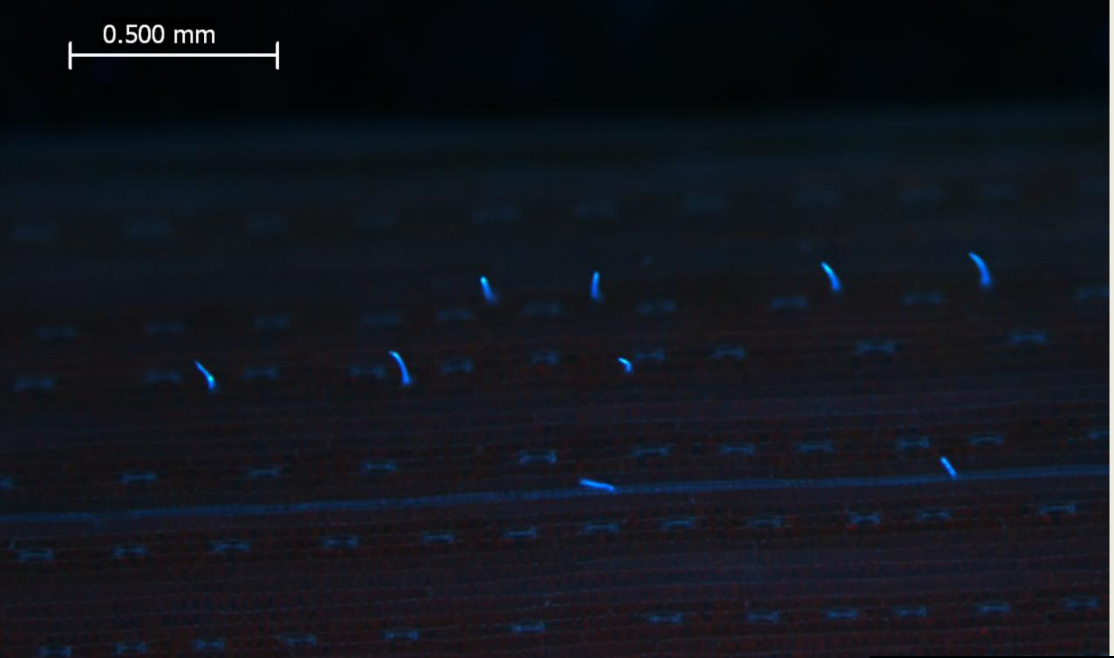
Rhopalosiphum padi **development assays with Spark x Rialto mapping lines. Mean Relative Growth Rate as a proportion of MRGR on Solstice = 1**



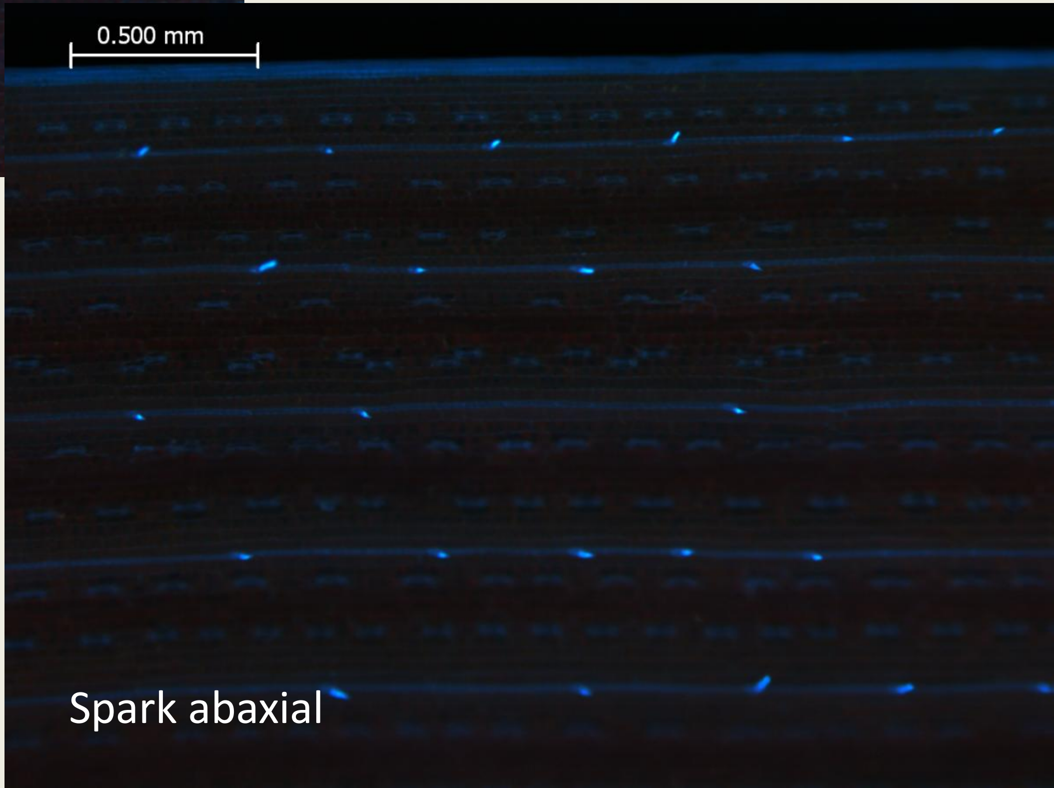
Sitobion avenae **development assays with Spark x Rialto mapping lines. Mean Relative Growth Rate as a proportion of MRGR on Solstice = 1**



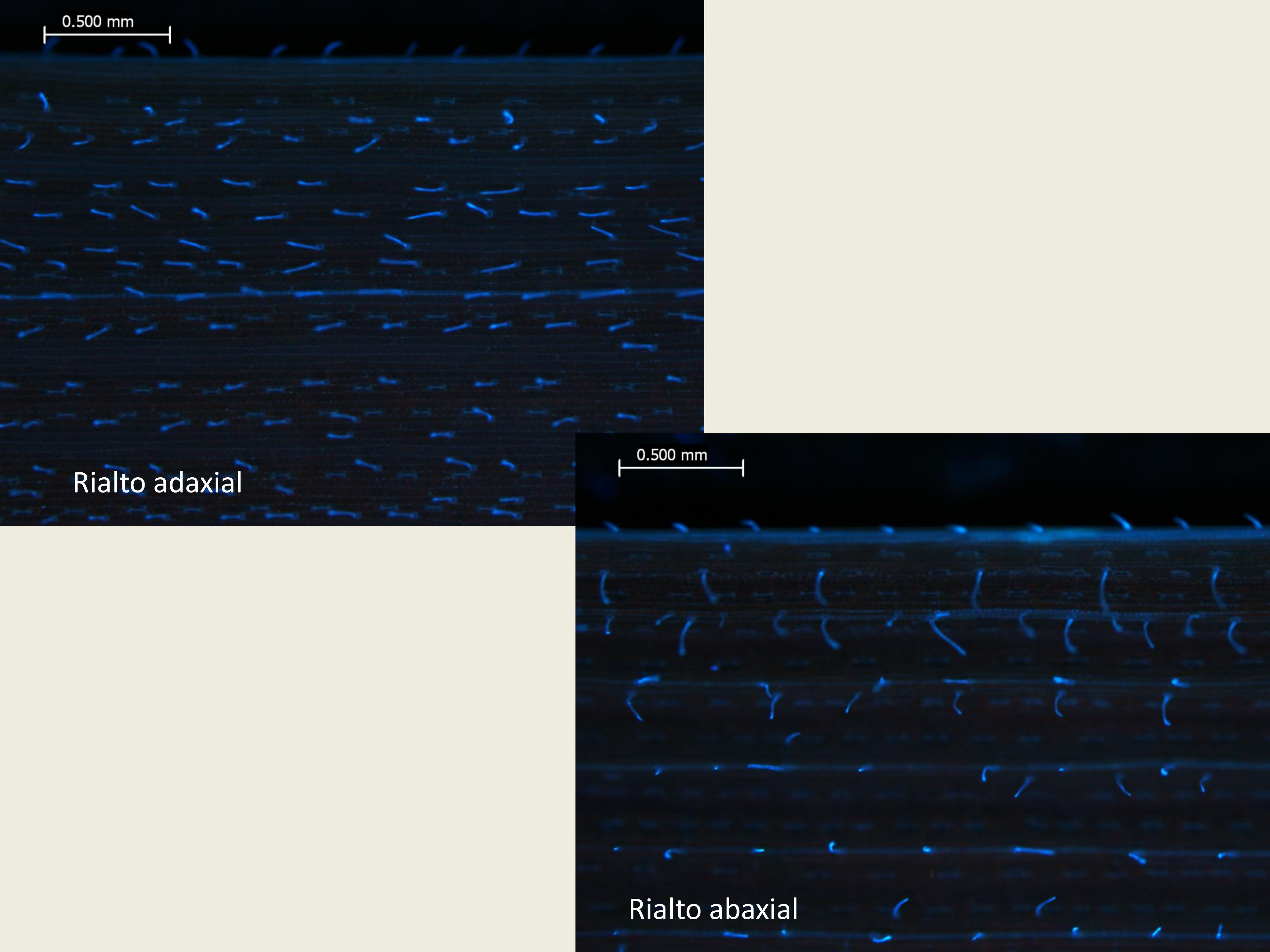
	Alate settlement		Nymphs at 24h		MRGR	
	S. avenae	***R. padi***	***S. avenae***	***R. padi***	***S. avenae***	***R. padi***
most preferred	SR92	SR120	SR120	SR120	SR120	SPARK
	SR7	RIALTO	SR10	SR111	SR110	SR120
	SR120	SR144	SR92	SR144	SR98	SR98
	SR110	SR110	SR7	SR110	SR111	SR6
	SR39	SR7	SR110	SR4	SR39	RIALTO
					SR67	SR39
	SR122	SR21	SR8	SR96	SR10	SR111
	SR98	SR92	SR122	SR39	RIALTO	SR10
	SR6	SR39	SR95	SR21	SR6	SR110
	SR111	SR67	SR111	SR6	SPARK	SR67
least preferred	SR95	SR6	SR98	SR67		

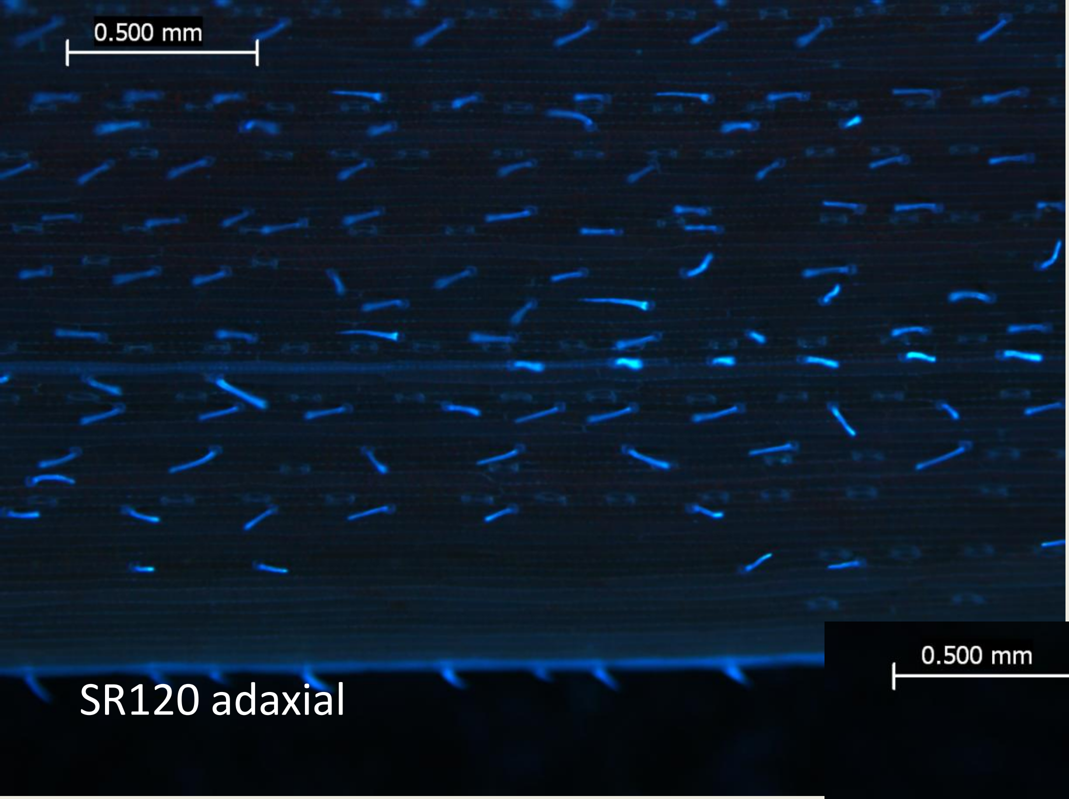


Spark adaxial

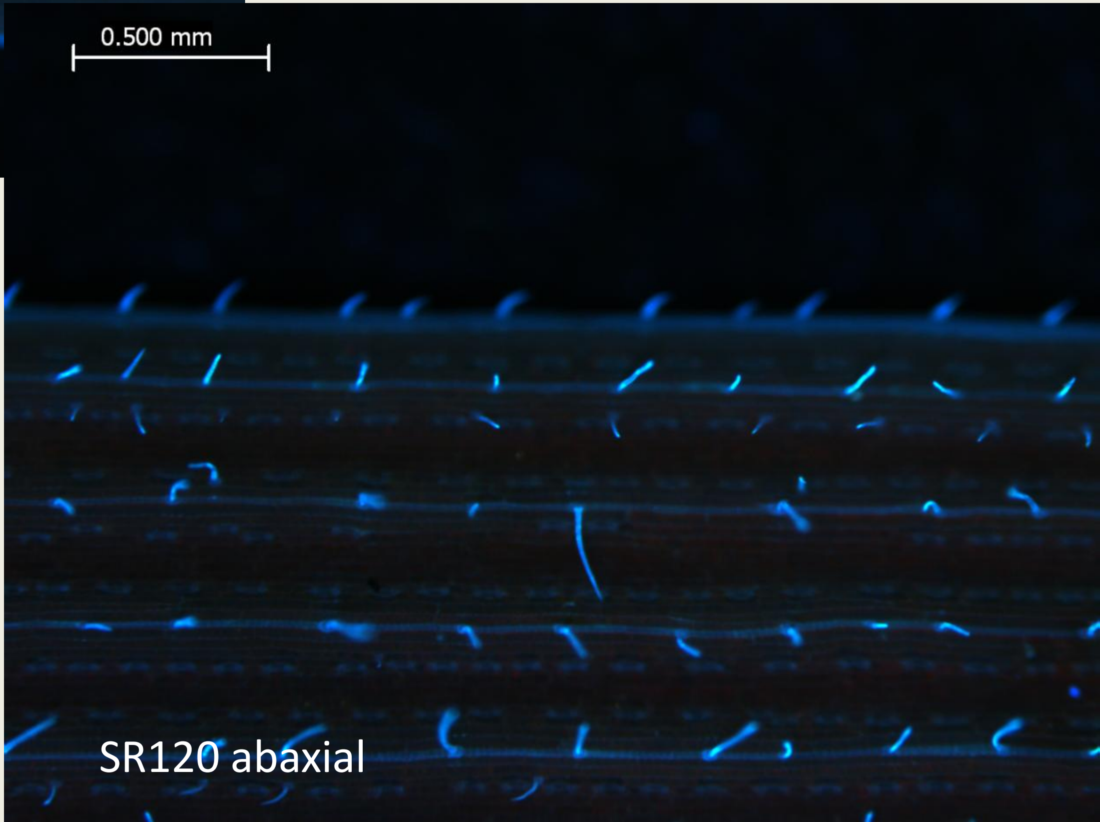


Spark abaxial


0.500 mm
Rialto adaxial
0.500 mm
Rialto abaxial



SR120 adaxial



SR120 abaxial

Summary

- Line SR120 was the most preferred for settlement and nymph production over 24h by *R. padi* and for 24h nymph production by *S. avenae*. Development of nymphs was not improved significantly.

- Line SR67 was the least preferred for 24h nymph production by *R. padi* and the development of *R. padi* nymphs was significantly reduced.

- Overall there was little consistency in results for behavioural and developmental assays between the aphid species.

- Are there any differences between the least and most preferred genotypes?

- Investigate leaf chemistry, in particular for SR120

Resistance to Take-all

Richard Gutteridge
Kim Hammond-Kosack

Wheat
Genetic
Improvement
Network

defra
Department for Environment
Food and Rural Affairs

BBSRC
bioscience for the future

ROTHAMSTED
RESEARCH

WGIN MM@RRes
16th Feb 2011

Take-all disease of wheat

- *Gaeumannomyces graminis* var. *tritici* (***Ggt***)

  - ascomycete soil borne fungus

  - related to rice blast fungus *Magnaporthe oryzae* (previously *M. grisea*)

Severely infected take-all plant

A *Ggt* infected wheat root

Take-all disease – soil-borne fungus

In 1st wheats - no disease problem

A major problem
for 2nd / 3rd wheat crops

2nd wheat syndrome

Typical take-all patch showing stunting and premature ripening of the crop

The risk of take-all is largely dependent on the amount of fungal inoculum in the soil at the time of sowing

Objective 10 - Talk Outline

- **Hexaploid wheat – Watkins / Gediflux collections**
  Diploid wheat

  - field evaluation to identify potentially resistance genotypes

- **Diploid wheat**
  - mapping populations
  - introgression to *T. aestivum*

- **Hexaploid wheat – inoculum build-up in 1st wheats – 2010**

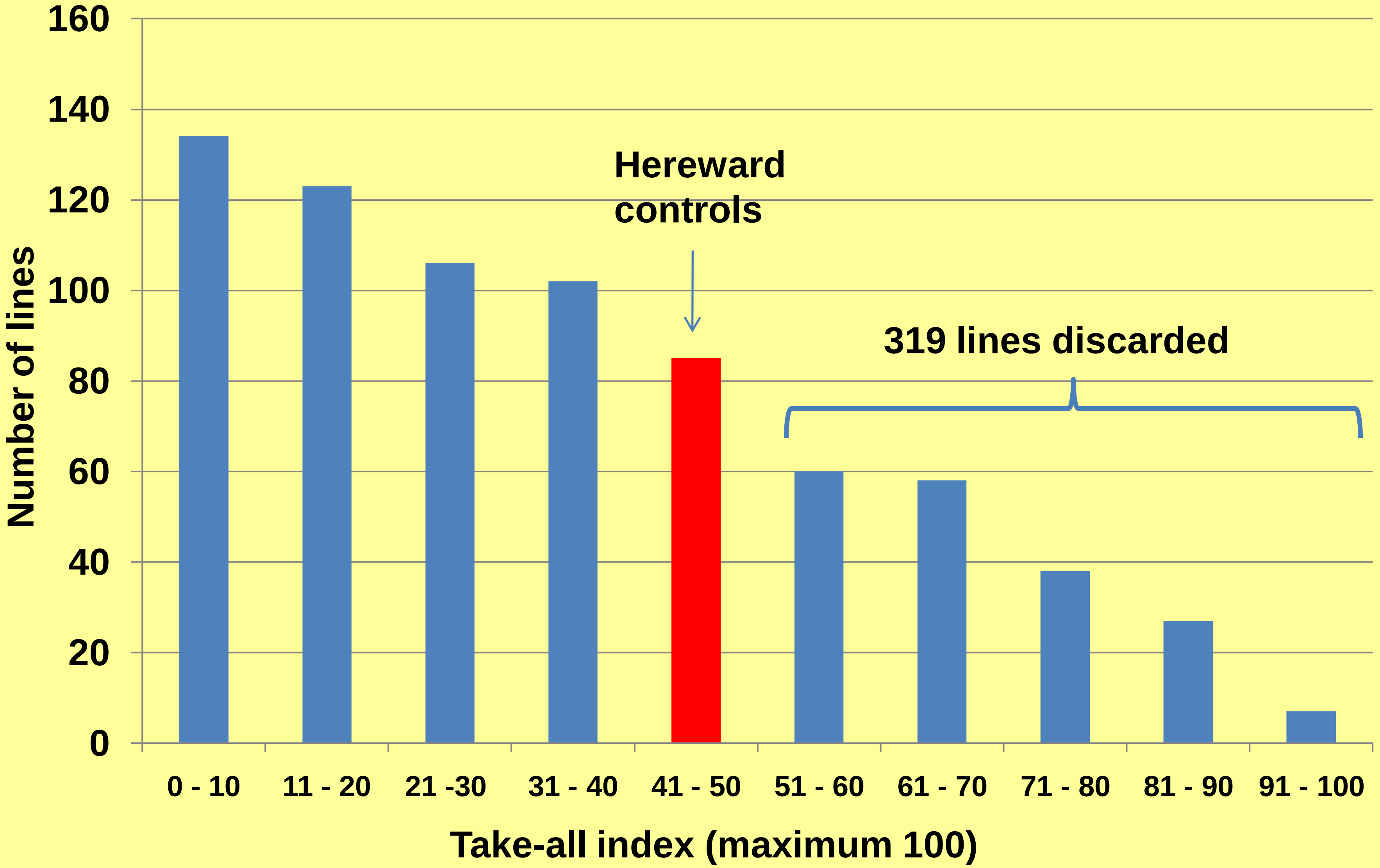
- results so far / current activities

Watkins Hexaploid wheat collection
Take-all assessments

- **2008 and 2009 field season – one plot / genotype –** established from 45 seeds
- **823 lines from the collection (both years – 740 lines)**

3rd wheat situation

Watkins 2008 Take-all data

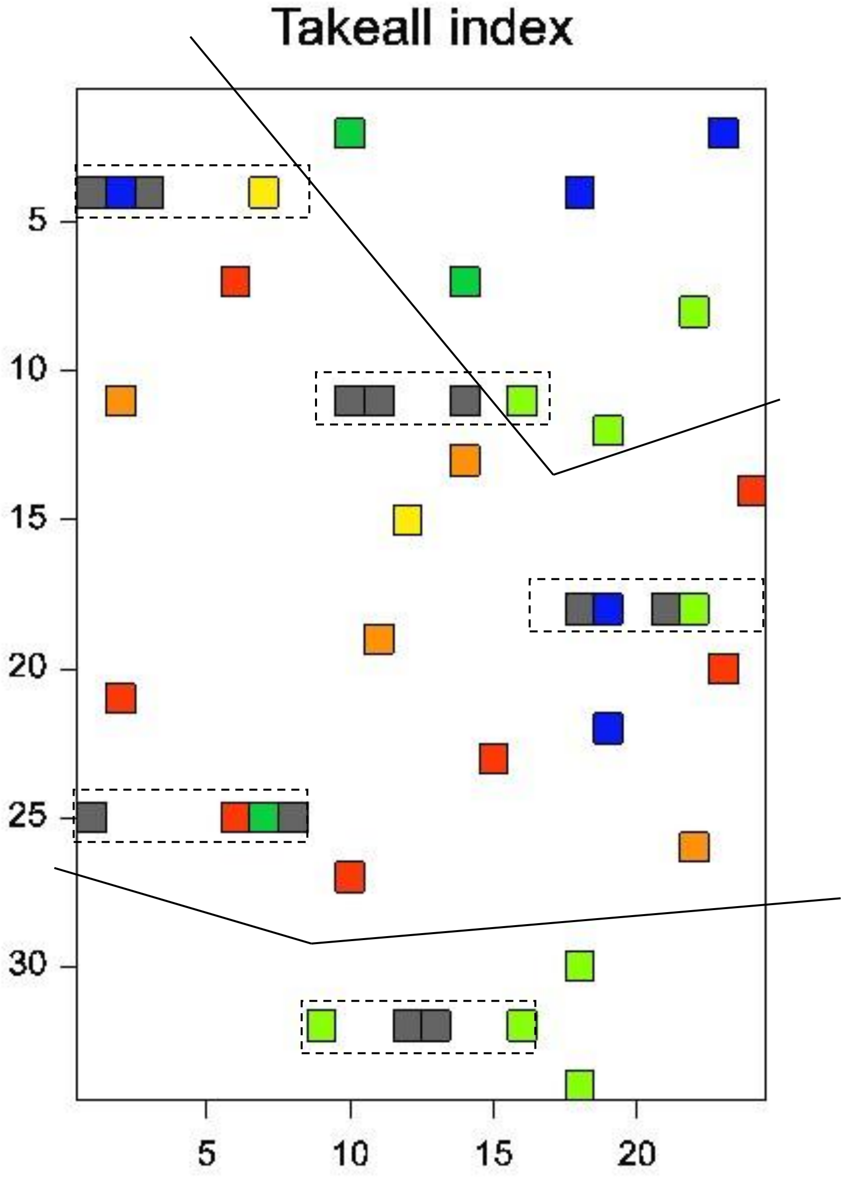


Watkins Experiment 2008 RRes Take-all severity - control plots

5 control blocks

Variety	TAI
Hereward	35.6
Triticale	18.4
Rye	1.7
Oats	0.0

	TAI
⬜	0-5
🟦	6-15
🟩	16-25
🟩	26-35
🟨	36-45
🟧	46- 55
🟥	> 55



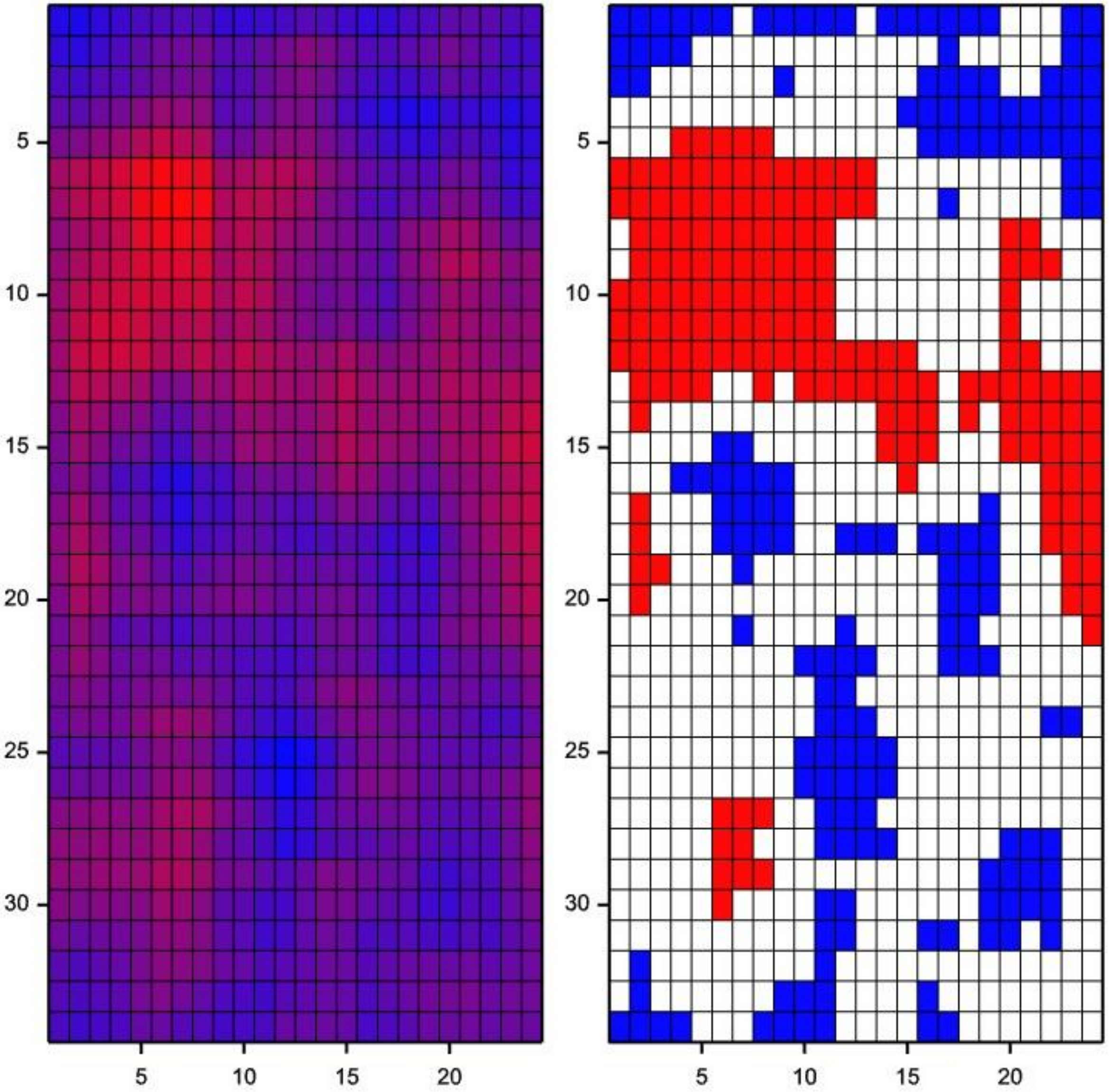
Hereward - Extra 20 plots - mean TAI = 45.3

Alpha design

N = 800 plots

Mean of all plots
Hereward = 43.4

Spatial trend for 2008 Watkins trial



Analysis by Sue Welham, Stats, RRes

Red indicates high take-all values

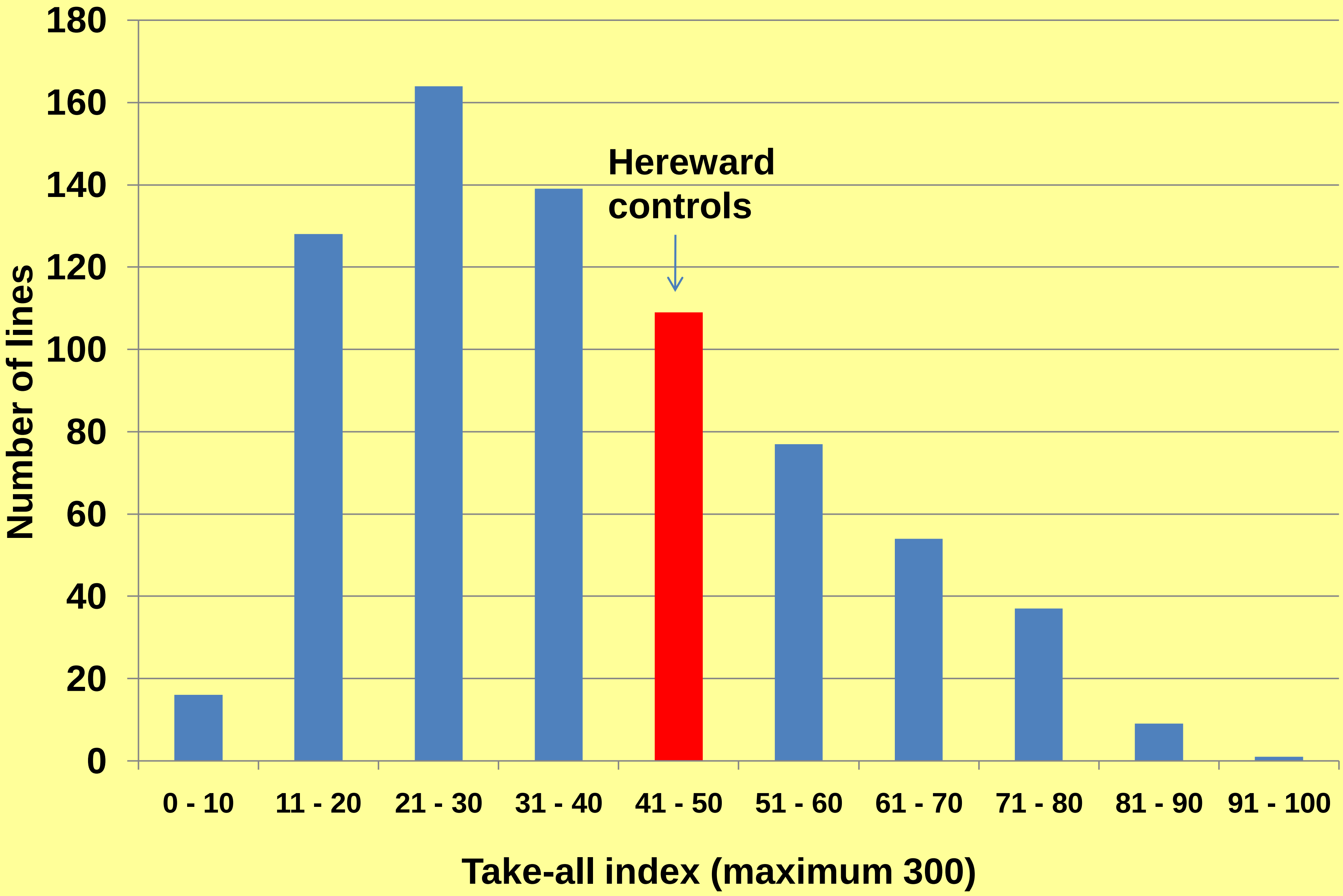
White indicates mid take-all values

Blue indicates low take-all values

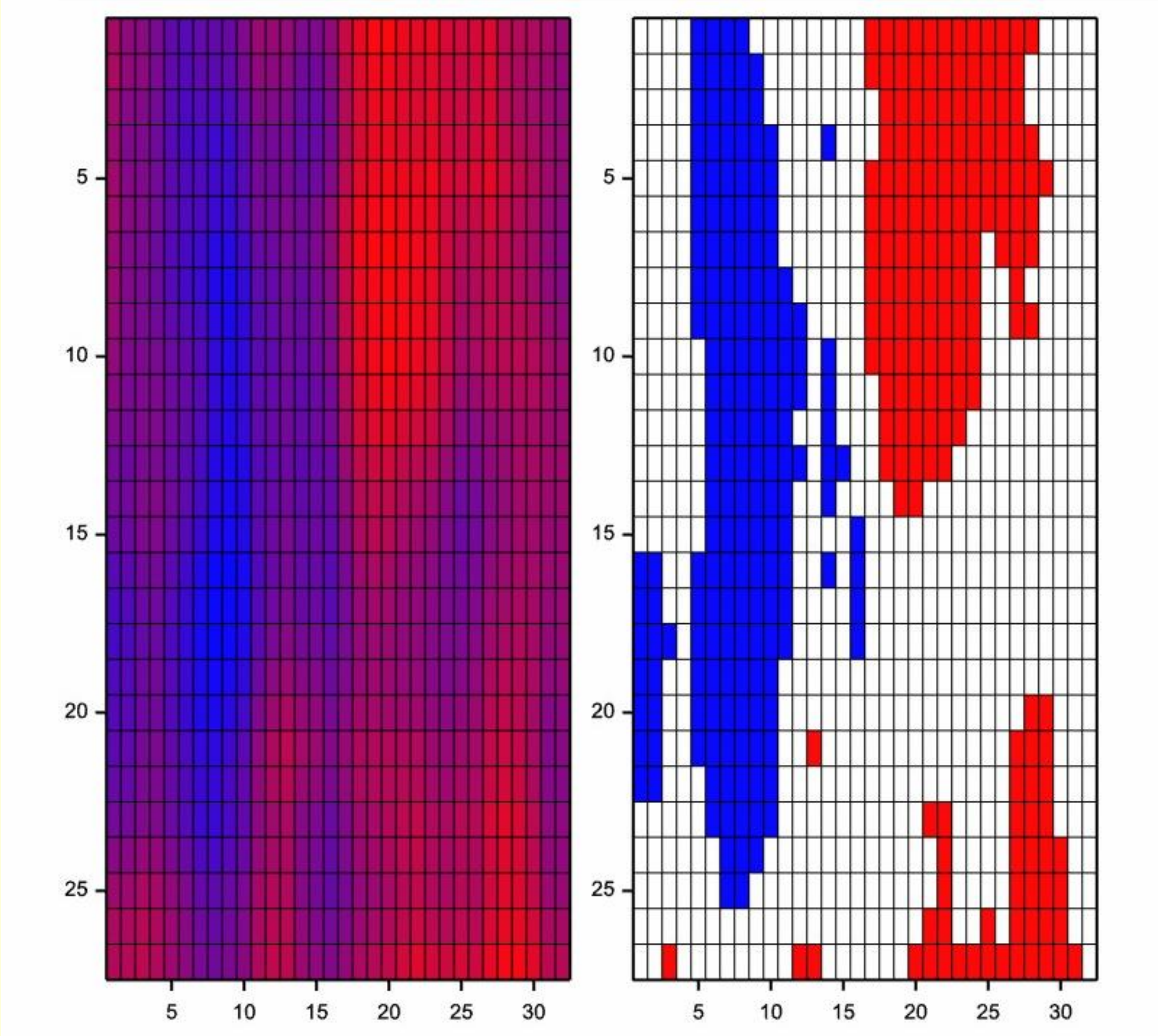
20:60:20 split

Spatial trend accounted for 36% of background variation

Watkins 2009 Take-all data



Spatial trend for 2009 Watkins trial



Analysis by Sue Welham, Stats, RRes

Red indicates high take-all values

White indicates mid take-all values

Blue indicates low take-all values

20:60:20 split

Spatial trend accounted for 11% of background variation

Note: Some lines are within an area of general high readings, but still outside of a patch of infection.

Spatial Analysis- Watkins 2008 and 2009

Hypothesis 1 : Lines with a **low** take-all score in areas of **high spatial background** exhibit **resistance**

- **32** lines of this type observed either in year 1 or year 2

Hypothesis 2 : Lines with a **low** take-all score in areas of **low spatial background** may either exhibit **resistance** or **have not been properly challenged**

- **164** lines of this type observed either in year 1 or year 2

But only

- **8** lines in areas with a low spatial trend background both years
  - **not properly challenged** (**1.08%**)

Watkins/Gediflux Hexaploid wheat collection

Aim: To identify genotypes with tissue based resistance

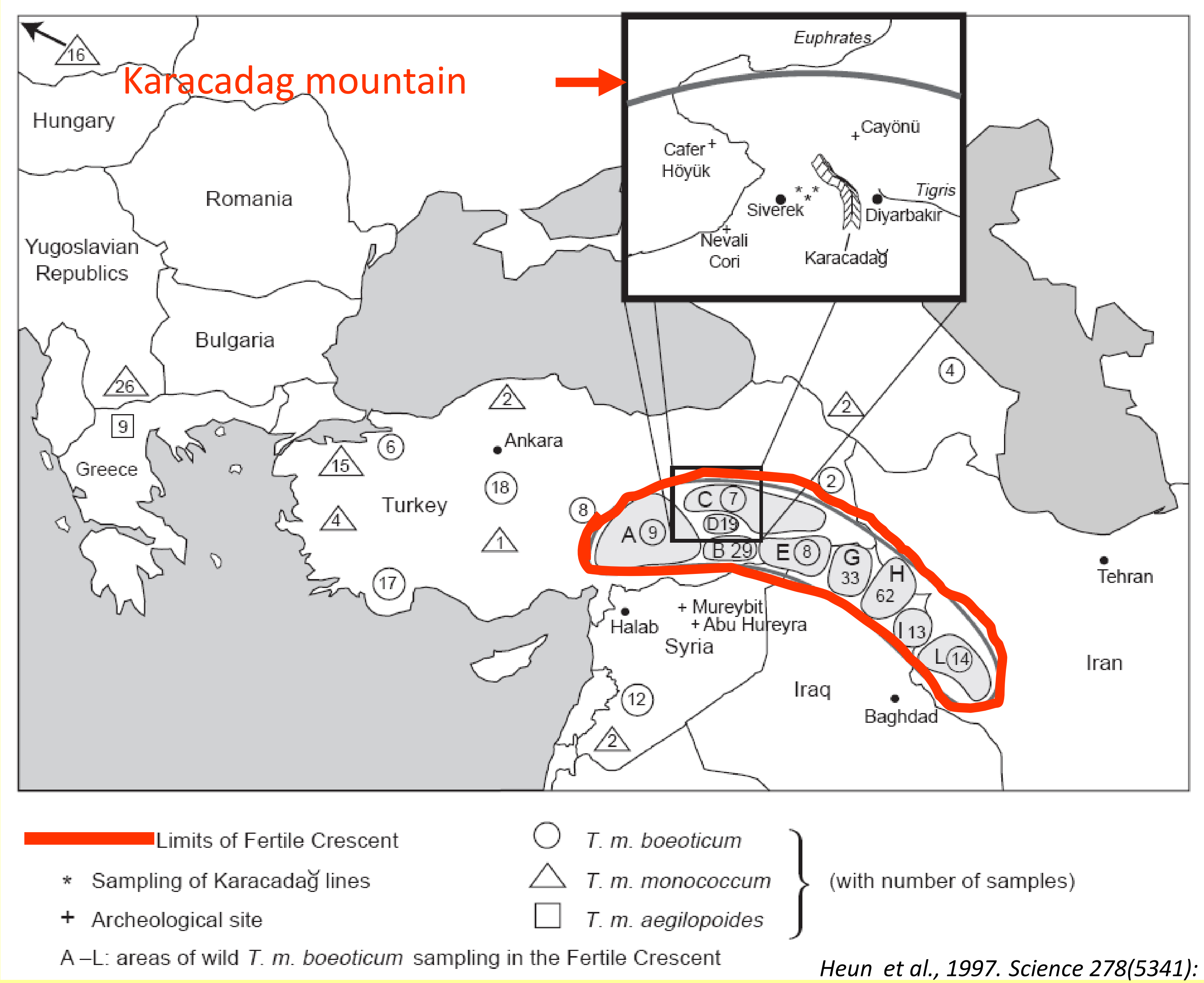
Watkins lines
823 lines tested of which **319 lines** discarded as take-all susceptible (2008 season).

Gediflux collection – **24 lines** discarded from 60 lines originally tested in 2009

2010 – 2011 field season (year 3)

504 Watkins lines and **36 Gediflux lines**
5 blocks of 8 controls
20 Hereward control plots.
Sown 21st October 2010 – Claycroft field 3rd wheat

T. monococcum (AA genome) domesticated from *T. boeoticum*

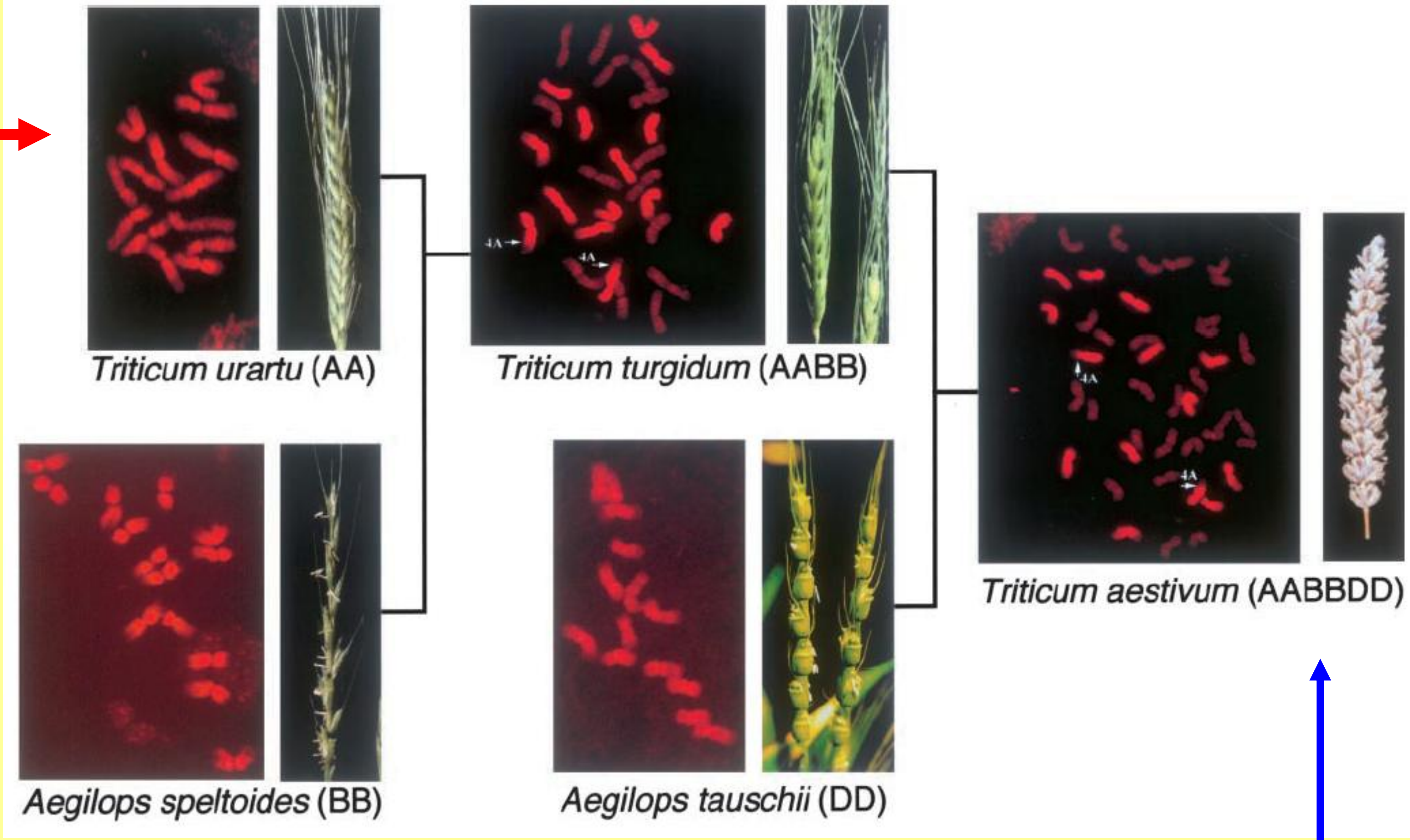


Karacadag mountain

Heun et al., 1997. Science 278(5341): 1312-1314.

Origin of bread wheat

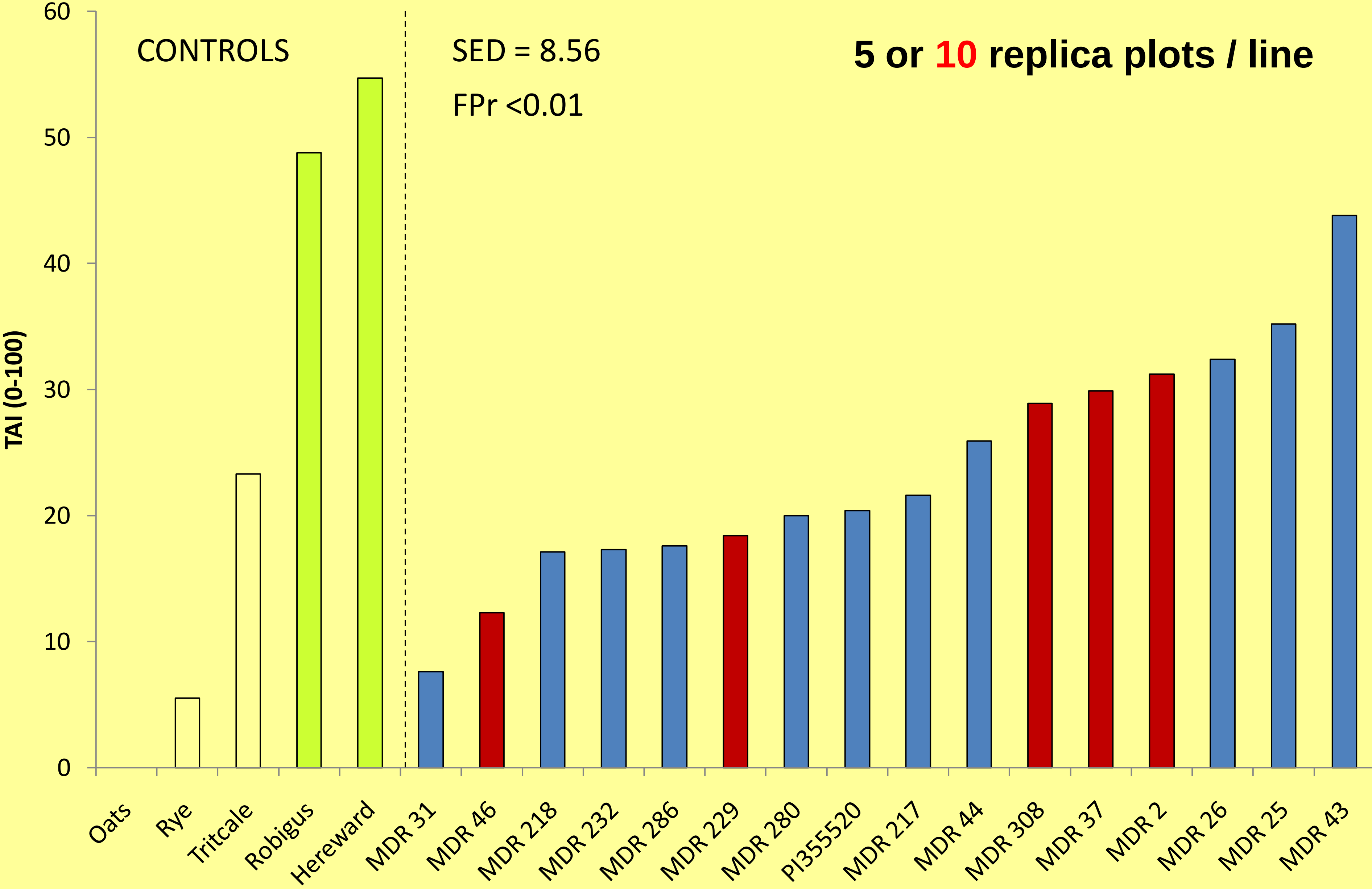
T. monococcum A^mA^m



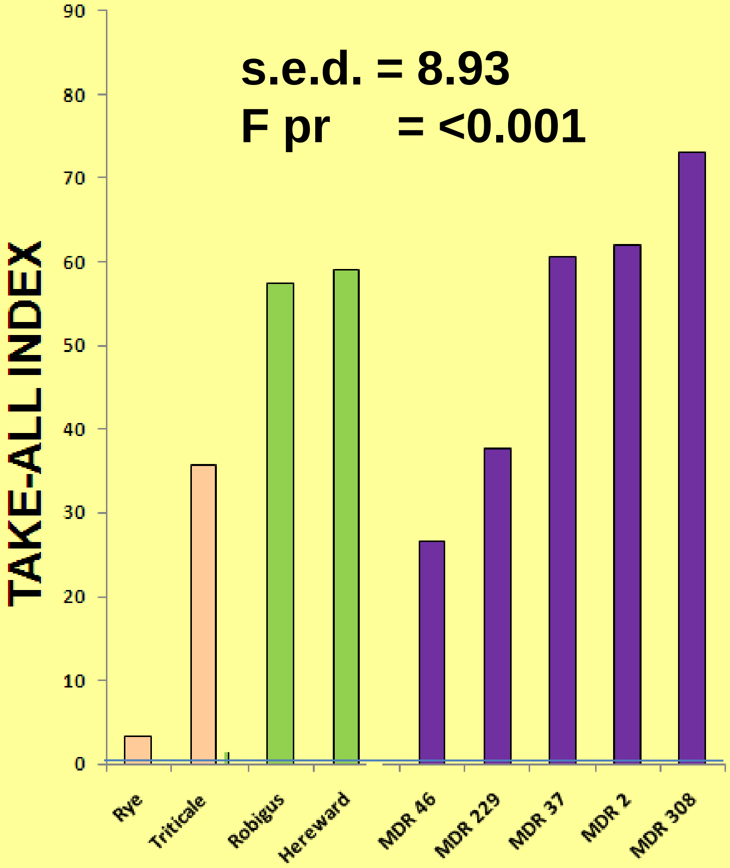
Sexual gene transfer

Gill *et al.* (2004) *Genetics* 168: 1087–1096

Diploid wheat field experiment 2008



Diploid *T. monococcum* - Field experiment 2009

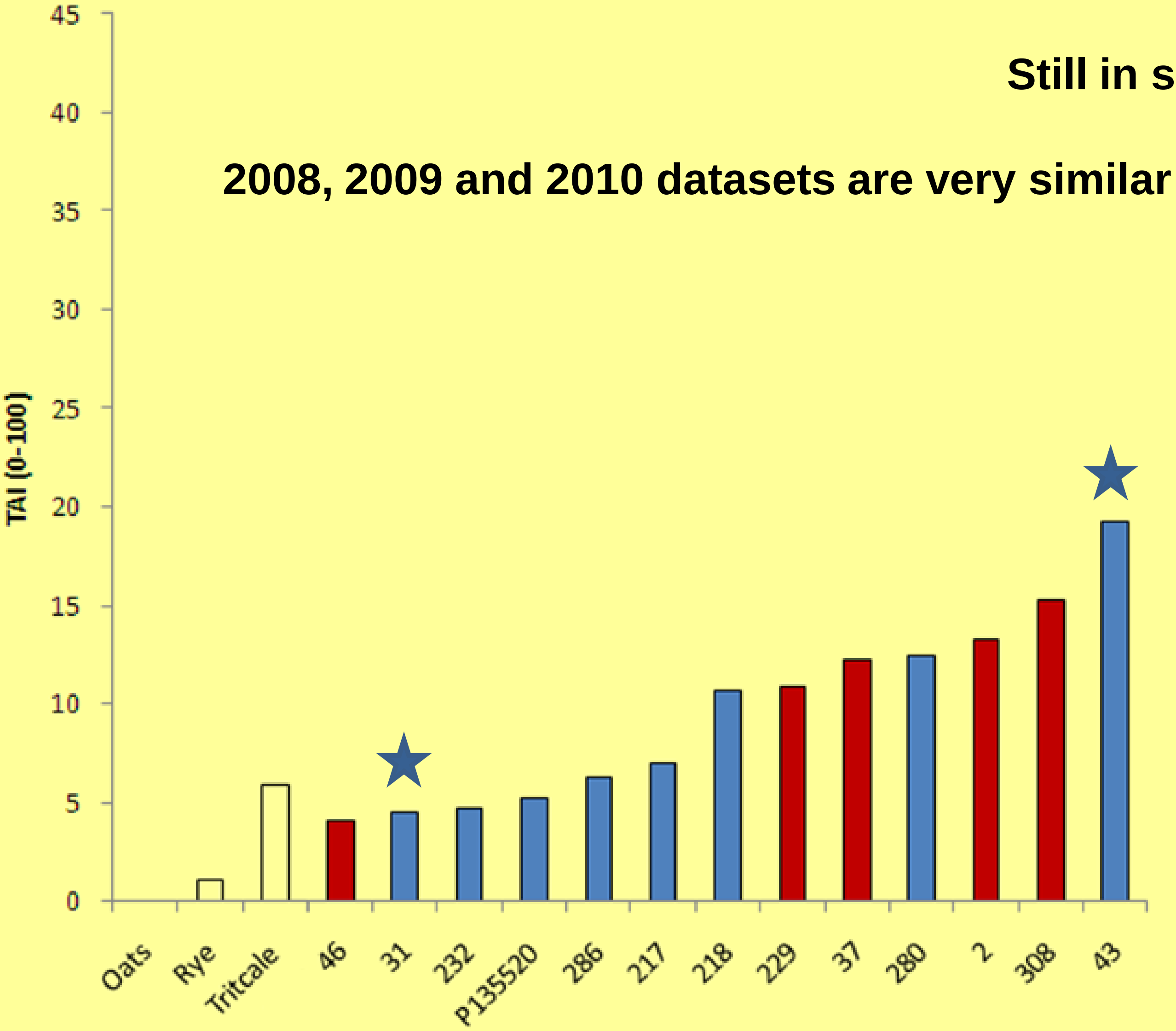


s.e.d. = 8.93
F pr = <0.001

MDR 308 is DV92 (Dubcovsky)

10 replica plots / line

Diploid wheat field experiment 2010



Still in stats

2008, 2009 and 2010 datasets are very similar

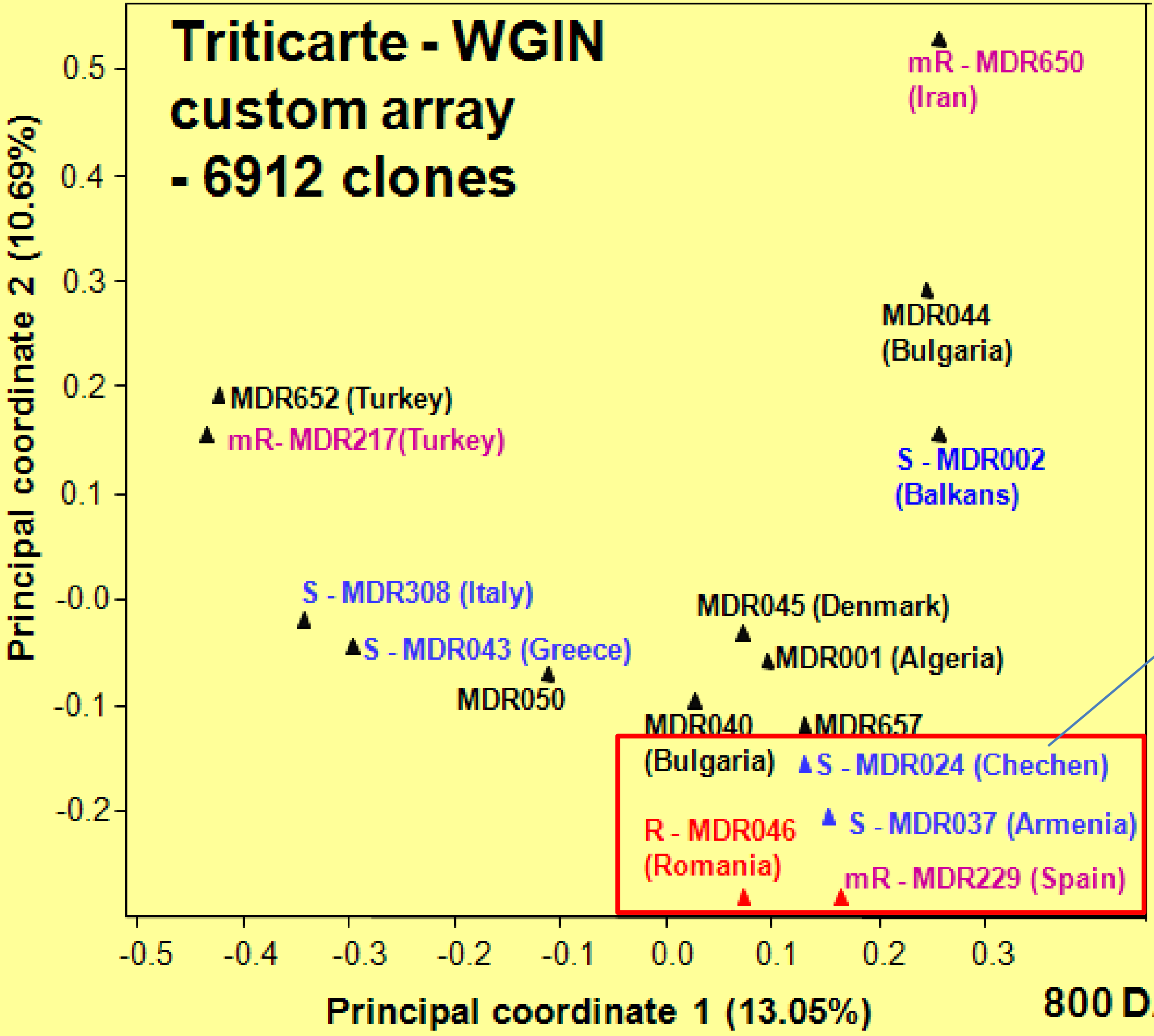
10 replica plots / line

Diploid Field experiments 2009 - 2011

2009	2010		2011	
37	31	280	31	280
229	46	286	46	286
2	217	P135520	217	P135520
308	218	2	218	2
46	229	308	229	308
	232	37	232	37

Sown 22nd October 2010 - Claycroft field 3rd wheat

DArT marker and PCA analysis of *T. monococcum* accessions



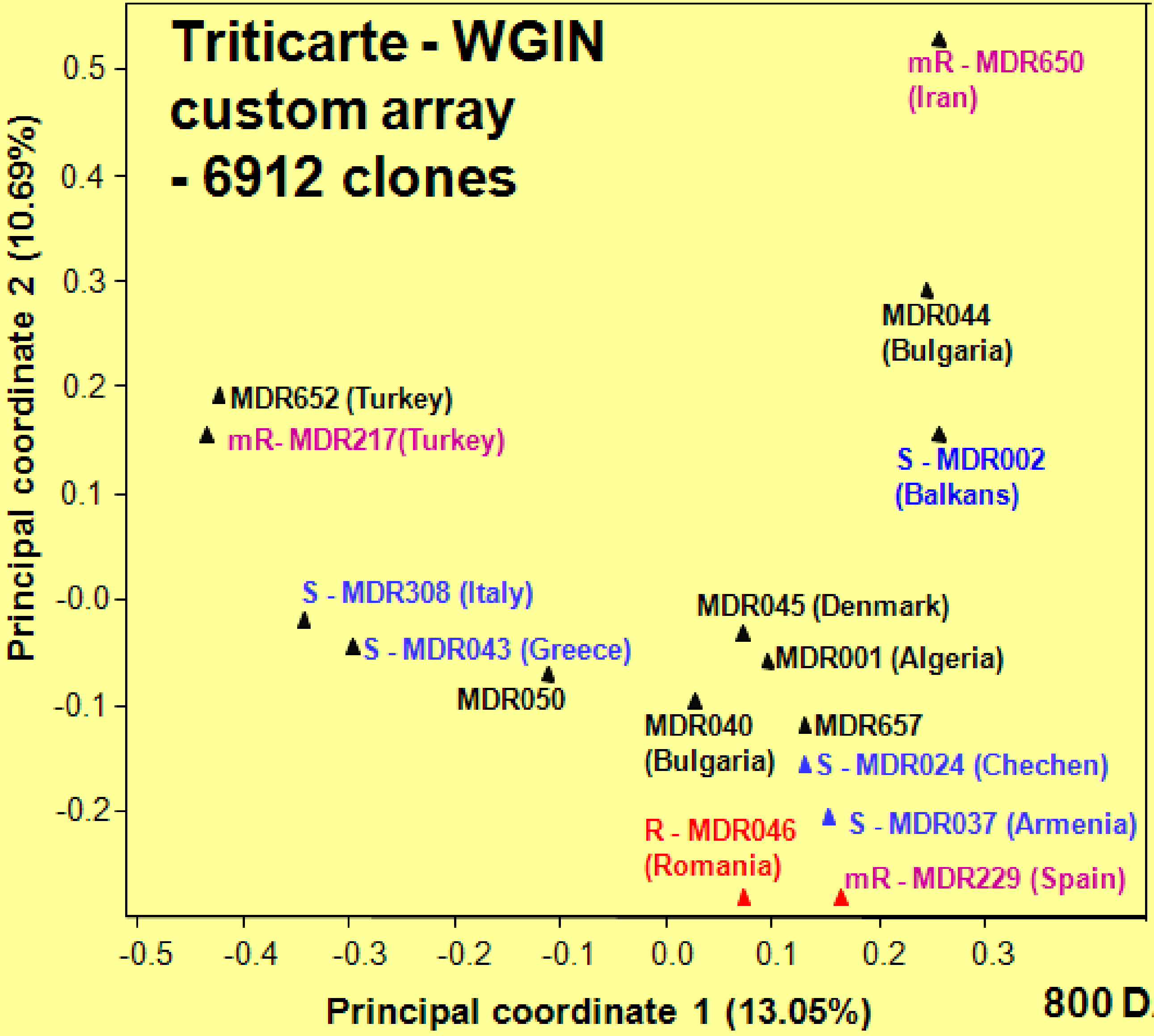
Triticarte - WGIN custom array - 6912 clones

One Chr is enriched for DArT markers in both *R* lines

800 DArT markers
297 mapped in *Tm*

Hai-Chun Jing, unpublished

DArT marker and PCA analysis of *T. monococcum* accessions



Not yet in DArT analysis

MDR218

MDR232

MDR280

MDR286

MDR031

+

MDR049 (insect)

800 DArT markers
297 mapped in *Tm*

Hai-Chun Jing, unpublished

T. monococcum - Glasshouse crosses

2008

MDR037 x **MDR046** →
MDR037 x **MDR229** →

2009

F_2

2010

F_3

~ 120 lines
SSD for
each pop^{n}
(resown)

→

2011

Harvest F_4
Mid Feb

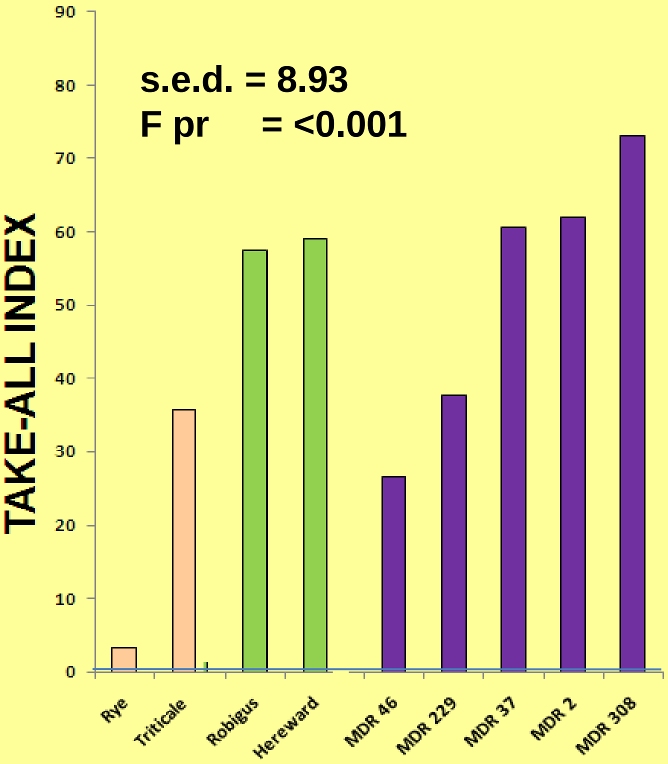
→

F_5

↓

(~90% homozygosity)

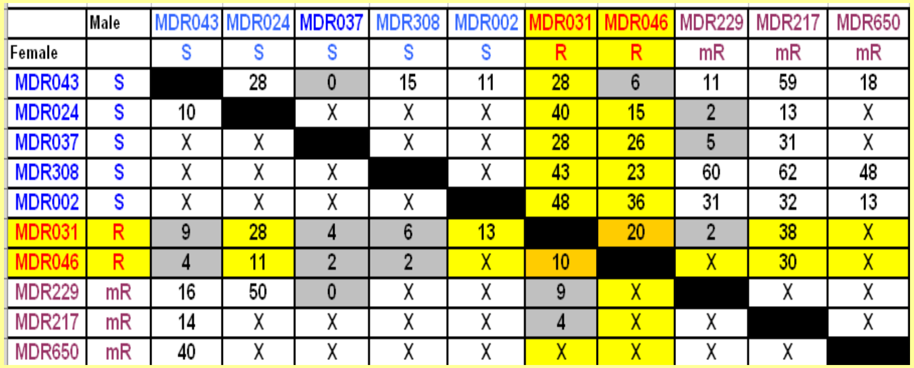
Take-all pot test
(~12 seed / line)



s.e.d. = 8.93
F pr = <0.001

T. monococcum - Glasshouse crosses

2009 - 2010



	Male	MDR043	MDR024	MDR037	MDR308	MDR002	MDR031	MDR046	MDR229	MDR217	MDR650
Female		S	S	S	S	S	R	R	mR	mR	mR
MDR043	S		28	0	15	11	28	6	11	59	18
MDR024	S	10		X	X	X	40	15	2	13	X
MDR037	S	X	X		X	X	28	26	5	31	X
MDR308	S	X	X	X		X	43	23	60	62	48
MDR002	S	X	X	X	X		48	36	31	32	13
MDR031	R	9	28	4	6	13		20	2	38	X
MDR046	R	4	11	2	2	X	10		X	30	X
MDR229	mR	16	50	0	X	X	9	X		X	X
MDR217	mR	14	X	X	X	X	4	X	X		X
MDR650	mR	40	X	X	X	X	X	X	X	X	

▨ < 10 grain X = not done

2010

Sown many of the F_1s

- seed harvested Feb- April 2011

2011

More reciprocal crosses

Main focus

R / mR – MDR031, MDR046, MDR 229, MDR650

S – MDR037, MDR 043, MDR308

Generating F_1 populations (~ 60 seed per cross)

To test for additive / synergistic effects on resistance (*R* gene pyramiding)

To determine the phenotype of resistance in a heterozygous state (semi-dominance)

Differences in crossing potential of the *Tm* lines

Typical results – 1 to 4 F_1 grain per ear crossed (pollinations)

cross	female	male	pollinations	assessed	grains
A	31	46	23	22	**20**
B	46	31	22	19	**28**
K	31	2	2	2	**11**

Line 229 exhibits higher fertility

20	650	229	4	4	**16**
H	31	229	4	4	**15**
11	229	37	2	2	**22**
13	229	308	3	3	**29**

Talk Outline

- Hexaploid wheat – Watkins / Gediflux collections
  Diploid wheat

  - field evaluation to identify potentially resistance genotypes

- Diploid wheat
  - mapping populations
  - **introgression to *T. aestivum***

- Hexaploid wheat – inoculum build-up in 1st wheats

  - **results so far / current activities**

T. monococcum introgression to *T. aestivum*

Hexaploid genotypes

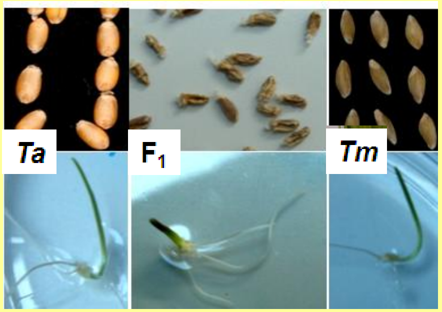
Avalon
Cadenza
Xi19
Chinese Spring

Various *Tm* accessions

x

13 days post pollination

Seed set



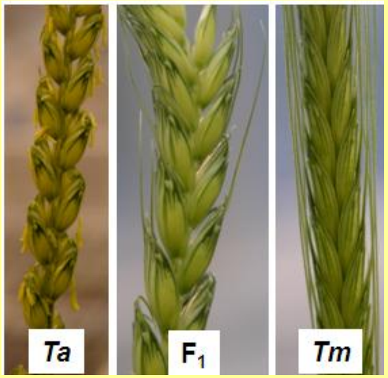
Embryo rescue

28 plants

4 weeks

Vernalisation

High quality glasshouse

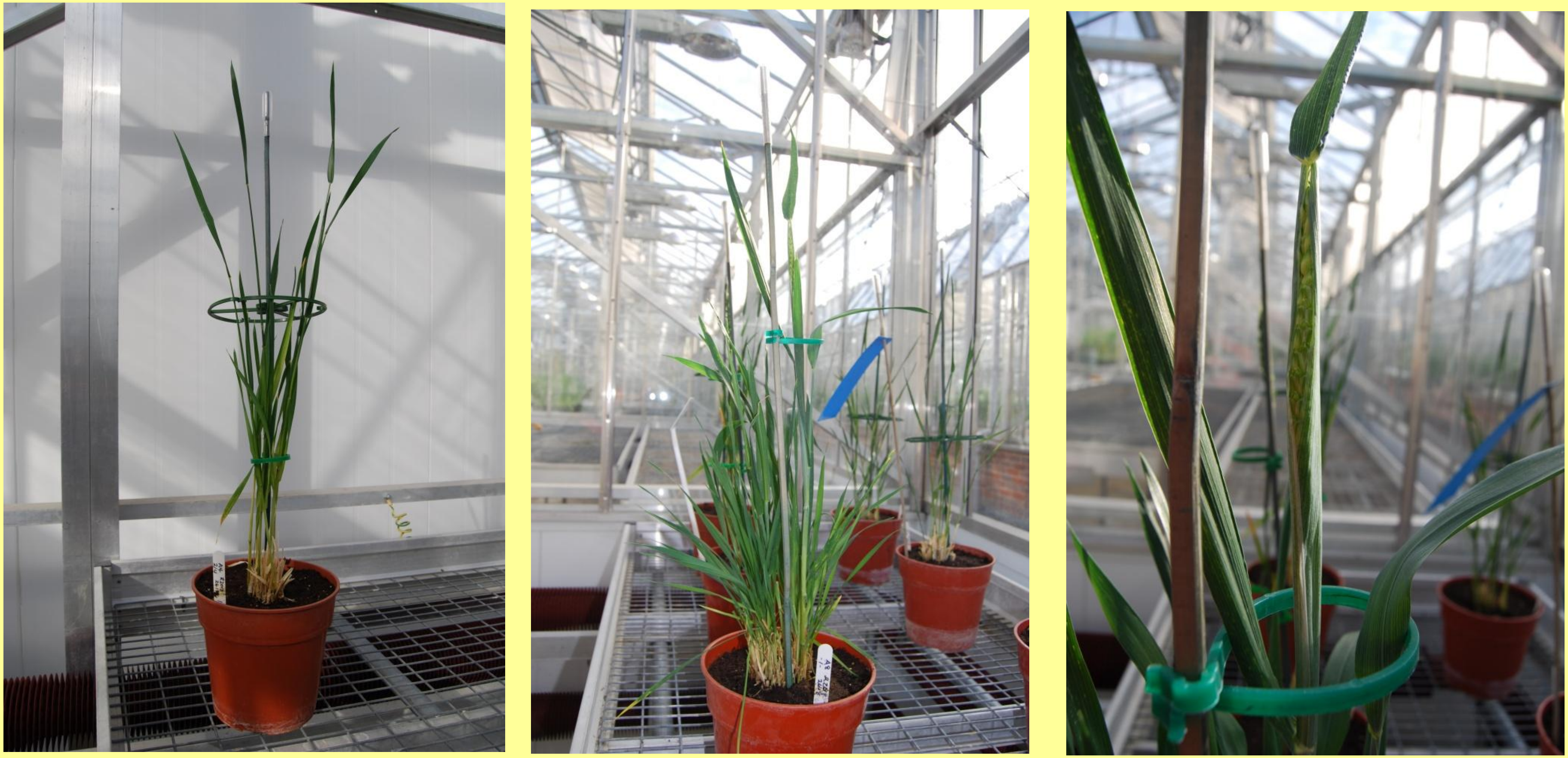


Minimal fertile ears

8 weeks vernalisation - 12 plants

F_1 *Ta* x *Tm* plants prior to going back into vernalisation

March 2010



T. monococcum introgression to *T. aestivum*

Outcome

One cross Avalon x MDR037

~200 F_2 seed of varying sizes

Not very effective use of time and resources

T. monococcum introgression to *T. aestivum*

New strategies – emerging

1. Ian King (University of Nottinghham)
New *T. aestivum* sources

Paragon	**- *ph1* mutant and wild-type**
Chinese Spring	**- *ph1* mutant and wild-type**

2. Martha Molnar Lang - cereal cytogenetist at Martonvasar, Hungary

3. Literature search for *T. monococcum* introgression lines made by other groups

EUPHYTICA
Volume 176, Number 2, 213-222, DOI: 10.1007/s10681-010-0227-7

Molecular mapping of cereal cyst nematode resistance in *Triticum monococcum* L. and its transfer to the genetic background of cultivated wheat

Kuldeep Singh, Parveen Chhuneja, Inderjit Singh, S. K. Sharma, Tosh Garg, Monika Garg, Beat Keller and Harcharan S. Dhaliwal

Abstract

Triticum monococcum, the diploid A genome species, harbours enormous variability for resistance to biotic stresses. A spring type *T. monococcum* acc. 14087 was found to be resistant to *Heterodera avenae* (cereal cyst nematode, CCN). A recombinant inbred line population (RIL) developed by crossing this accession with a CCN susceptible *T. boeoticum* acc. 5088 was used for studying the inheritance and map location of the CCN resistance. Based on composite interval mapping two QTL, one each on chromosome 1AS and 2AS, were detected. The QTL on 1A, designated as *Qcre.pau-1A*, appeared to be a major gene with 26% contribution to the overall phenotypic variance whereas the QTL on 2A designated as *Qcre.pau-2A* contributed 13% to total phenotypic variation. *Qcre.pau-1A* is novel, being the only CCN resistance gene mapped in any 'A' genome species and none of the other known genes have been mapped on chromosome 1A. The QTL *Qcre.pau-2A* might be allelic to *Cre5*, a CCN resistance gene transferred from *Ae. ventricosa* and mapped on 2AS. The *Qcre.pau-1A* was transferred to cultivated wheat using *T. durum* cv. PBW114 as the bridging species. Selected CCN resistant F_8 lines showed introgression for the molecular markers identified to be linked with CCN resistance locus *Qcre.pau*-1A. Thus, this gene alone could impart complete resistance against CCN. These introgression lines can be used for marker-assisted transfer of *Qcre.pau-1A* to elite wheat cultivars.

Objective 10 - Talk Outline

- **Hexaploid wheat – Watkins / Gediflux collections**
  Diploid wheat

  - field evaluation to identify potentially resistance genotypes

- **Diploid wheat**
  - **mapping populations**
  - **introgression to *T. aestivum***

- **Hexaploid wheat – inoculum build-up in 1st wheats –**

Result : 2010 low inoculum build-up year (rep1 diversity)
Pot tests still in progress

Many thanks to

RRes Farm staff

Richard Gutteridge
Vanessa McMillan (HGCA-BBSRC)

Kostya Kanyuka
Wing-Sham Lee
Mike H-K
Hai-Chun Jing
Steve Freeman (WGIN casual)
Elke Anzinger

Summer students
Nicola Phillips (HGCA)
Joseph Whittaker (BBSRC)
Marcin Czaban (WGIN)
James Bruce (HGCA-BBSRC)

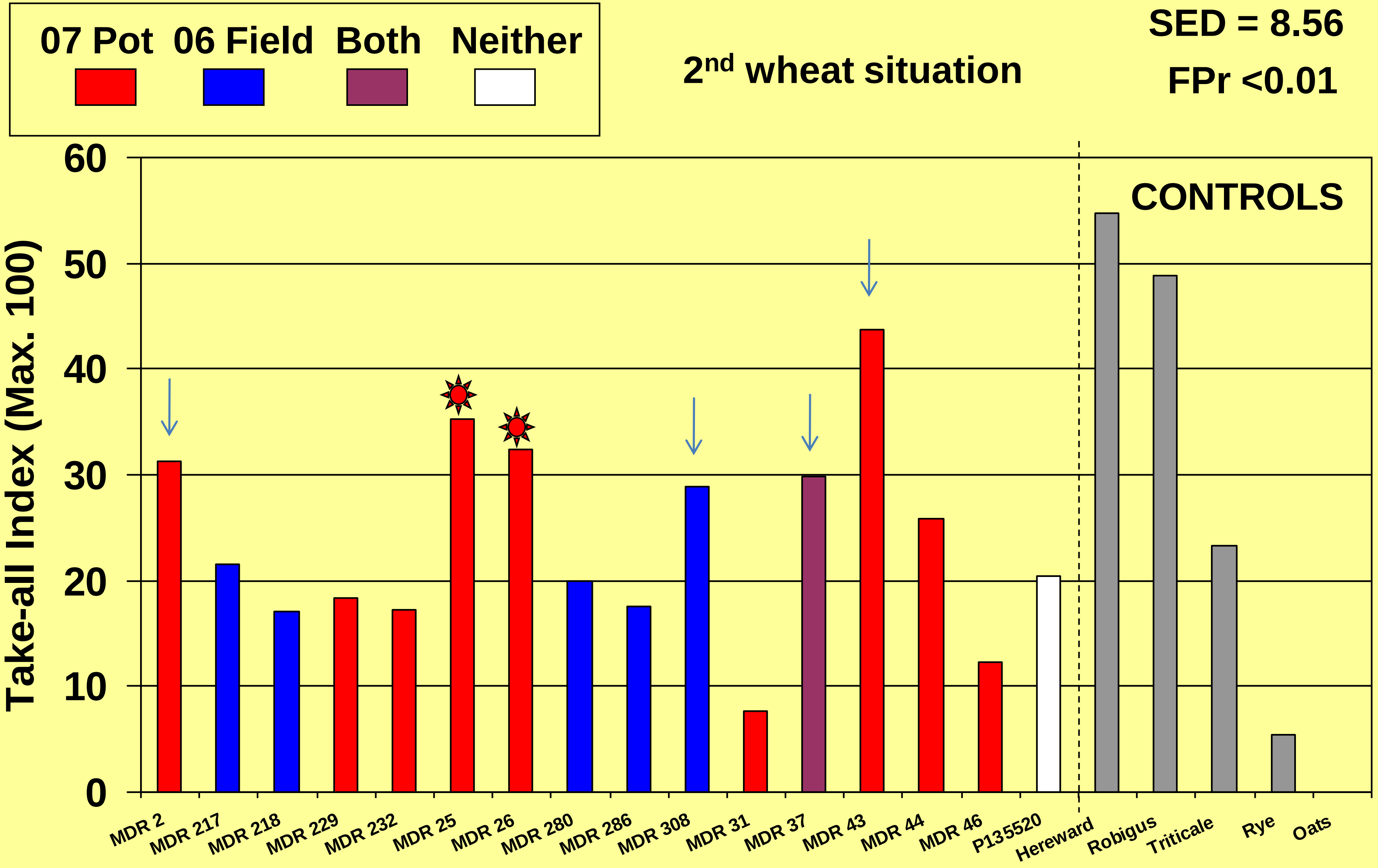
New look A C mapping population

- **205** ‘original’ lines (JIC) – lots of seed
- **467** new lines (Rothamsted) – seed for small pot experiments is already available; larger seed quantities will be available for field trials from late summer 2011
- **115 (98 + 17)** additional new lines (Rothamsted) – seed for small pot experiments and for field trials will be available from late summer 2011 and late summer 2012, respectively

Total = **787**

The A x C cross was originally selected by Steve Parker (CSL), late Tony Worland (JIC) and Darren Lovell (LARS-RRes) for studies of canopy architecture traits in collaboration with ADAS and the University of Nottingham

Field experiment 2008



2nd wheat situation

SED = 8.56

FPr <0.01

5 rep exp but 10 reps MDR 37, MDR 46 and MDR 229

Objective 8 – Nitrogen update

M J Hawkesford
WGIN Management Meeting
16th February 2011

Objectives

- Define important NUE traits
- Identify and evaluate diversity
- Determine mechanisms
- Provide leads for markers and genes
- Examine trait stability over multiple years

Diversity and mapping population trials

- To date:
  - Diversity since 2004 (7 completed)
  - 2004-07 published (Eur J Agric (2010) 33, 1-11)
  - Avalon x Cadenza (**2007**, 2008 (x2), 2009, **2010**) at **high**/low N
- Remaining trials
  - Diversity Trials: 2011, 12, 13
  - A x C 2011, (2012?), root screen
- 2011 Diversity (25 genotypes x 4N)
  - New varieties
  - Core set
  - New traits
- 2011 Avalon x Cadenza screening
  - High N (200 kg/ha)
  - New traits

diversity

Core set: long term trends and stability

New varieties for new traits (e.g. protein content, staygreen):
    2010: Marksman, Gallant, Oakley (Chablis)
    2011: Stigg, Crusoe

Inclusion (6 varieties) as part of BBSRC-IPA on quality-yield relationships (GPD)

Detailed analysis of selected A x C lines (since 2009)

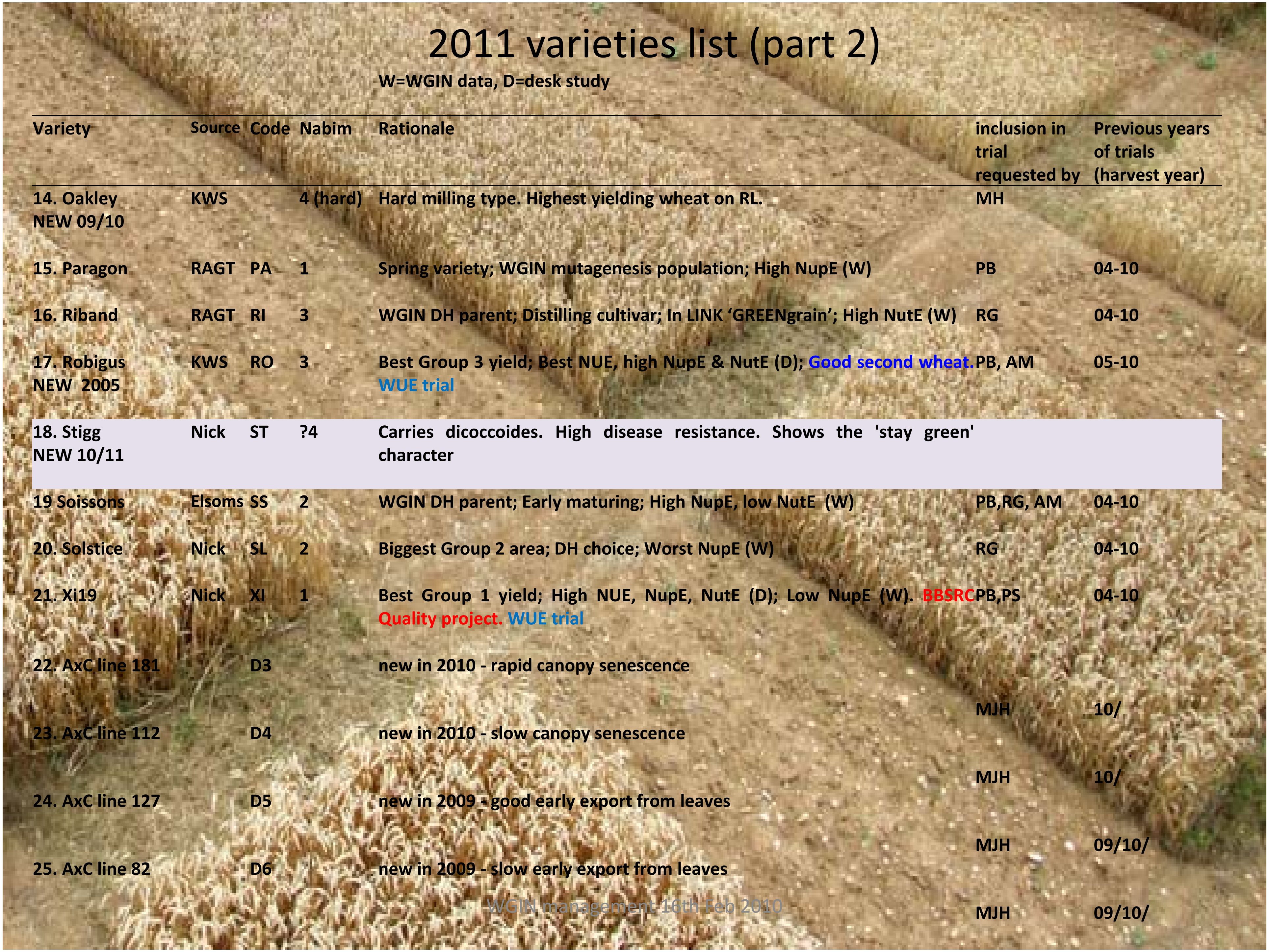
Examine root gene expression (in field) and link to NUpE and N-inputs (2011)

Take-All

2011 varieties list (part 1)

Wheat varieties for WGIN-NUE 2010/11 W=WGIN data, D=desk study

Variety	Source	Code	Nabim	Rationale	inclusion in trial requested by	Previous years of trials (harvest year)
1. Avalon	Av	AV	1	WGIN DH parent; Low NupE & NutE (D)	PB, RG, MJH	05-10
2. Cadenza	Ca	CA	2	WGIN DH parent; Best NupE (W)	PB, RG, MJH	04-10
3. Chablis NEW 09/10	KWS		2	SPRING variety (previous grown in 2004 trial) as very N-responsive variety	MH	only in 04 and 10
4. Claire NEW 2005	Nick	CL	3	Biggest area on RL; WGIN DH parent; Good second wheat	PB,PS	05-10
5. Cordiale NEW 2006	KWS	CO	2	Good second wheat. BBSRC Quality project	RG	06-10
6. Crusoe NEW 10/11	Nick	CR	2	Carries dicoccoides. Shows the 'stay green' character		
7. Gallant NEW 09/10	Syn	GA	1	new claimed high yield and high protein type	MH	
8. Hereward	RAGT	HE	1	Best protein on RL; benchmark bread variety. BBSRC Quality project	PB,PS	04-10
9. Istabraq NEW 2005	Nick	IS	4	Best yield on RL; Distilling cultivar; In LINK 'GREENgrain'; Good second wheat. BBSRC Quality project. WUE trial	PB,PS	05-10
10. Malacca	KWS	MA	1	Biggest Group 1 area; DH choice; Low NupE, high NutE (W). BBSRC Quality project	PS	04-10
11. Marksman	RAGT	MK	2	new for 2009, PRS request for BBSRC Quality project	PS	only 09 and 10
12. Maris Widgeon		MW	1	Tall (rht), old cultivar	PB, AM	04-10
13. Mercia		ME	1	Low NupE & NutE (desk); Low Canopy N requirement; In IGF micro-array. WUE trial. RHT series	RG	04 and 06-10

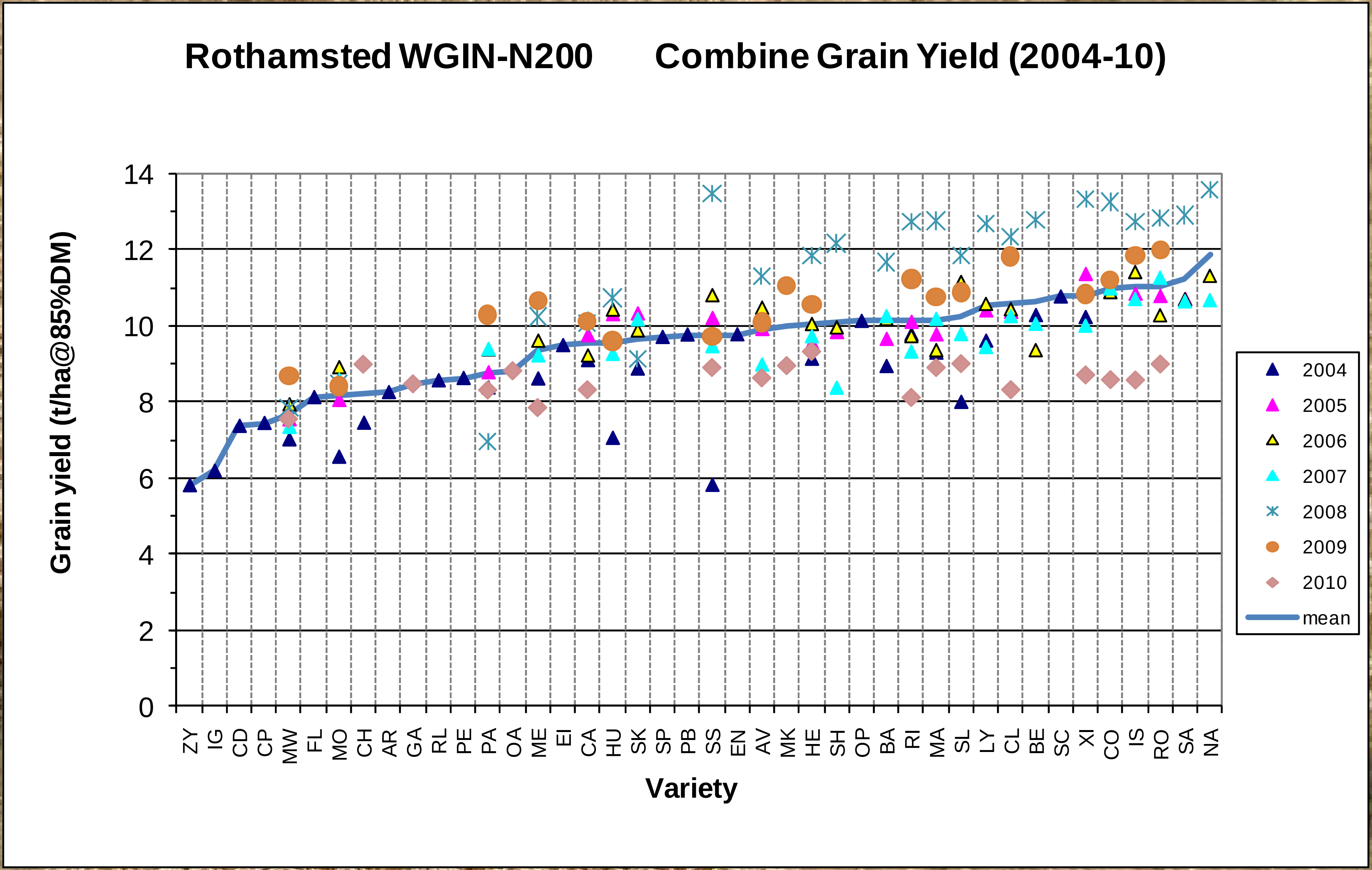


2011 varieties list (part 2)

W=WGIN data, D=desk study

Variety	Source	Code	Nabim	Rationale	inclusion in trial requested by	Previous years of trials (harvest year)
14. Oakley NEW 09/10	KWS		4 (hard)	Hard milling type. Highest yielding wheat on RL.	MH	
15. Paragon	RAGT	PA	1	Spring variety; WGIN mutagenesis population; High NupE (W)	PB	04-10
16. Riband	RAGT	RI	3	WGIN DH parent; Distilling cultivar; In LINK 'GREENgrain'; High NutE (W)	RG	04-10
17. Robigus NEW 2005	KWS	RO	3	Best Group 3 yield; Best NUE, high NupE & NutE (D); Good second wheat. WUE trial	PB, AM	05-10
18. Stigg NEW 10/11	Nick	ST	?4	Carries dicoccoides. High disease resistance. Shows the 'stay green' character		
19 Soissons	Elsoms	SS	2	WGIN DH parent; Early maturing; High NupE, low NutE (W)	PB,RG, AM	04-10
20. Solstice	Nick	SL	2	Biggest Group 2 area; DH choice; Worst NupE (W)	RG	04-10
21. Xi19	Nick	XI	1	Best Group 1 yield; High NUE, NupE, NutE (D); Low NupE (W). BBSRC Quality project. WUE trial	PB,PS	04-10
22. AxC line 181		D3		new in 2010 - rapid canopy senescence	MJH	10/
23. AxC line 112		D4		new in 2010 - slow canopy senescence	MJH	10/
24. AxC line 127		D5		new in 2009 - good early export from leaves	MJH	09/10/
25. AxC line 82		D6		new in 2009 - slow early export from leaves	MJH	09/10/

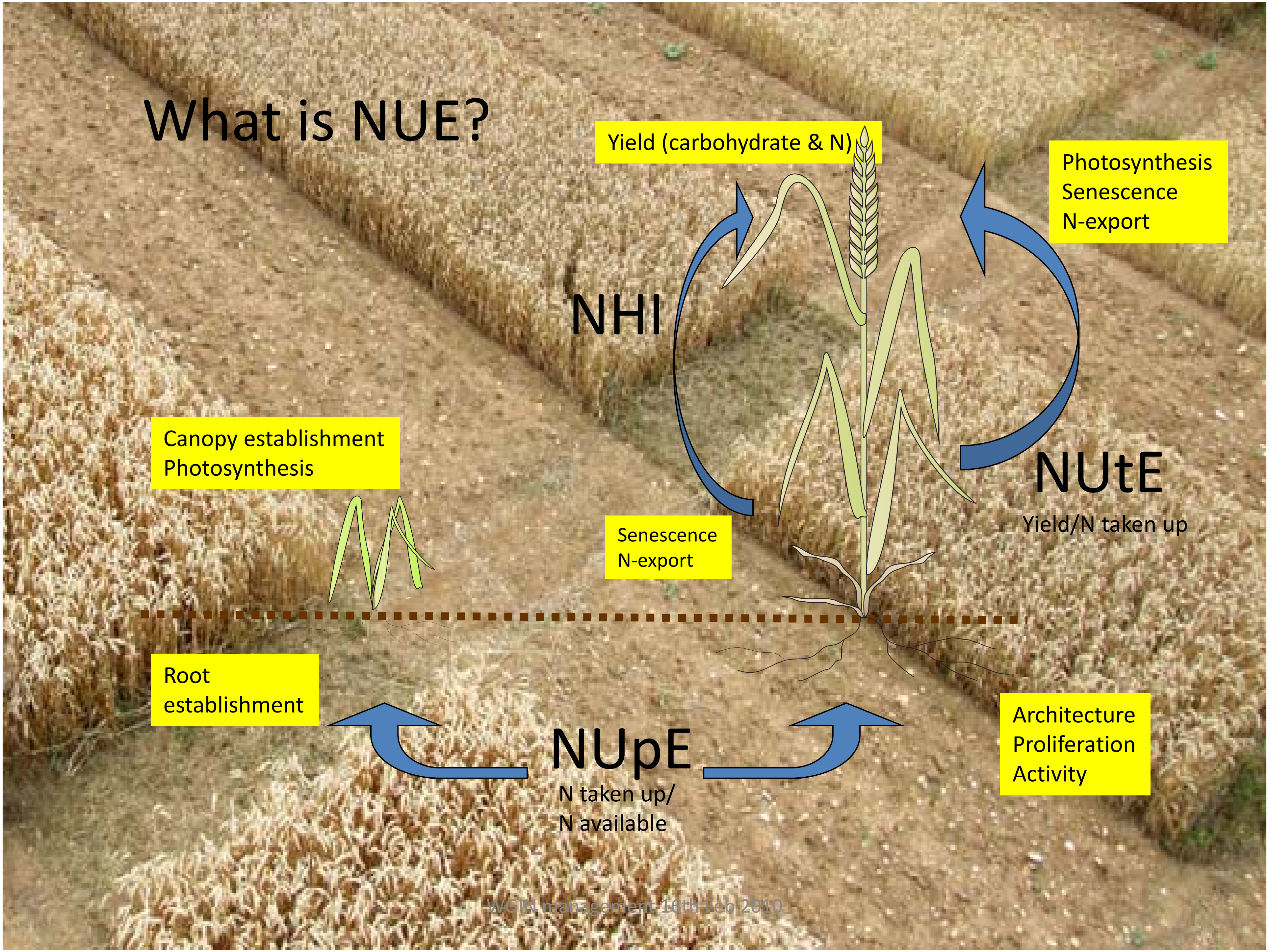
Yield summary



Avalon x Cadenza traits

- Core data (WGIN)
  - Flowering time and height
  - Yield (grain and straw) and tgw
  - Nitrogen (grain and straw)
  - NUtE, N uptake (final)
- Supplementary studies (other)
  - Leaf N and SPAD (anthesis and 21 dpa)
  - Leaf size (leaf 2)
  - Canopy longevity, reflectance (NDVI), rate of senescence
  - Early N uptake
  - Gene expression
  - Root traits
  - Grain minerals

What is NUE?



Yield (carbohydrate & N)

Photosynthesis
Senescence
N-export

NHI

NUtE

Yield/N taken up

Canopy establishment
Photosynthesis

Senescence
N-export

Root
establishment

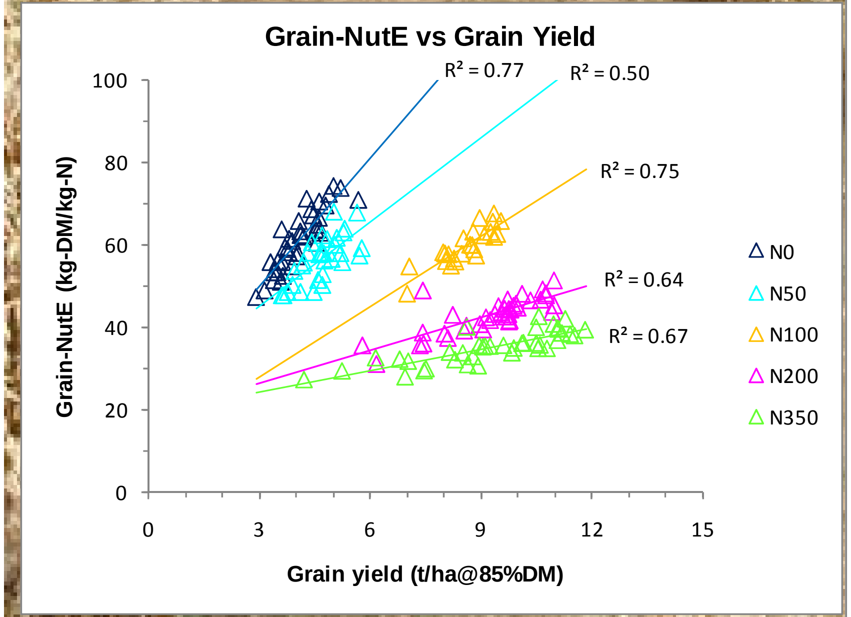
NUpE

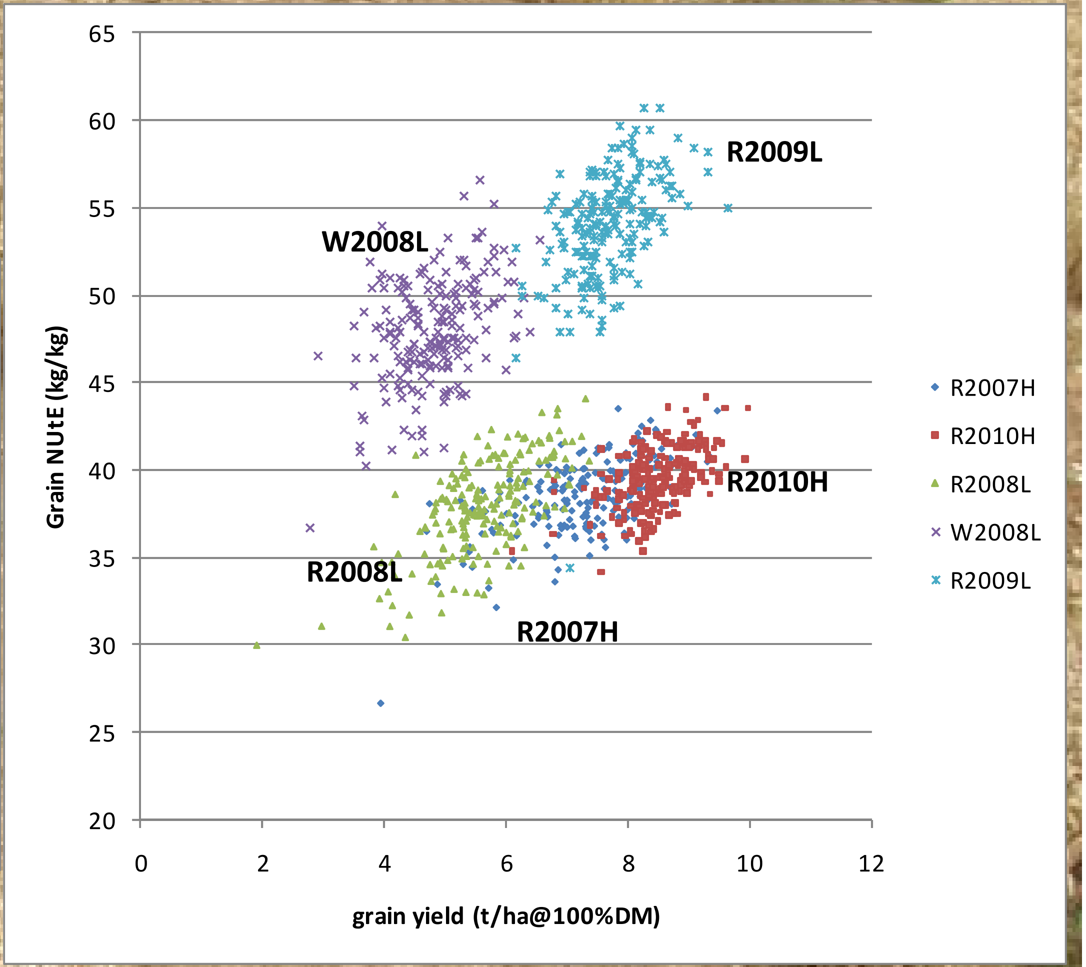
N taken up/
N available

Architecture
Proliferation
Activity

NUtE and yield

NUtE=yield/N taken up



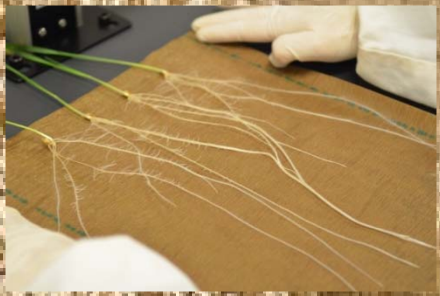


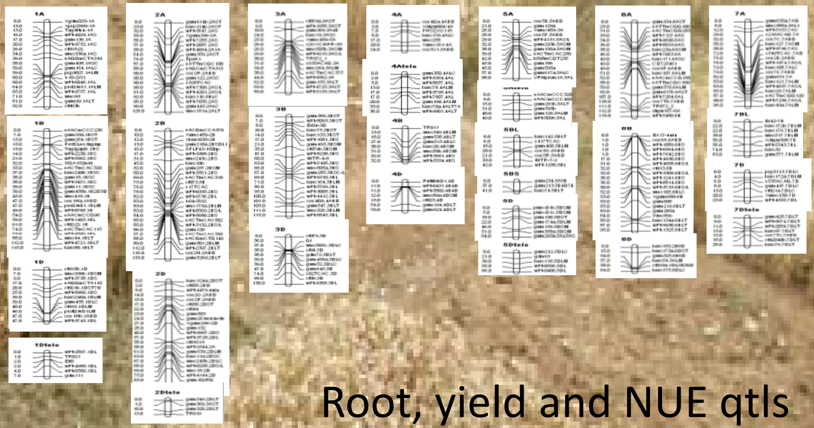
Diversity

Eur J Agric (2010) 33, 1-11

Avalon x Cadenza

Variation in root traits: mapping QTLs





Root, yield and NUE qtls

Wheat
Genetic
Improvement
Network

Thanks

defra

- RRes Farm staff
- Group and field team: Peter Barraclough, Peter Buchner, Yongfan Wan, Jonathan Howarth, Mark Durenkamp, Saroj Parmar, Janina Jones, Dan Godfrey, Emmanuelle Cabannes, Adinda Derkx, Fumie Shinmachi, Caihong Bai + many summer students

BBSRC
bioscience for the future

HGCA

ROTHAMSTED
RESEARCH

Drought tolerance

WGIN-2 SG meeting

KWS UK Ltd 16 February 2011

The University of Nottingham

John Innes Centre

Activity 9, Drought tolerance (2009-14)

Obj 1. **Identify traits for WUE and drought tolerance (DT) in elite winter wheat varieties. (*Yrs 1-2*)**

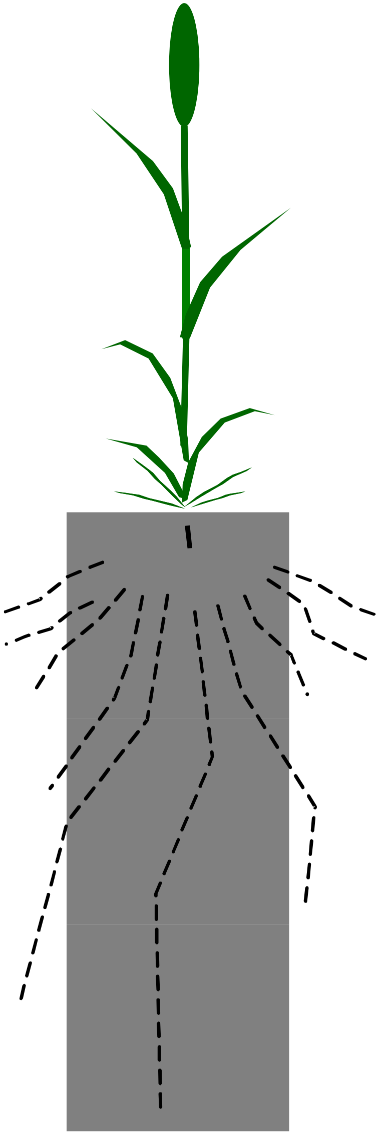
Obj 2. **Identify QTLs for WUE and DT traits using one DH pop in an elite background. (*Yrs 2-3*)**

Obj 3. **Develop one new DH pop for drought research. (*Yrs 2-4*)**

Obj 4. **Identify novel genes and alleles for WUE and DT using the AE Watkins and Gediflux collections. (*Yrs 2-4*)**

Obj 5. **Collate a diverse germplasm (cvs, advanced lines) for future association genetics studies. (*Yrs 4 -5*)**

Ideotype for high sustainable yield under drought



OPTIMIZE WUE

- High $^{13}C\ \Delta$
- Pn capacity
- Specific leaf N

MAXIMIZE HARVEST INDEX

- Stem CHO reserves
- Stay green

MAXIMIZE WATER CAPTURE

- RLD at depth
- β (distribute roots deeper)
- Specific root length

EARLINESS

- Extend stem elongation phase
- Early onset GS31

WUE trial 2009-10

Split plot design (3 reps): plot size 1.6 x 12 m

Main plot: Fully irrigated (trickle irrigation)
Unirrigated

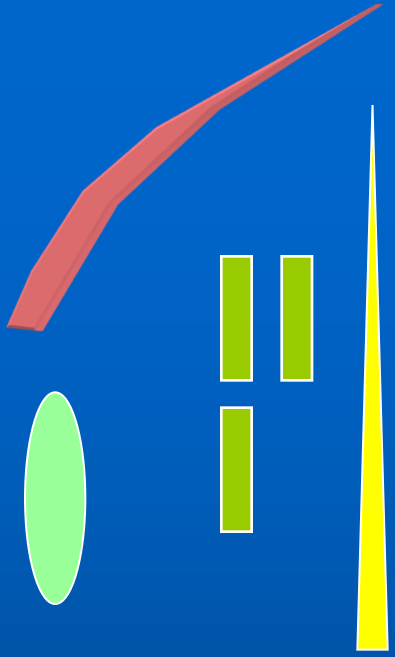
Split plot (variety):

1. Avalon *
2. Beaver
3. Cadenza *
4. Cappelle Deprez
5. Cordiale
6. Glasgow
7. Hereward *
8. Hobbit
9. Istabraq
10. M. Widgeon *
11. Oakley
12. Panorama
13. Paragon*
14. Rialto
15. Savannah
16. Soissons
17. Xi 19 *
18. Zebedee

* Common with NUE trial

Measurements

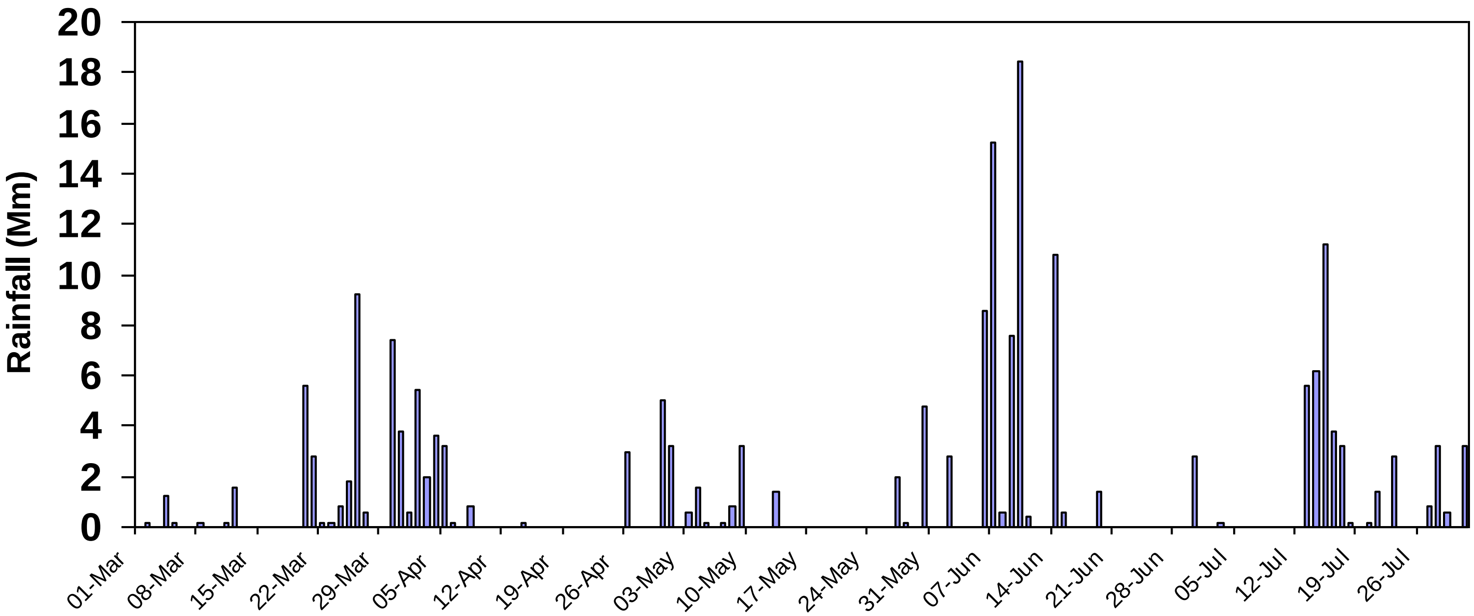
- **Combine grain yield, yield components**
- **DM & partitioning at GS31, GS61, harvest**
- **% stem WSC at GS61+10d**
- **Leaf senescence kinetics for L1, L2 and L3.**
- **Stomatal conductance/photosynthetic rate using Licor (unirrigated)**
- **Canopy temperature**
- **Water use ~ gravimetric analysis of soil cores (unirrigated, 18 varieties)**
- **^{13}C Δ grain ~ leaf WUE**
- **^{18}O Δ flag leaf ~ leaf transpiration**



Leaf gas exchange

Canopy temp.

Sutton Bonington 2010 rainfall data

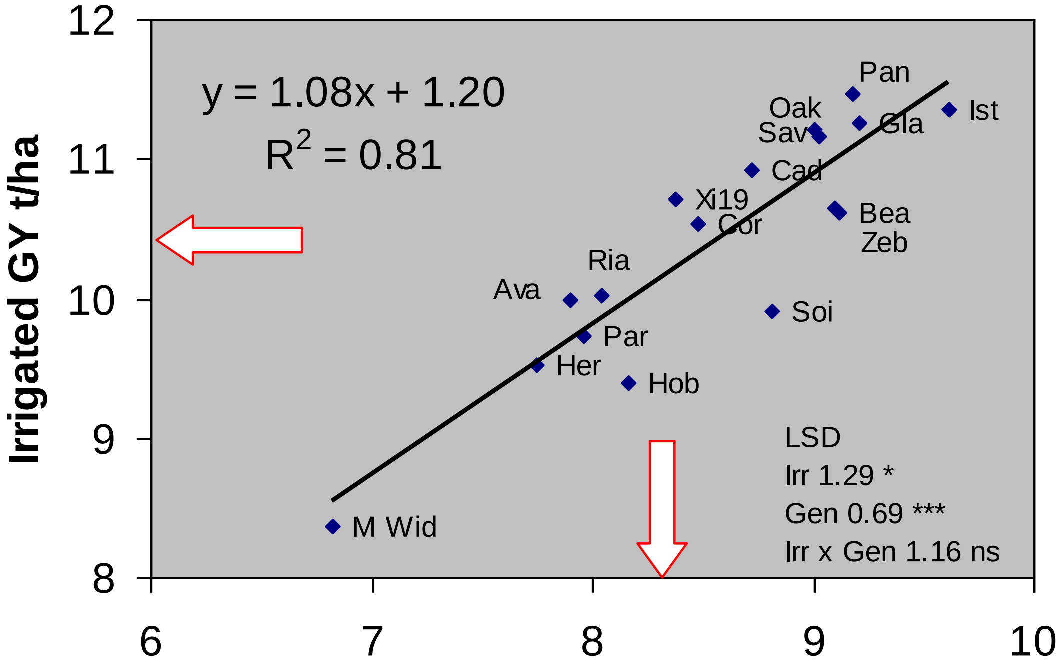


	Rainfall (mm)	
	2010	LTM 75-09
Jan	33	54.1
Feb	41.6	43.4
Mar	36	45.7
Apr	24	44.4
May	18.2	45.6
Jun	69.2	58.7
Jul	42.6	49.8

Glasgow Irrigated vs Unirrigated 19 July

Wheat
Genetic
Improvement
Network

Grain yield responses to irrigation

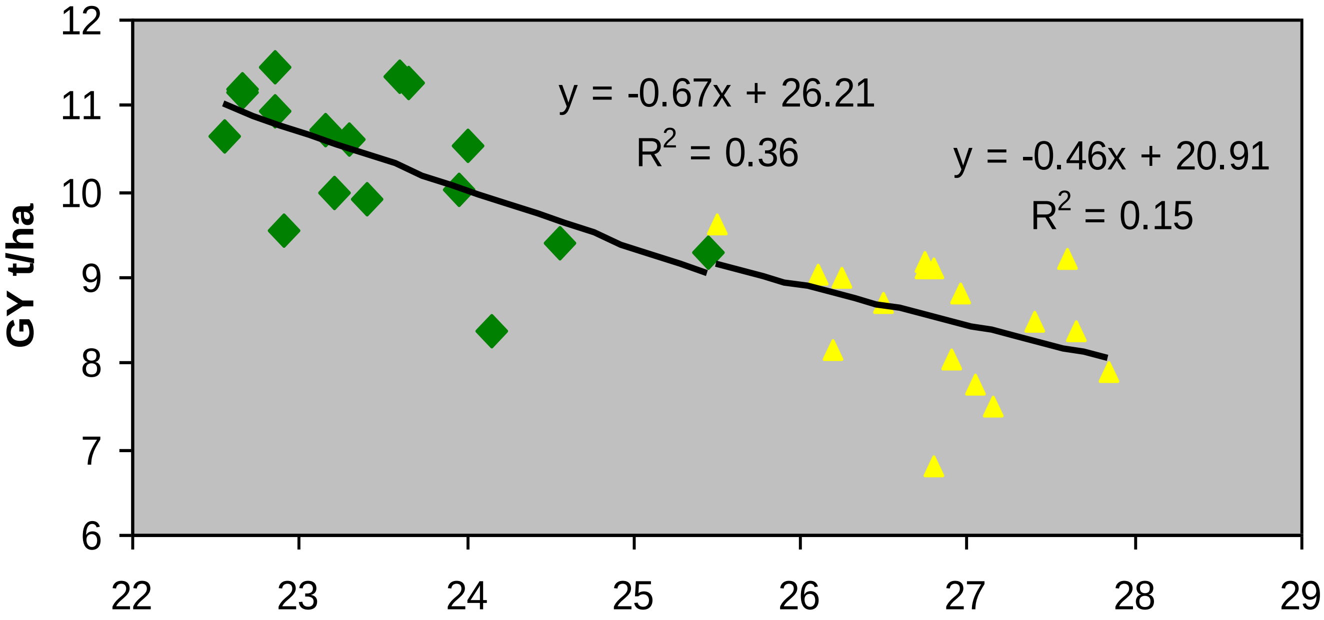


Sutton Bonington 2009-10

	Rainfall (mm)	
	2010	LTM 75-09
Jan	33	54.1
Feb	41.6	43.4
Mar	36	45.7
Apr	24	44.4
May	18.2	45.6
Jun	69.2	58.7
Jul	42.6	49.8

Glasgow Irrigated vs Unirrigated 19 July

Canopy Temperature (indicative of access to water) post-anthesis vs grain yield

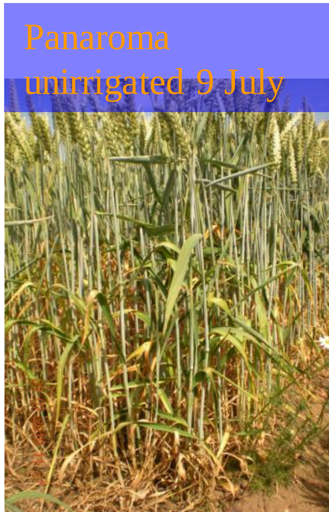


Sutton Bonington 2009-10

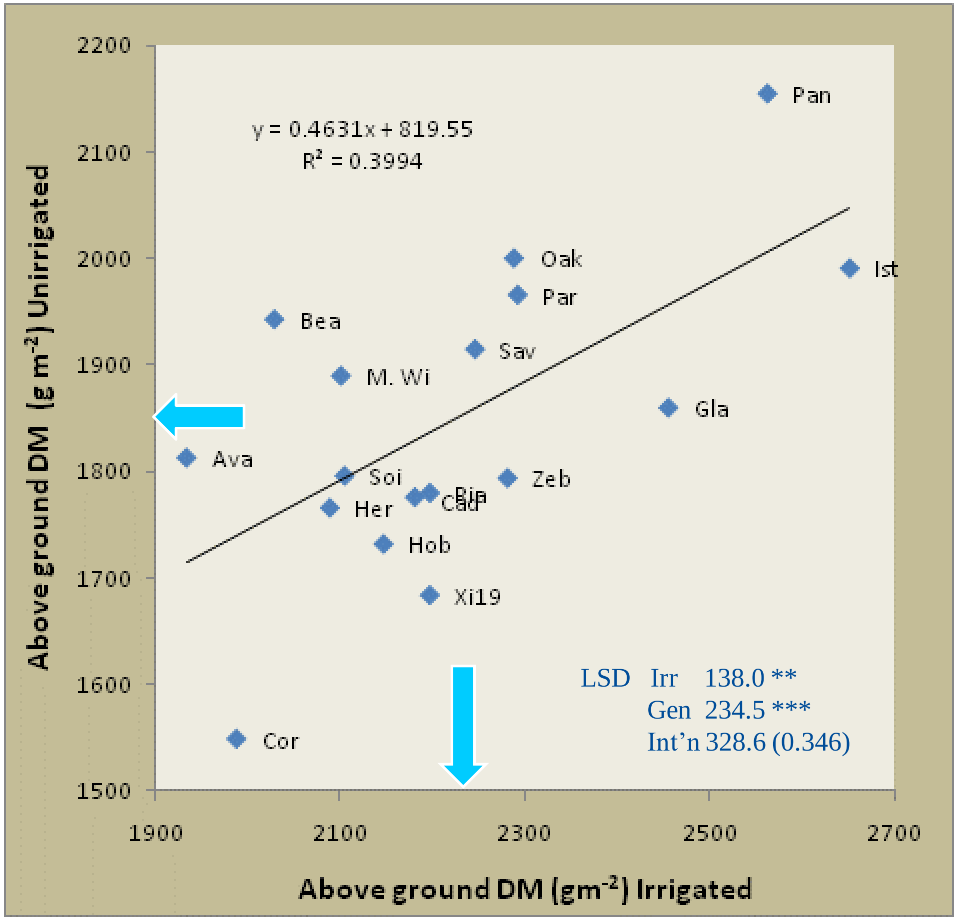
Drought tolerance index: $(Y_{Dr}/Y_{Irr}) / (\text{mean } Y_{Dr} / \text{mean } Y_{Irr})$

	R^2	Prob
Canopy T°C vs DTI	**0.16**	**0.11**
Anthesis date vs DTI	**0.04**	**0.43**
Plant height vs DTI	**0.01**	**0.81**

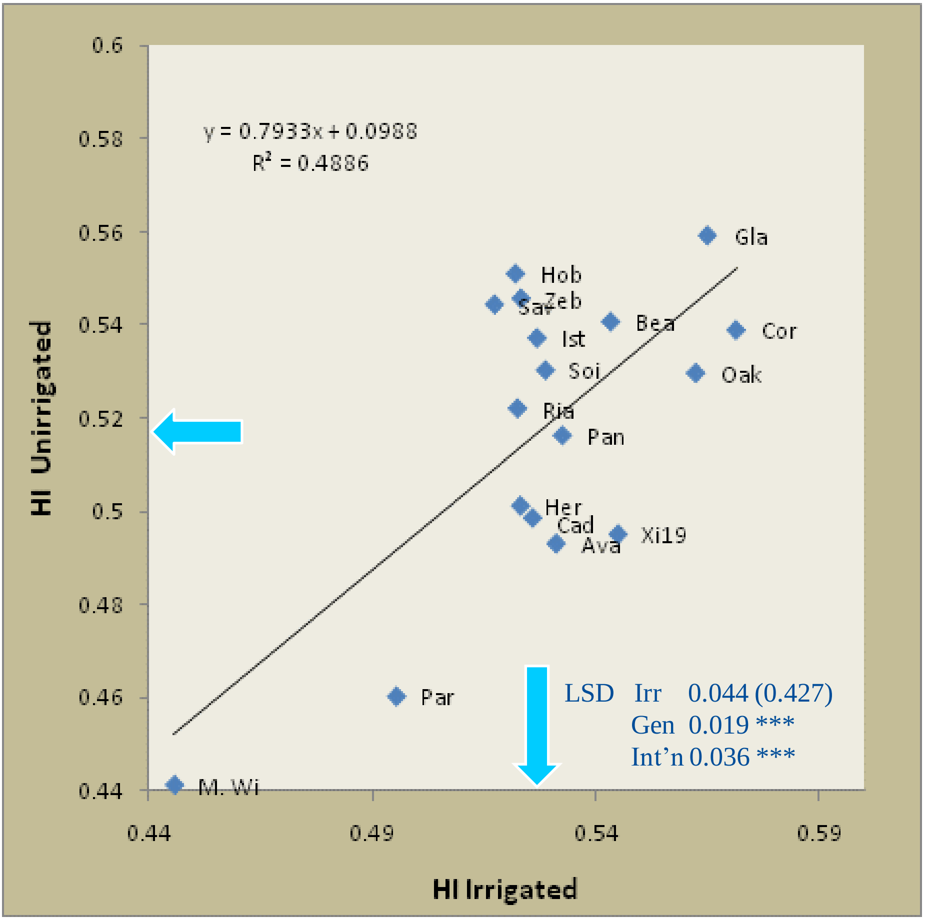

Panaroma irrigated 9 July


Panaroma unirrigated 9 July

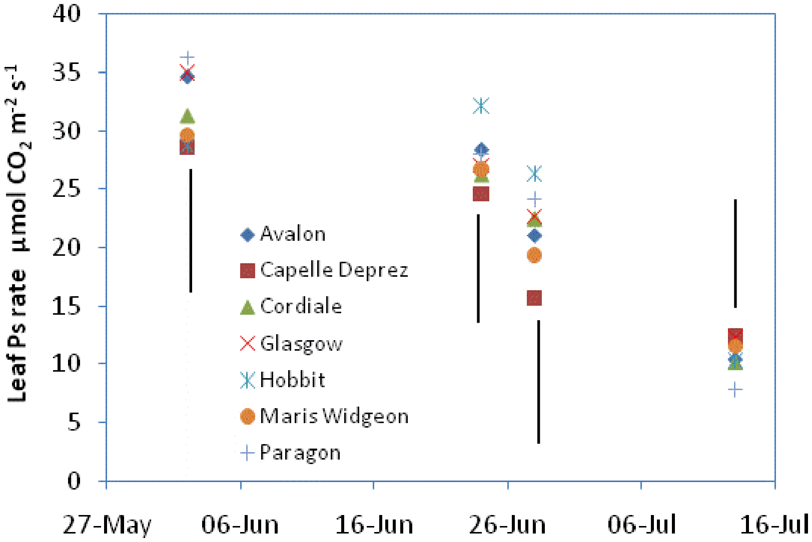
Harvest biomass



Harvest index

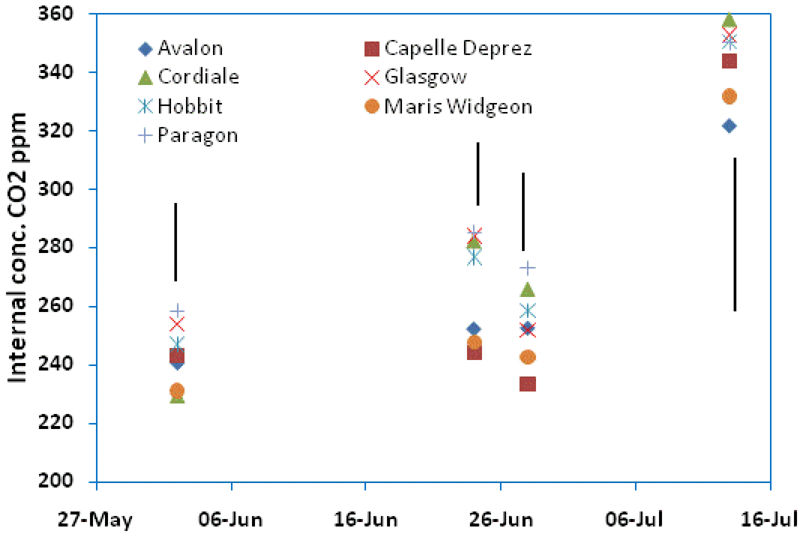


Leaf photosynthesis rate and internal conc. CO$_2$ (unirrigated trt)



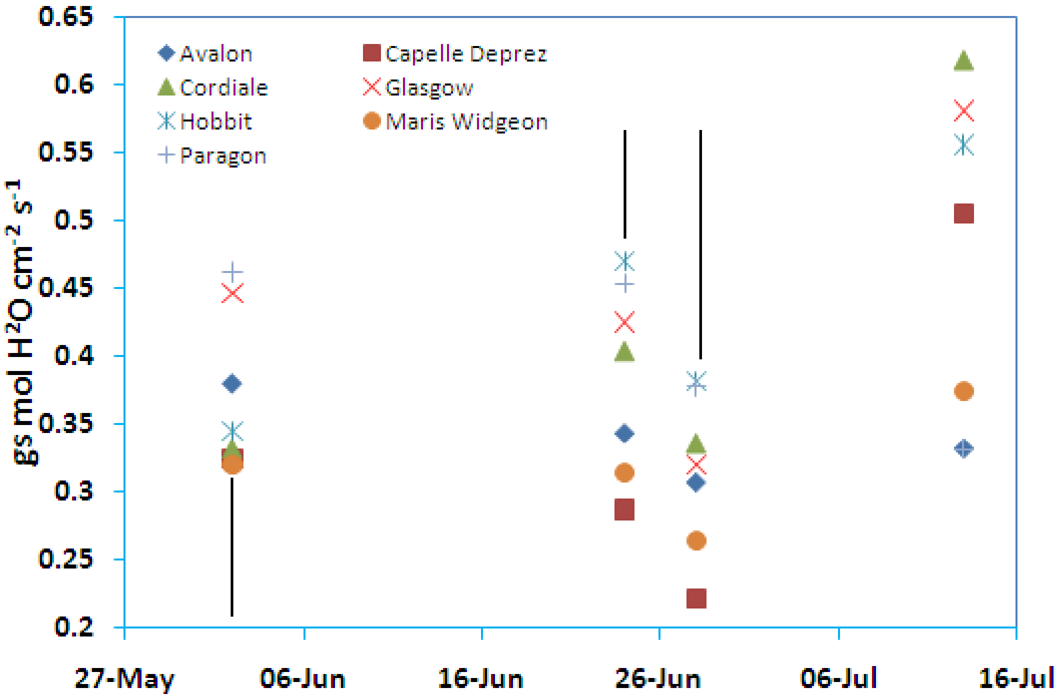
- Trend for differences in leaf ps rate: Hobbit > M. Widgeon, C. Desprez

- Sig. differences in Ci: Cordiale, Glasgow > Avalon, M. Widgeon, C. Desprez :



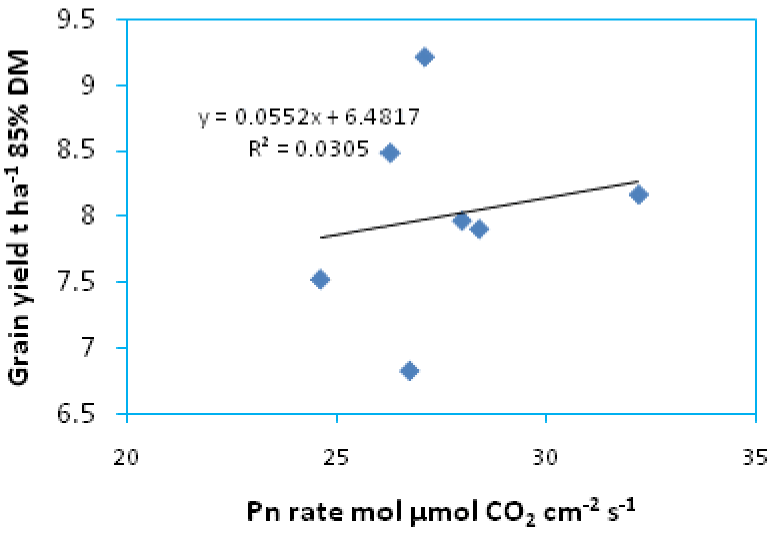
Instrumentation: Gas exchange (C assimilation) : Licor 6400

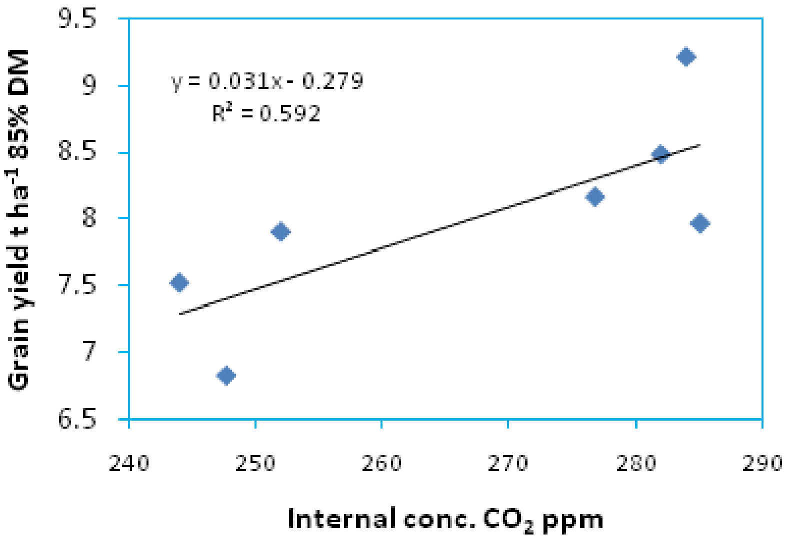
Stomatal conductance (unirrigated trt)

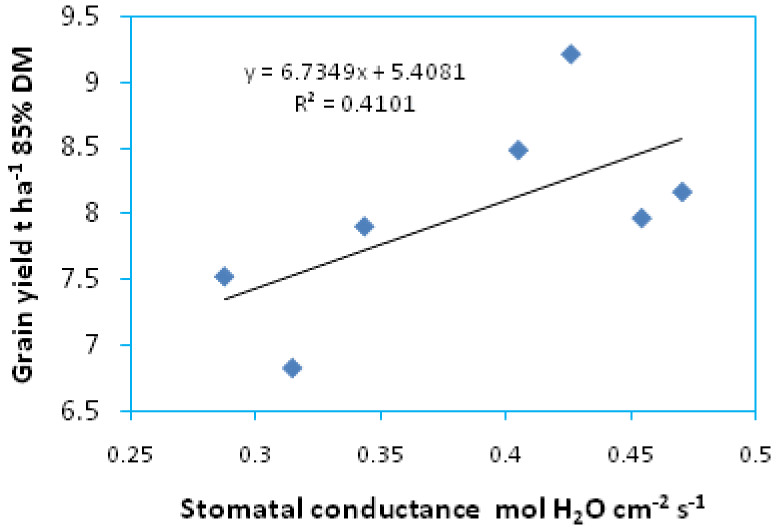


- Sig. differences in stomatal conductance: Glasgow, Hobbit, Paragon, Cordiale > M. Widgeon, C. Desprez :

Relationship between leaf activity traits (24 June) and yield



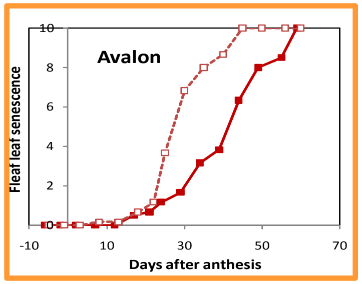


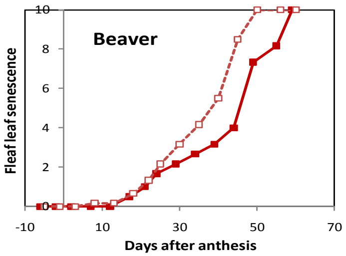


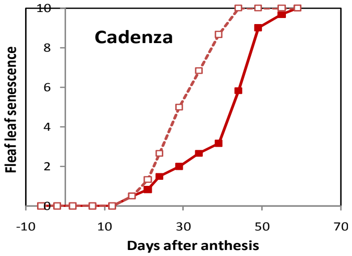
	02-Jun	24-Jun	28-Jun	13-Jul
Ps rate	0.22	0.03	0.26	0.00
Ci	0.18	0.59	0.20	0.36
Gs	0.31	0.41	0.25	0.37

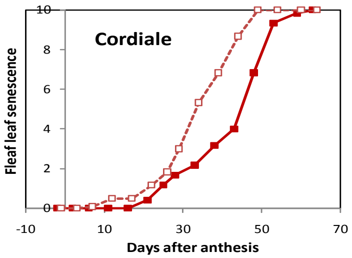
Effect of drought on gas exchange parameters (Glasgow)

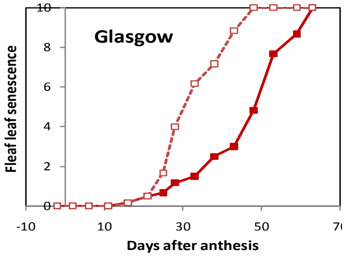
		Irr	Unirr	Sig.
Pn rate µmol cm^{-2} s^{-1}	24-Jun	30.9	27.1	$P < 0.10$
	28-Jun	32.5	22.6	***
Ci ppm	24-Jun	0.51	0.43	*
	28-Jun	0.52	0.22	***
Gs mol cm^{-2} s^{-1}	24-Jun	291.0	284.0	ns
	28-Jun	285.4	220.1	***

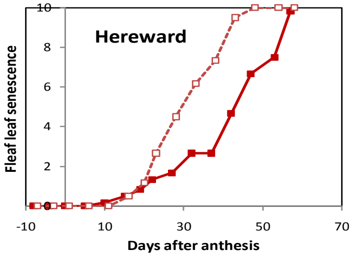


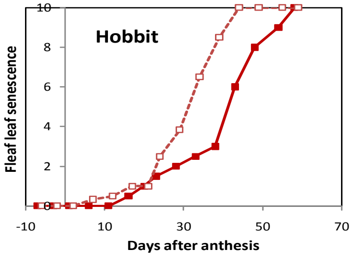


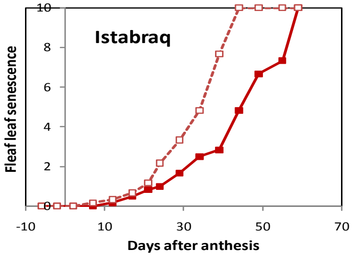


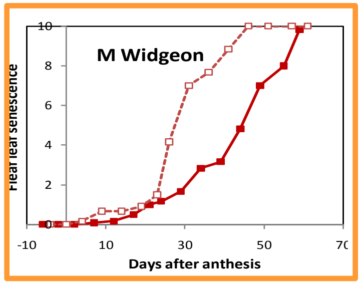


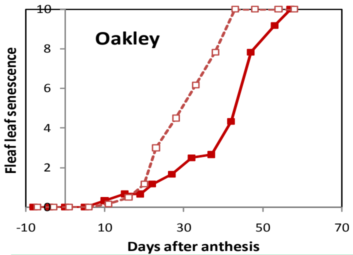


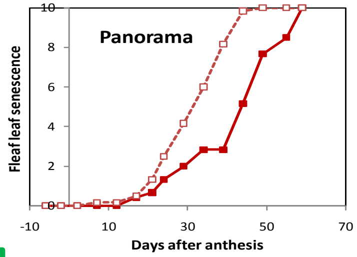


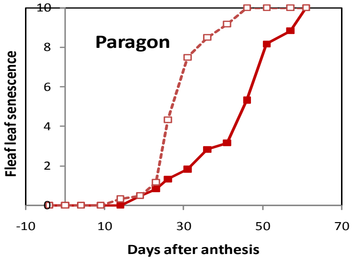


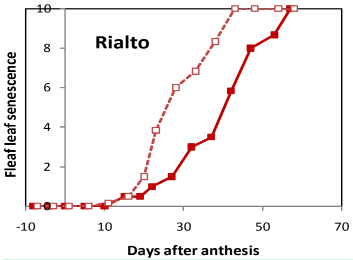


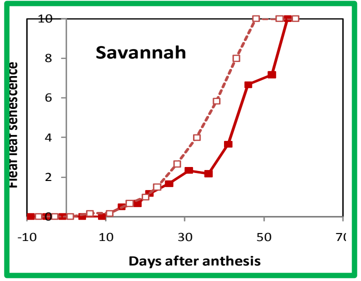


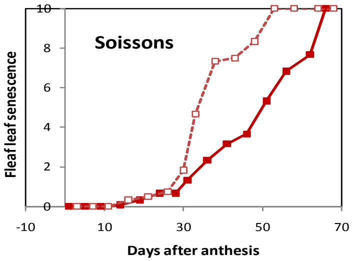


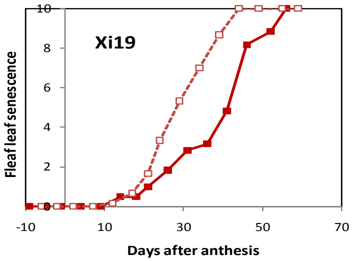


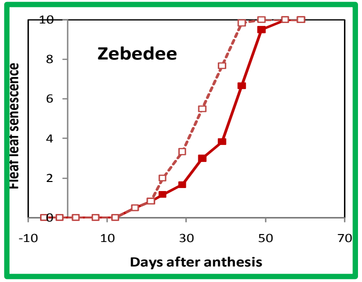




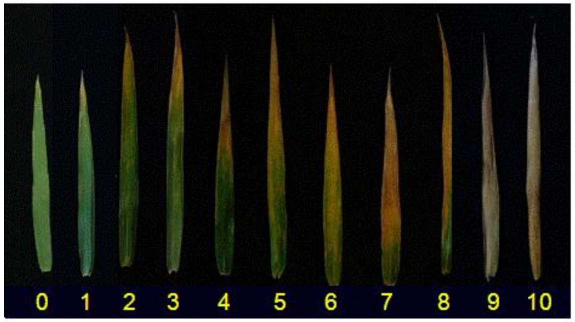




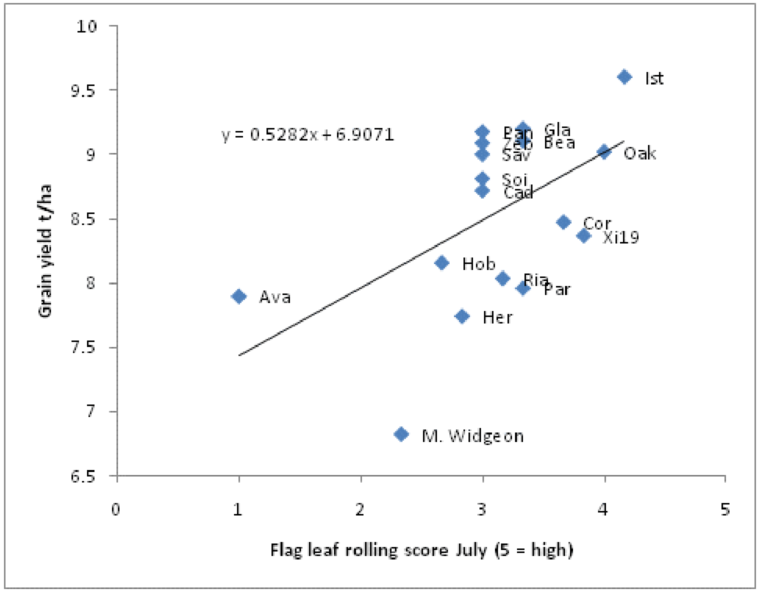


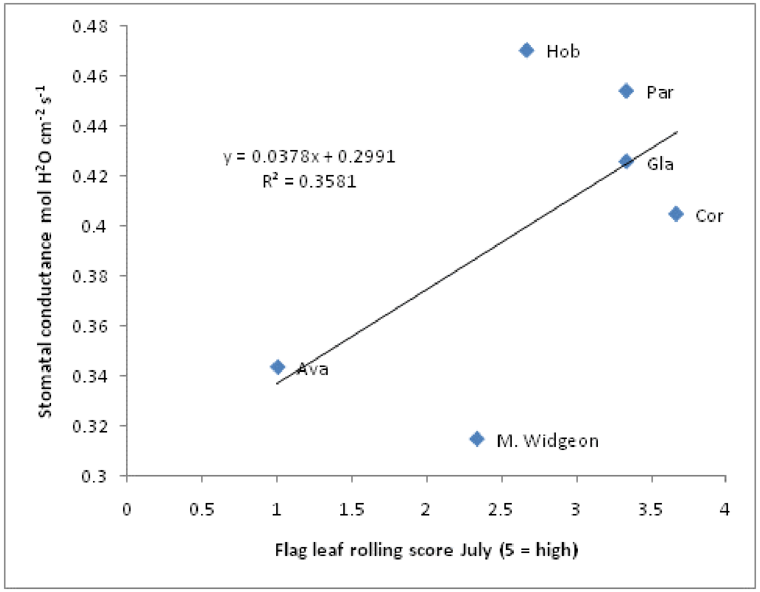


Flag leaf senescence



Flag leaf rolling score (5 July) Unirrigated trt





WGIN 2 (Drought tolerance, 9.1)

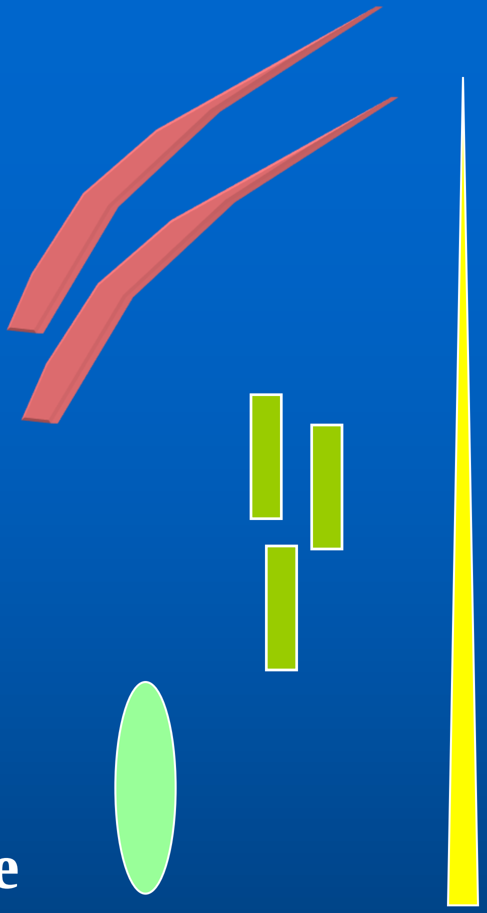
2010-11 expt

Split plot design (3 reps): plot size 1.6 x 12 m
Main plot: Fully irrigated (trickle irrigation)
Unirrigated

Split plot (variety):

1. Avalon *
2. Beaver
3. Cadenza *
4. Sterling (C. Deprez)
5. Cordiale
6. Gallant *
7. Glasgow
8. Hereward *
9. Hobbit
10. Istabraq *
11. M. Widgeon
12. Oakley *
13. Panorama
14. Paragon
15. Cappelle Deprez
16. Soissons
17. Xi 19 *
18. Zebedee

Measurements



- **Combine grain yield, yield components**
- **DM and partitioning at GS31, GS61, harvest**
- **% stem WSC at GS61+10d**
- **Leaf senescence kinetics for flag-leaf, L2 and L3.**
- **Stomatal conductance/photosynthetic rate using Licor (unirrigated subset , 8 varieties)**
- **Canopy temperature**
- **Water use ~ gravimetric analysis of soil cores (unirrigated, 18 varieties)**

WGIN 2 (Drought tolerance, 9.2)

	Project Month	Milestone
30/11/2012	48	Act 9 Obj2: QTL analysis to identify genome locations associated with WUE and drought tolerance traits completed.

2010-11 expts

Rialto x Savannah DH population for phenotying for yield physiological traits (94 lines and 2 parents)

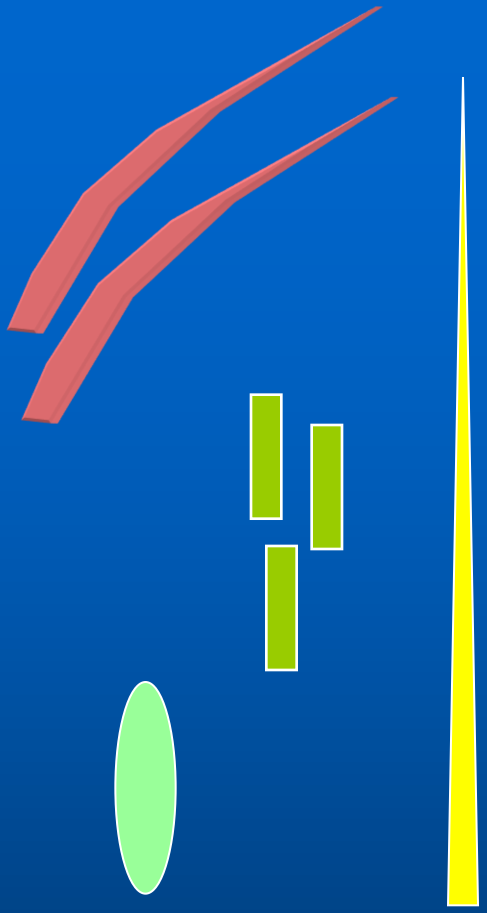
~ 2 sites: Nottingham - irrigated and unirrigated

JIC - unirrigated

~ extend molecular map as necessary with Dart and SSR

Measurements on DH pop

- Combine grain yield, yield components
- % stem WSC at GS61+10d (unirrigated)
- Leaf senescence kinetics for flag-leaf, L2 and L3.
- Canopy temperature
- grain △ 13C (unirrigated)



WGIN 2 (Drought tolerance, 9.3)

	Project Month	Milestone
31/03/2012	40	Act 9 Obj3. Complete development of one new DH population in an elite modern background segregating for drought-tolerance traits.

- Candidate F1(s) made at JIC crosses to maize informed by data analysis from LK0986 project
- F1 crossed with maize
- Population segregating for Ppd1a:
  - use WGIN resource to select against PpdD1a - ie make the pop photoperiod sensitive.
  - keep the pop large, so we can have flowering time strata and perform analysis within them

WGIN 2 (Activity 9, Drought tolerance)

	Project Month	Milestone
30/11//2011	36	Act 9 Obj1: Complete phenotyping and data analysis for drought tolerance traits in elite winter wheat varieties in 2009/10 &10/11.
30/11/2012	48	Act 9 Obj2: QTL analysis to identify genome locations associated with WUE and drought tolerance traits completed.
31/03/2012	40	Act 9 Obj3. Complete development of one new DH population in an elite modern background segregating for drought-tolerance traits.
28/02/2013	51	Act 9 Obj4: Association genetics analysis of drought tolerance traits using AE Watkins & Gediflux collections completed.
28/02/2013	51	Act 9 Obj5: Collation of diverse germplasm collection (cultivars, advanced lines) from worldwide drought-tolerance wheat breeding programmes completed.

Acknowledgments:

Nottingham
J. DeSilva
J. Alcock
M. Tovey

The University of Nottingham

Defra
Department for Environment Food and Rural Affairs

JIC
J. Snape
S. Griffiths
S. Orford

John Innes Centre

Chemical analysis In WGIN drought tolerance trial in 2009/10 & 2010/11

Samples (per year) on 18 cultivars x 2 Irr trts x 3 reps (=108 plots)

	Chemical analysis			Total
No. samples	**13C**	**18O**	**Ash%**	
Flag leaf @ GS61	**108**	***108***	***108***	**324**
Grain @ harvest	***108***		***108***	**216**

Core funding

Sub-contract funding

Sub-contract budget

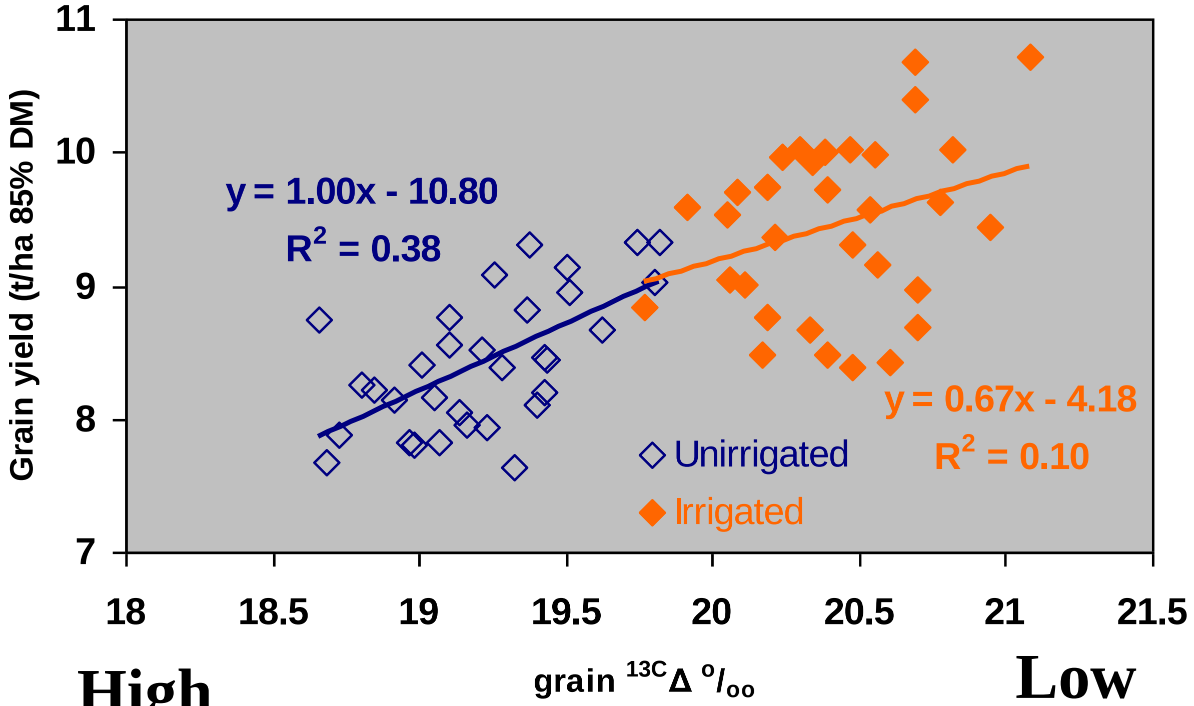
Estimated costs	
Salaries	£3,512 (2 months Research technician)
Other expenses	£15,012 (Chemical analysis for $\Delta^{18}0$, $\Delta^{18}0$, ash content)
	£ 3,849 Indirect costs (OHs)
VAT	£2,627
Total	£25,000

Use of 13CO_2 discrimination technique in breeding programmes

- C^{12}/C^{13} isotope ratio of fixed CO_2 can be used as an indicator of WUE

- Low discrimination against $^{13}CO_2$ → high WUE

WUE vs grain yield: Beaver x Soissons DH population



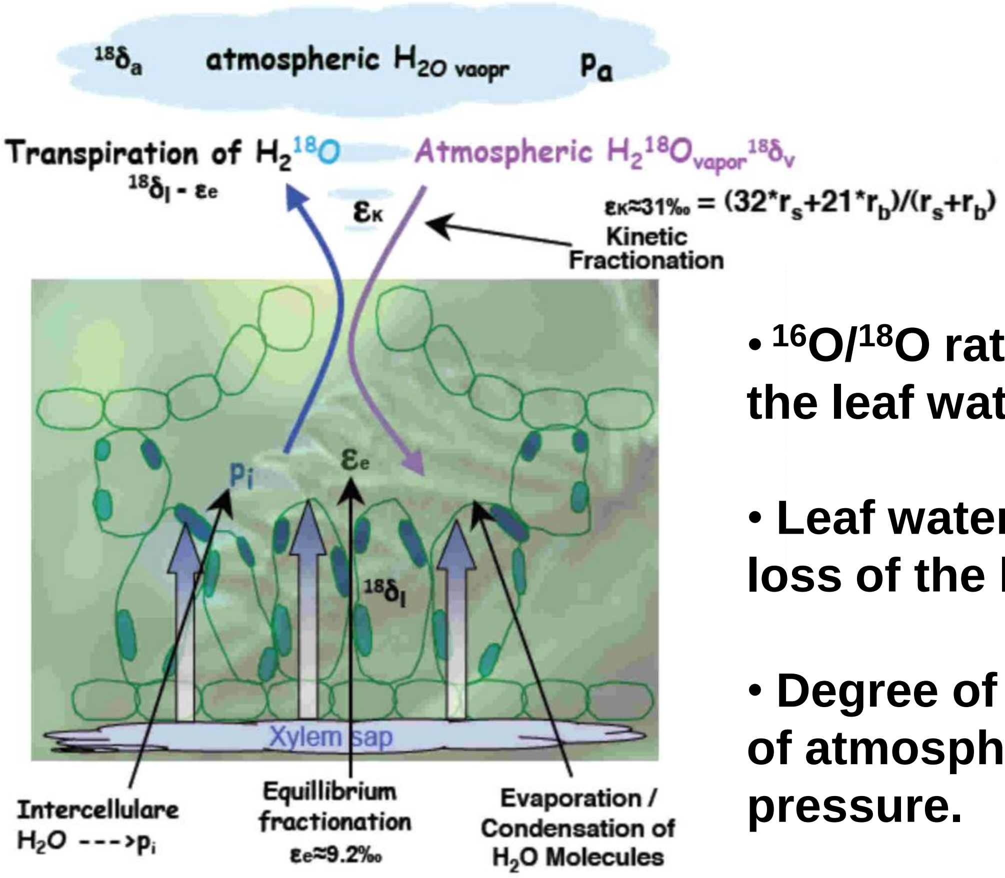
High WUE ← **Low WUE**

→grain $^{13C}\Delta$ positively associated with yield under drought – indicator of ability to access water
→ trade-off between WUE and season-long water use

Mean GL 2002-3 and SB 2004-5

Kumar et al. J Agric Sci 2010

Techniques: Oxygen isotope ratio ~ <u>leaf transpiration</u>



- **$^{16}O/^{18}O$ ratio determined by enrichment in the leaf water due to transpiration.**

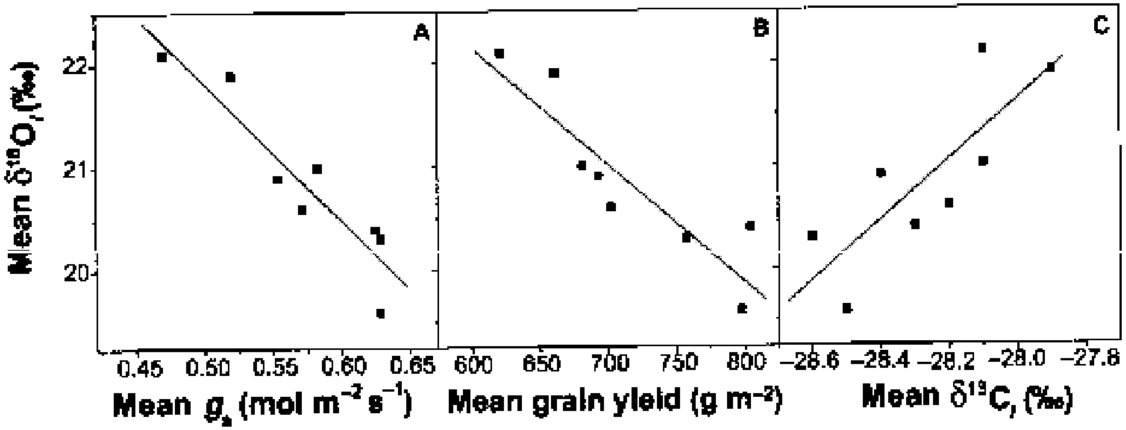
- **Leaf water enriched due to the preferential loss of the lighter $H_2{}^{16}O$ during evaporation.**

- **Degree of enrichment is related to the ratio of atmospheric to intercellular vapour pressure.**

- **An increase in stomatal conductance should decrease leaf temp. hence intercellular vapour pressure, resulting in less enrichment at the evaporating site.**

Barbour et al. (2000) Aust. J. Plant Physiol., **27**, 625–637

Oxygen isotope ratio of leaf and grain material correlates with stomatal conductance and grain yield in irrigated wheat



The relationship between the 3 year mean of cultivar $\delta^{18}O_{leaf}$ and corresponding means of stomatal conductance (gs) measured pre-anthesis, grain yield and δ $13C_{leaf}$ for eight CIMMYT spring wheat cvs

$\delta^{18}O$ is not thought to be strongly influenced by photosynthetic rate, so that combined measurement of both $\delta^{13}C$ and $\delta^{18}O$ should allow stomatal and photosynthetic effects on δ13C to be teased apart

Techniques: Mineral ash content **~ <u>water use</u>**

- Total leaf ash content of plant tissues is suggested as a useful tool to predict yield under drought.

- The mechanism of mineral accumulation in plant tissues appears to be explained through the passive transport of minerals via xylem driven by transpiration.

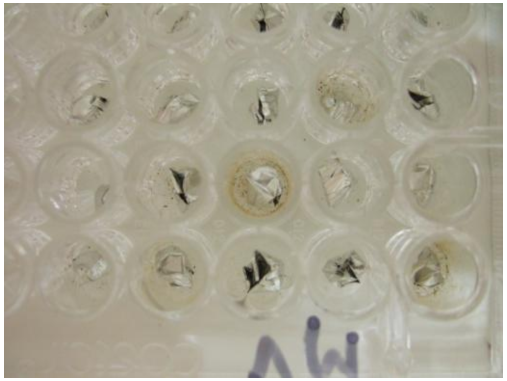
- Thus, ash content measured in plant tissues provides an indicator of the total water transpired.

- The analysis of mineral ash content analysis is significantly less expensive than Δ13C or Δ18O, so may be a useful alternative for these screens in trials.

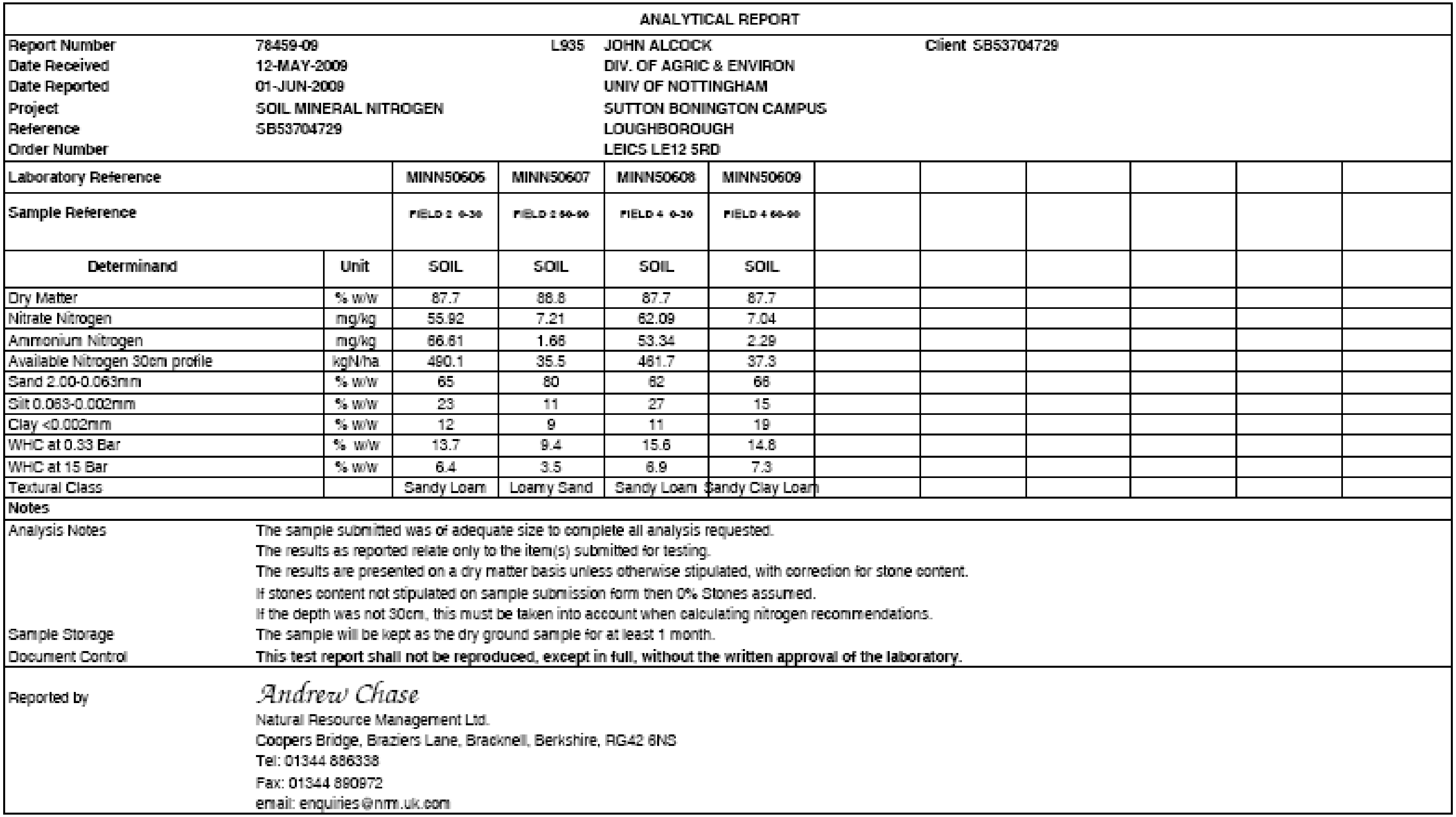
Isotope analysis, sample submission: :Weighing and encapsulate of milled samples samples for 13C and O18 isotope analysis

Encapsulation of 2 mg sample

Submit samples to Mylnefield Isotope lab at SCRI



All 2009/10 samples submitted to lab on 25 Jan 2011 (data returned in 4-6 wks)



ANALYTICAL REPORT

Report Number 78459-09 L935

Date Received 12-MAY-2009

Date Reported 01-JUN-2009

Project SOIL MINERAL NITROGEN

Reference SB53704729

Order Number

JOHN ALCOCK
DIV. OF AGRIC & ENVIRON
UNIV OF NOTTINGHAM
SUTTON BONINGTON CAMPUS
LOUGHBOROUGH
LEICS LE12 5RD

Client SB53704729

Laboratory Reference		MINN50606	MINN50607	MINN50608	MINN50609						
Sample Reference		FIELD 2 0-30	FIELD 2 60-90	FIELD 4 0-30	FIELD 4 60-90						
Determinand	**Unit**	SOIL	SOIL	SOIL	SOIL						
Dry Matter	% w/w	87.7	88.8	87.7	87.7						
Nitrate Nitrogen	mg/kg	55.92	7.21	62.09	7.04						
Ammonium Nitrogen	mg/kg	66.61	1.68	53.34	2.29						
Available Nitrogen 30cm profile	kgN/ha	490.1	35.5	461.7	37.3						
Sand 2.00-0.063mm	% w/w	65	80	62	66						
Silt 0.063-0.002mm	% w/w	23	11	27	15						
Clay <0.002mm	% w/w	12	9	11	19						
WHC at 0.33 Bar	% w/w	13.7	9.4	15.6	14.8						
WHC at 15 Bar	% w/w	6.4	3.5	6.9	7.3						
Textural Class		Sandy Loam	Loamy Sand	Sandy Loam	Sandy Clay Loam						

Notes

Analysis Notes The sample submitted was of adequate size to complete all analysis requested.
The results as reported relate only to the item(s) submitted for testing.
The results are presented on a dry matter basis unless otherwise stipulated, with correction for stone content.
If stones content not stipulated on sample submission form then 0% Stones assumed.
If the depth was not 30cm, this must be taken into account when calculating nitrogen recommendations.

Sample Storage The sample will be kept as the dry ground sample for at least 1 month.

Document Control **This test report shall not be reproduced, except in full, without the written approval of the laboratory.**

Reported by *Andrew Chase*
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Tel: 01344 886338
Fax: 01344 890972
email: enquiries@nrm.uk.com

Page 1 of 1

WGIN 2 (Drought tolerance, 9.3)

	Project Month	Milestone
31/03/2012	40	Act 9 Obj3. Complete development of one new DH population in an elite modern background segregating for drought-tolerance traits.

Candidate F1(s) made at JIC crosses to maize informed by data analysis from LK0986 project:

Timber
Gatsby
Consort
Clare
Zebedee
Garcia
Paragon

Evaluation of novel genetic resources

- NIAB backcrossing CIMMYT synthetic wheats (shown in Mexico to have improved drought tolerance) in Xi19 background.

- 29 BC1F3 families grown in small plots (4 x 1 m) and the recurrent parent (Xi19) on the drought-prone light sand at Bunny Park Farm.

WUE trial 2010-11

Split plot design (3 reps): plot size 1.6 x 12 m

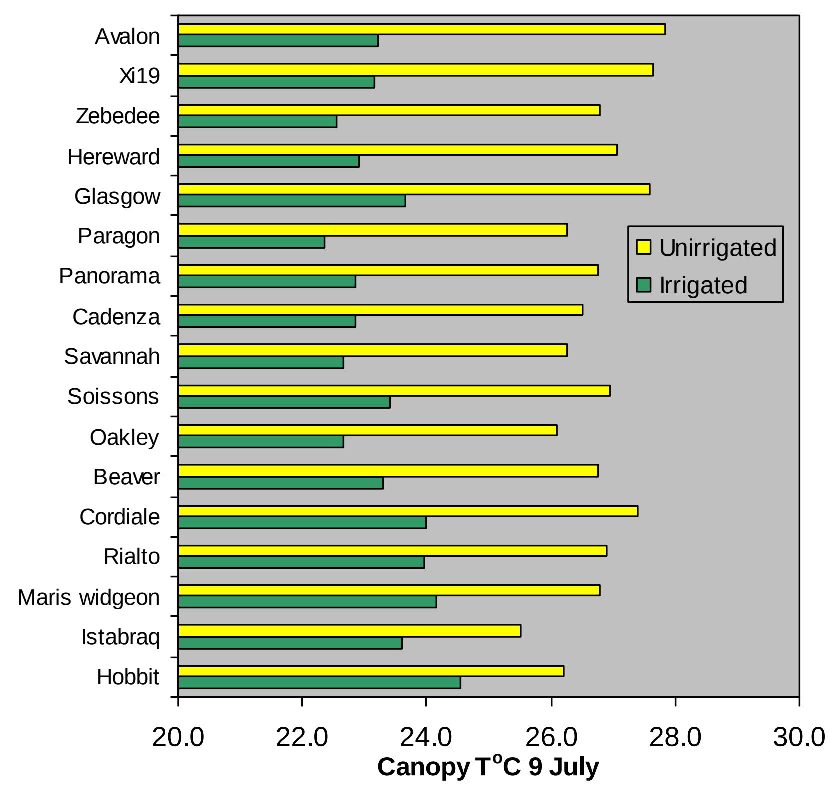
Main plot: Fully irrigated (trickle irrigation)
Unirrigated

Split plot (variety):

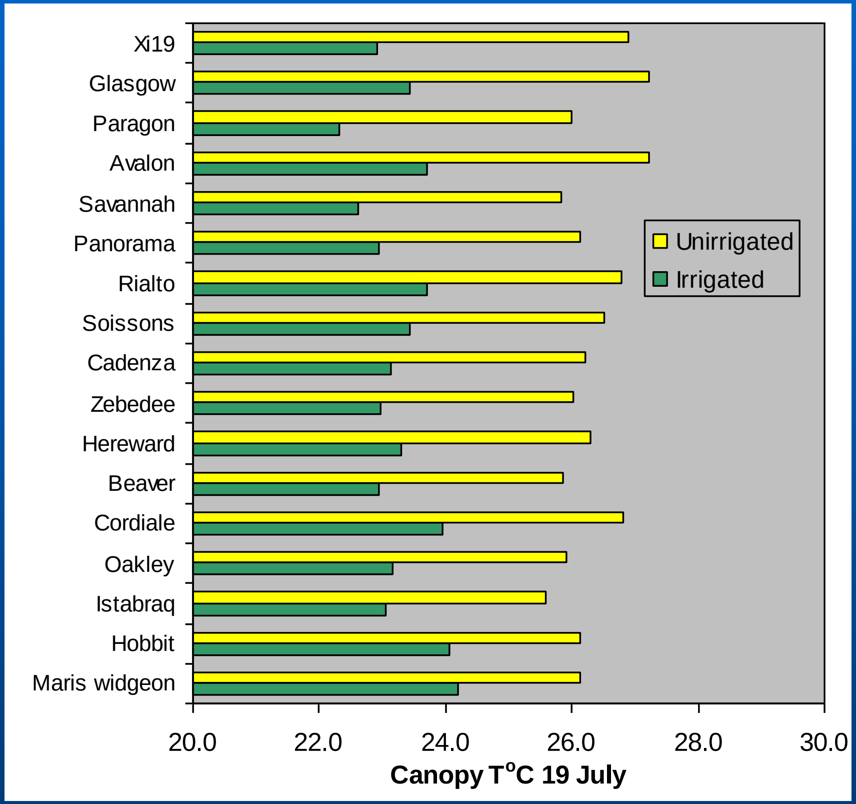
1. Avalon *
2. Beaver
3. Cadenza *
4. Sterling (C. Deprez)
5. Cordiale
6. Gallant *
7. Glasgow
8. Hereward *
9. Hobbit
10. Istabraq *
11. M. Widgeon
12. Oakley *
13. Panorama
14. Paragon
15. Cappelle Deprez
16. Soissons
17. Xi 19 *
18. Zebedee

* Common with NUE trial

Canopy Temperature post-anthesis



LSD Irr 4.37 (P 0.06)
LED Gen 1.29 ns
LSD Irr x Gen 10.94 ns



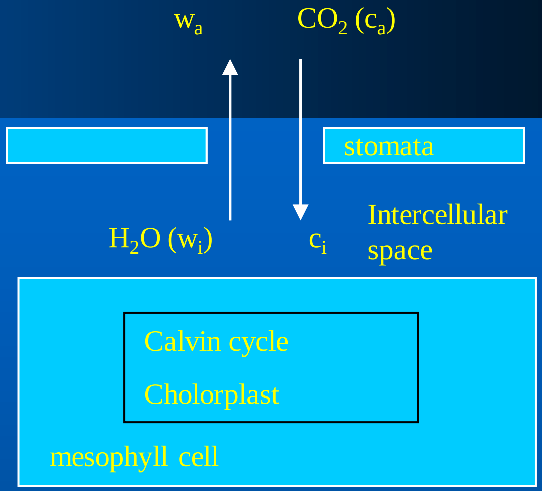
LSD Irr 6.50 ns
LED Gen 0.89 (P< 0.001)
LSD Irr x Gen 1.99 ns

Effects of leaf traits and canopy traits on WUE

- ***N or Rubisco content per unit leaf area:*** Greater photosynthetic activity ↓ c_i , hence ↑ WUE.

- ***Stomatal conductance:***. Lower conductance ↓ c_i hence ↑ WUE.

- ***Canopy size and architecture:*** Taller crops with rougher surfaces ↓ aerodynamic resistance, hence ↓ WUE.



Condon et al. (2002). Crop Science

Stomata open (irrigated conditions): Discrimination in favour of 12C0$_2$ isotope form at high internal C0$_2$ concentration.

Irrigated conditions

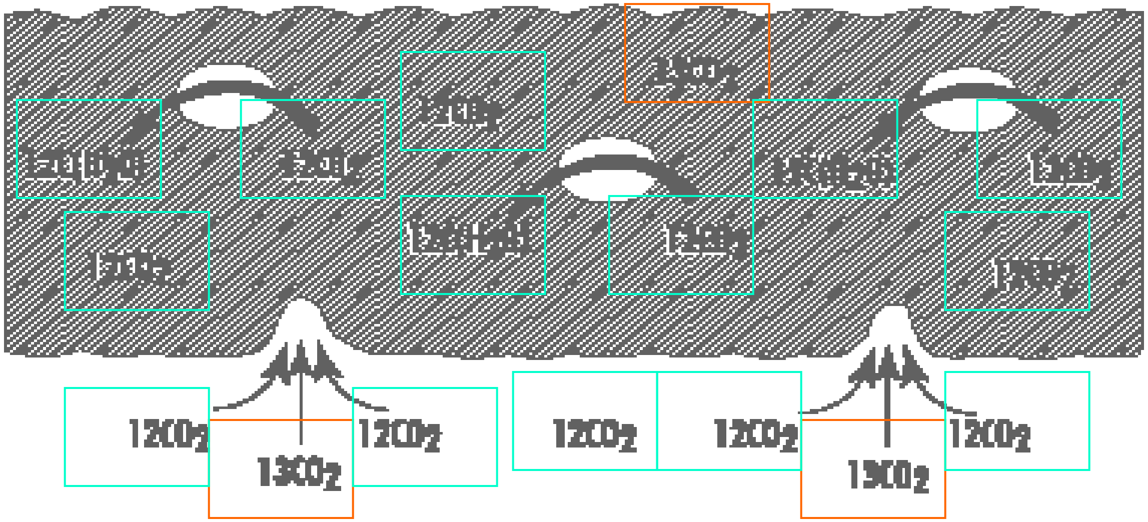
Stomata open (high stomatal conductance)

↓

High Ci

↙ ↘

High Discrimination against $^{13}CO_2$ - - - → **Low WUE**



Stomata closed (moisture stress): Discrimination less favourably to 12C0$_2$ as internal C0$_2$ concentration falling.

Drought conditions

Stomata close (low stomatal conductance)

↓

Low Ci

↙ ↘

Low Discrimination against $^{13}CO_2$ - - - → **High WUE**

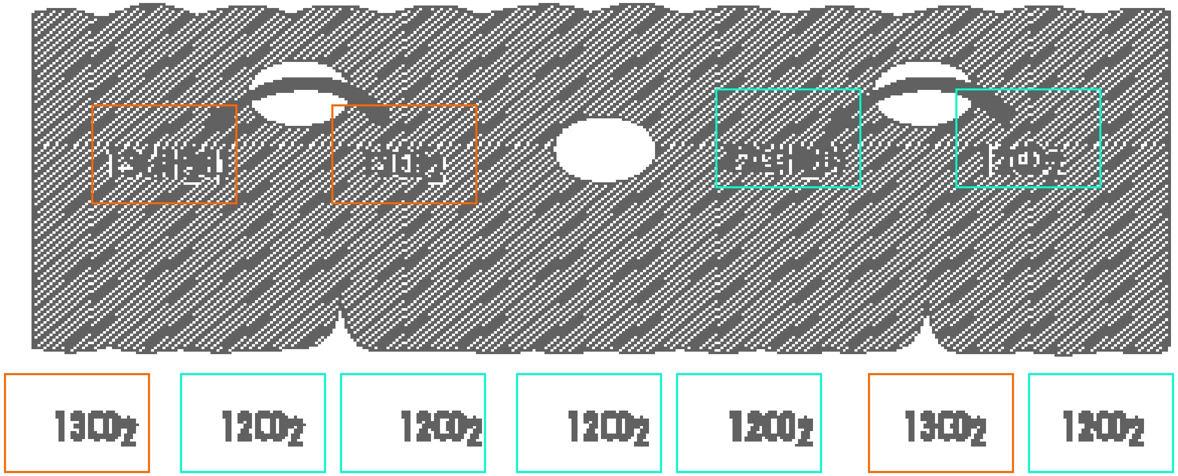
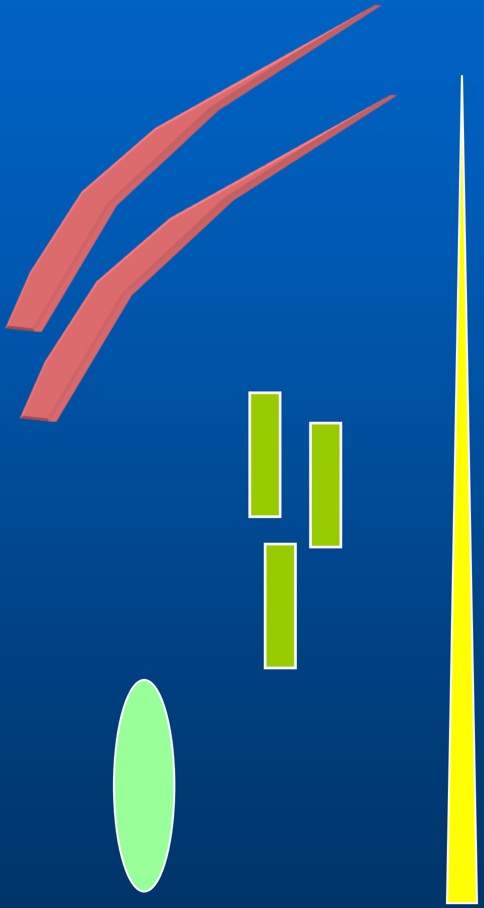


Diagram 1. Carbon isotope discrimination under irrigated and dry conditions.

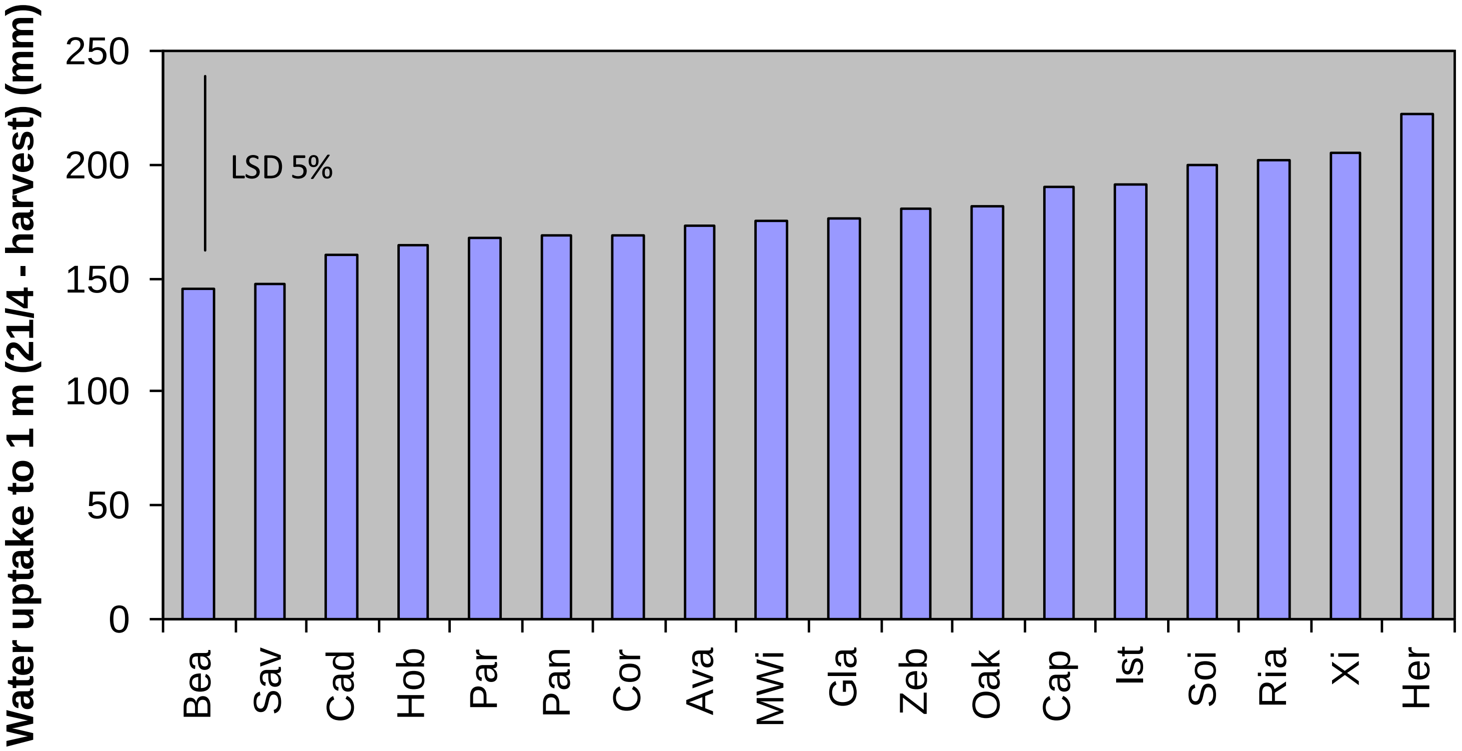
Measurements: isotope analysis of plant samples

Analyses on all varieties in both irrigation trts (108 plots):



- **Δ ^{13}C ~ flag leaf @ flowering and grain @ harvest**
- **Δ ^{18}O ~ flag leaf @ flowering**
- **Total mineral ash content ~ flag leaf @ GS61 and grain @ harvest**

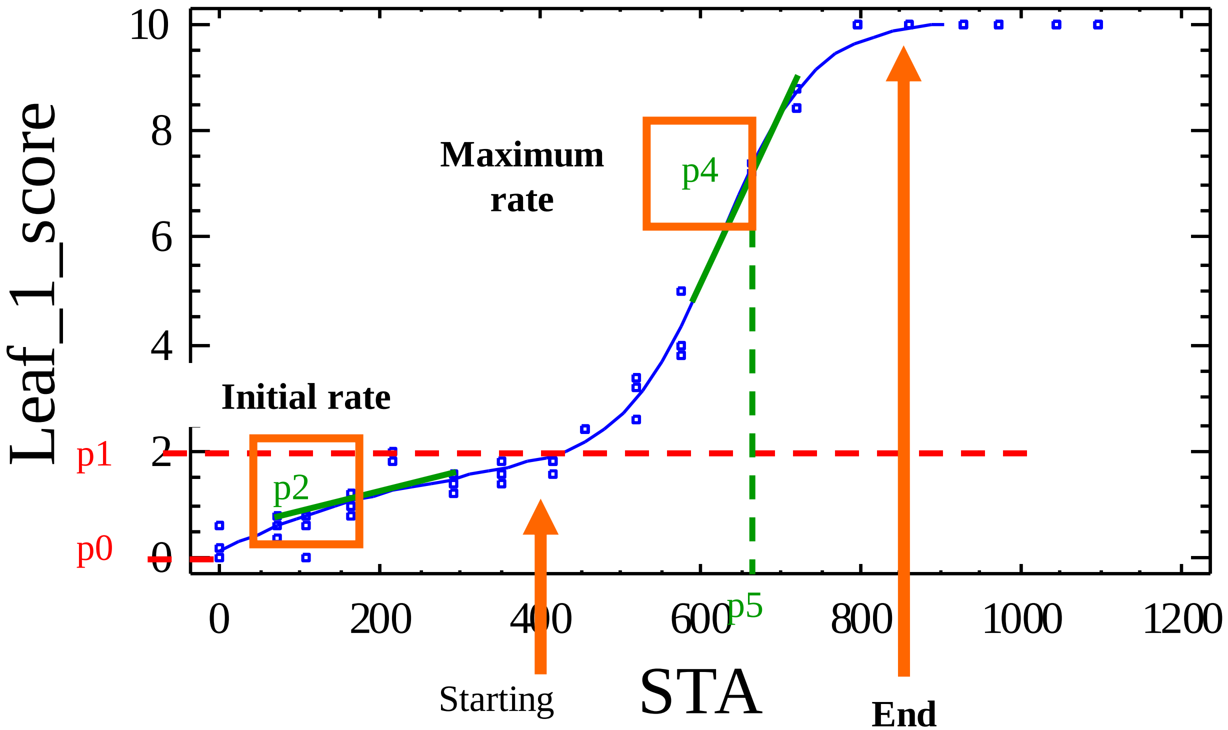
Water uptake from gravimetric analysis of soil cores (unirrigated)



Senescence scoring per flag leaf

Equation with 5 parameters = a monomolecular + a logistic function

Génard et al. (1999 Journal of horticultural science & biotechnology 74 : 772-776)



P0=initial score at GS61

P1=score of 1st phase

P2= max. rate of 1st phase

P4= max. rate of 2nd phase

P5= time when rate is max. in 2nd phase

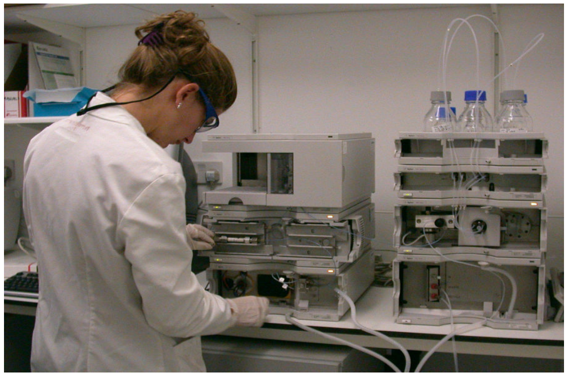
Starting

= date at which the second derivative is nil

End

= date at which score is 9.5

Score = p0+p1*(1-exp((-p2*STA)/p1))+(10-p1-p0)/(1+exp(-4*p4*(STA-p5)/(10-p1-p0)))



Non-destructive screening of WGIN Paragon mutants for grain NUE traits

Richard Weightman, ADAS Boxworth

WGIN management meeting 16/02/11

ADAS

www.adas.co.uk

Agenda

- Partners
- Background
- Development of NIR calibrations
- Results to date
- Work programme/timescale for completion

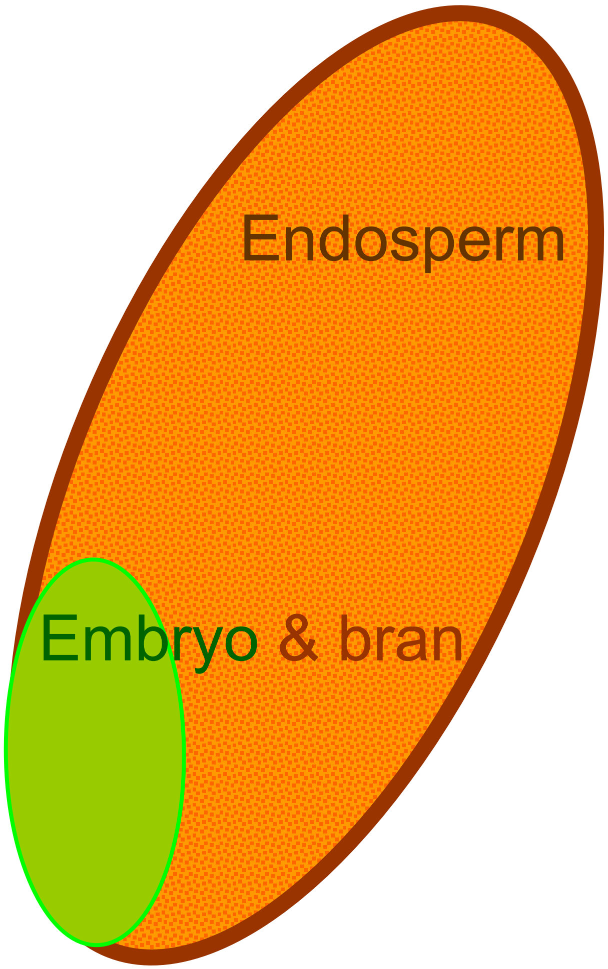
Partners

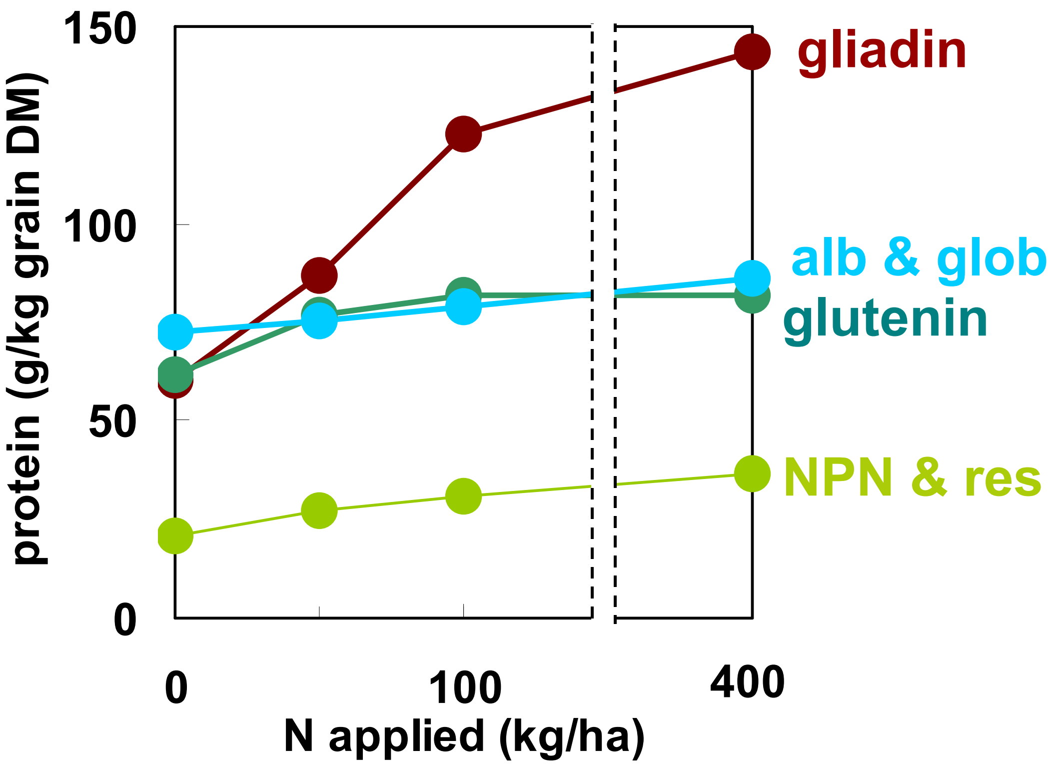
ADAS	R Weightman, D Kindred
JIC	S Orford, S Griffiths
SCRI	Stuart Swanston
Aunir	Chris Piotrowski

Storage protein fractions

- GG hypothesis relates to reducing gliadins in grain
    - Increase in response to applied N
    - Major storage protein
    - Need rapid screening tool
    - Tool could then be used to screen for ‘mutants’ or null gliadin lines

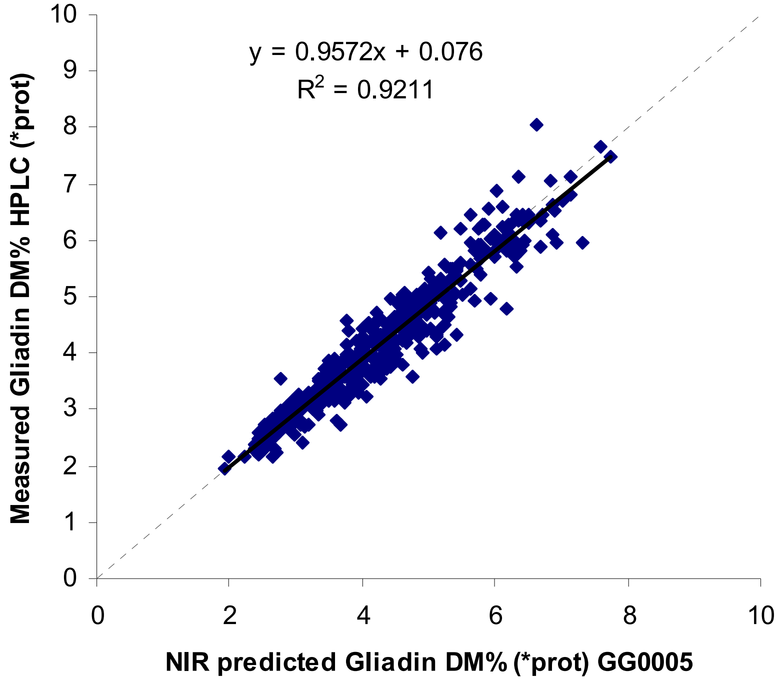
Wheat grain … response to N supply

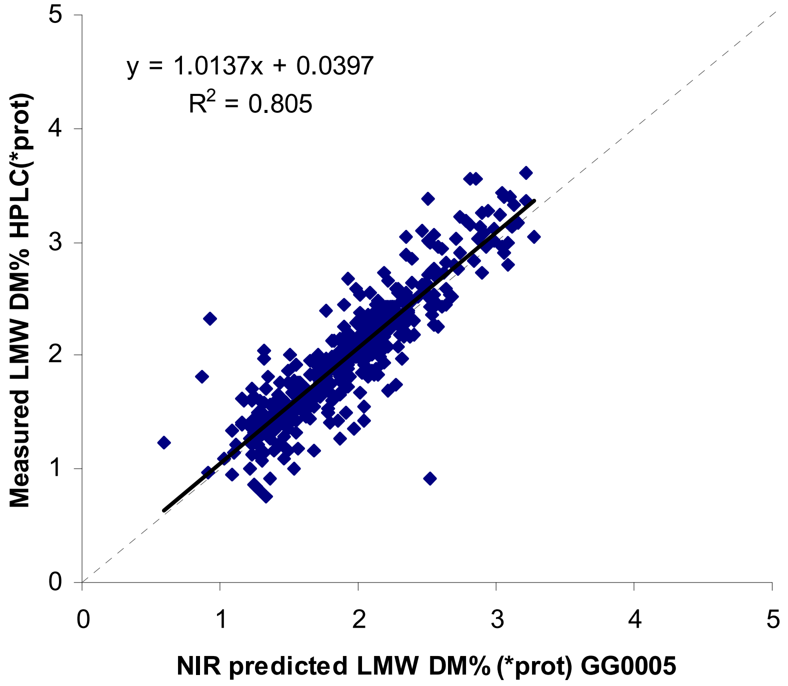




Dubetz, Gardiner, Flynn & de la Roche (1979).

NIR calibrations – protein fractions





Reasonable calibrations for gliadins and LMW glutenins

… but don’t know if the calibration is mainly detecting total protein

NIR calibrations – protein fractions

- Previous work was not able to fully test the calibrations, in the sense that:
  - Need null gliadin lines to break any relationship between total protein and gliadin in the calibration
  - Attempted to screen Paragon mutants at JIC
    - not possible logistically

Original Milestones 2010

1. Samples from SCRI & ref data from ADAS to Aunir	15th June
2. Aunir develop NIR calibrations	15th July
3. Transfer FOSS 6500 and calibrations to JIC	1st August
4. Transfer data from JIC to ADAS	31st October
5. Final report	30th November

Actual Milestones 2010/11

Contract finalised	26th May
1. Samples & ref data to Aunir	15th June
Samples from SCRI & forwarded to Aunir with data	23rd July
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FOSS 6500 transferred to JIC	13th Jan 2011
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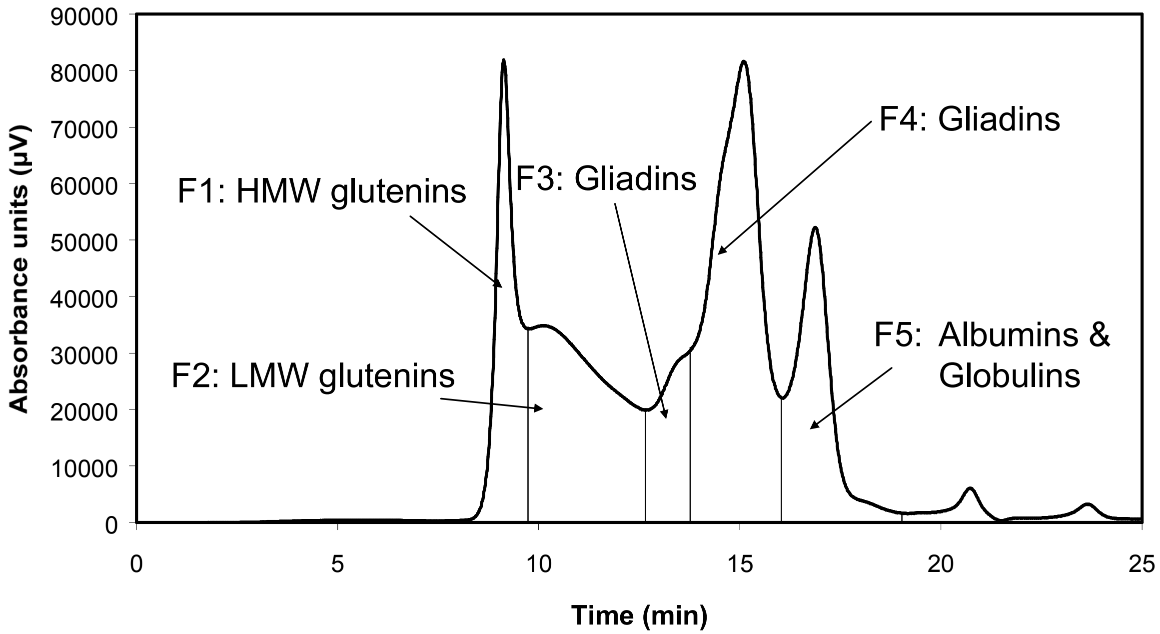
NIR performance (1)

Constituent	N	Mean	SD	SEC	RSQ	SECV	SECV/mean (%)
PAYProtein	552	455	13.5	2.08	0.98	2.32	0.51
AlcYieldldryt	533	452	14.8	7.17	0.77	7.52	1.66
PAYTGWWL	525	449	13.8	7.01	0.74	7.52	1.67
GrainLength	515	6.67	0.30	0.21	0.51	0.23	3.48
Protein	552	9.33	1.93	0.30	0.98	0.33	3.56
LengthWidth	511	1.80	0.09	0.06	0.54	0.06	3.59
GrainWidth	519	3.70	0.20	0.12	0.62	0.14	3.84
SKCSMC	399	13.2	1.49	0.46	0.90	0.57	4.30

NIR performance (2)

Constituent	N	Mean	SD	SEC	RSQ	SECV	SECV/mean (%)
ResViscosy	545	1.48	0.137	0.065	0.774	0.069	4.67
GliadFraction	466	0.42	0.037	0.027	0.461	0.028	6.61
TGW85DM	531	46.76	4.788	3.098	0.581	3.451	7.38
SKCSTGW	395	48.46	5.221	3.596	0.526	3.809	7.86
AGDMProt	469	2.56	0.363	0.233	0.588	0.242	9.46
LMWFraction	464	0.21	0.023	0.019	0.288	0.020	9.63
AlbGlobFract	472	0.28	0.045	0.026	0.661	0.028	9.96
AGDMHPLC	470	3.08	0.441	0.299	0.541	0.307	9.98
ExtractProt	462	11.40	2.416	1.262	0.727	1.303	11.4
GLDDMProt	448	4.06	1.117	0.471	0.822	0.488	12.0
LMWDMProt	463	1.96	0.554	0.263	0.774	0.274	14.0
GLDDMHPLC	454	4.95	1.360	0.680	0.750	0.700	14.1
LMWDMHPLC	464	2.34	0.669	0.378	0.680	0.390	16.7
HMWFraction	476	0.09	0.023	0.014	0.612	0.016	17.5

Typical chromatogram



Typical SE-HPLC chromatogram for wheat protein

NIR performance - comparison

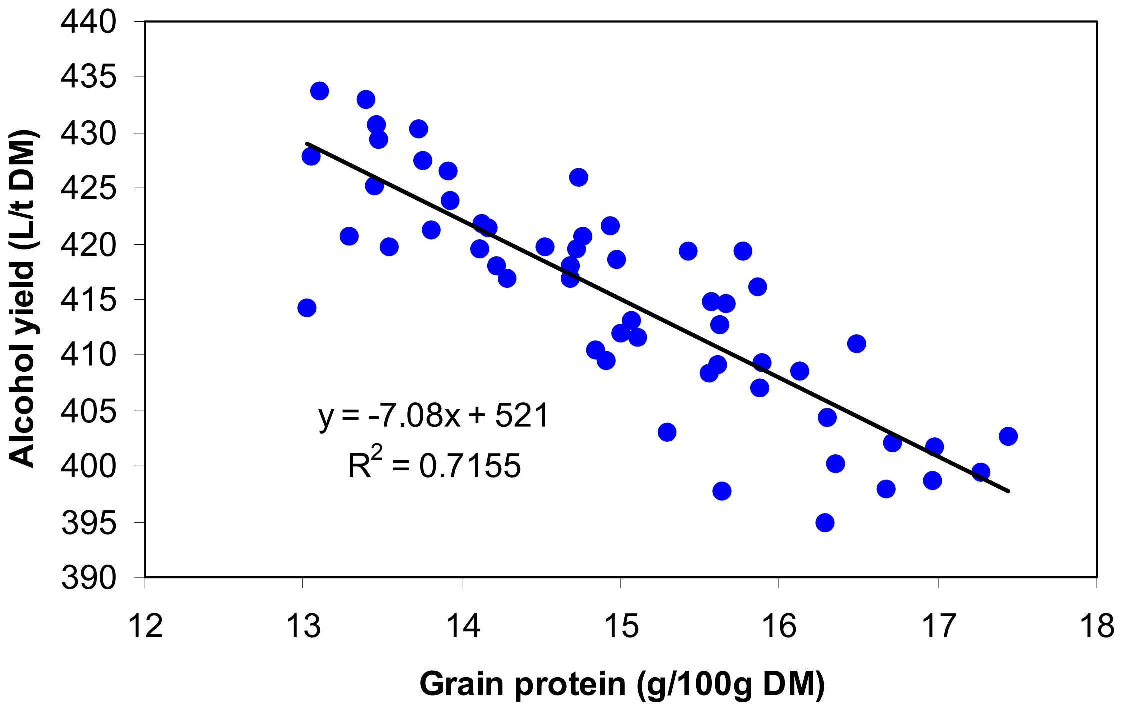
- **HGCA report No. 310 (Sam Millar, 2003)**

UK whole wheat

Parameter	**n**	**mean**	**SD**	**R2**	**SECV**	**CV(%)**
Protein (% as is)	284	10.7	1.06	0.99	0.15	1.4
CBP loaf volume (ml)	282	3332	185	0.41	149	4.5
F1/F2	298	0.584	0.058	0.57	0.045	7.7
(F3+F4)/F1	296	3.39	0.609	0.49	0.454	13.4

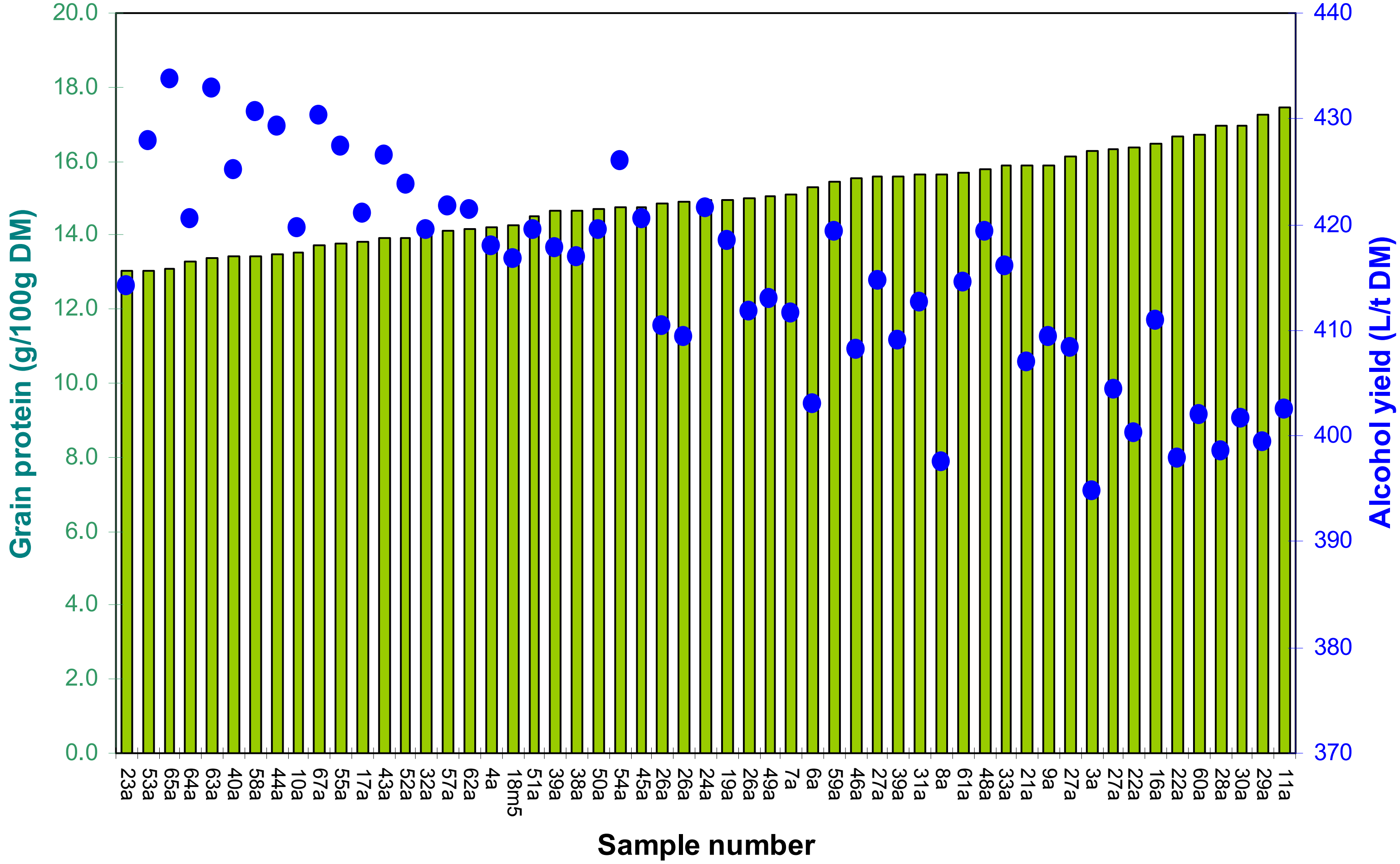
AY vs protein relationship

NIR predictions - 55 samples from Paragon mutant population

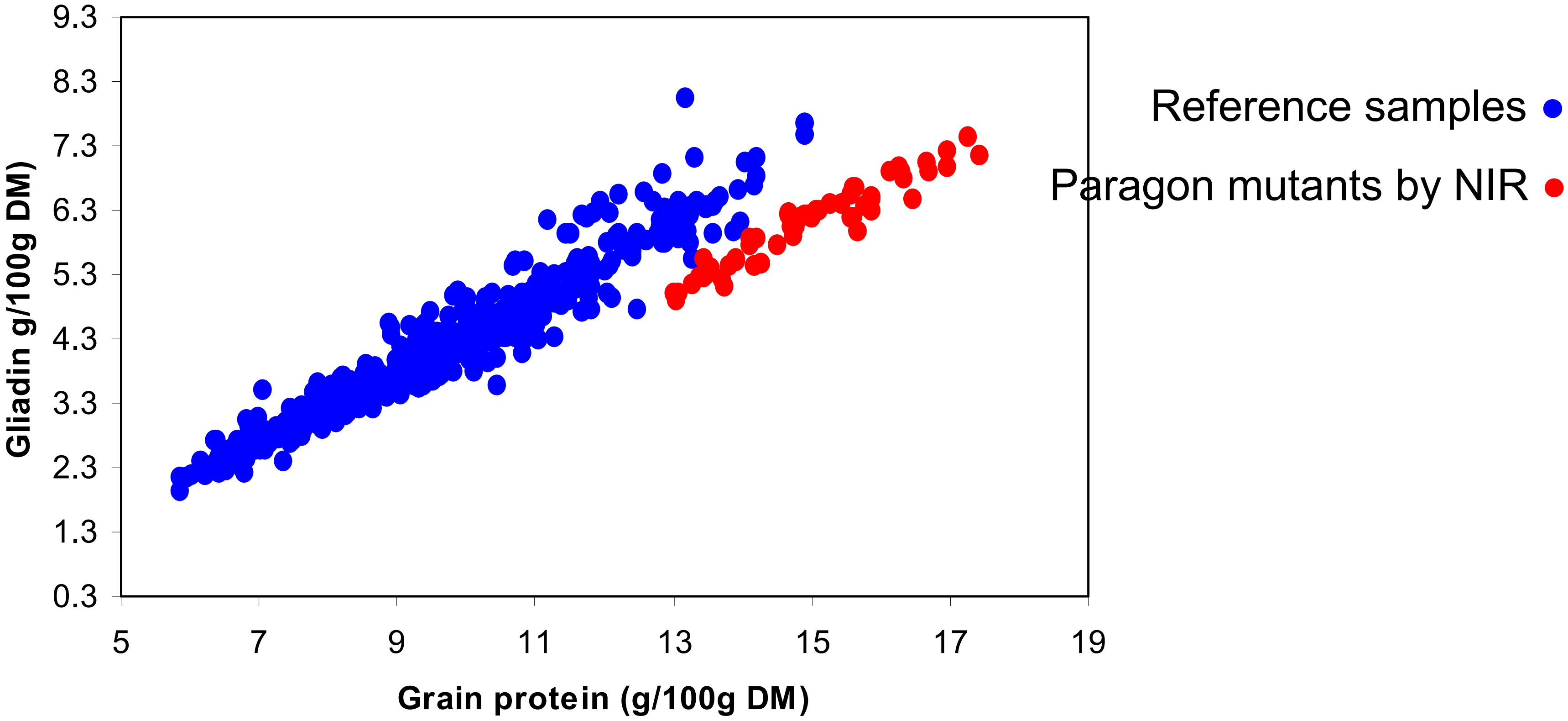


NB: Kindred *et al*. 2008, *AAB, 90, 143-152*
AY = 520 – (protein x 7.2)

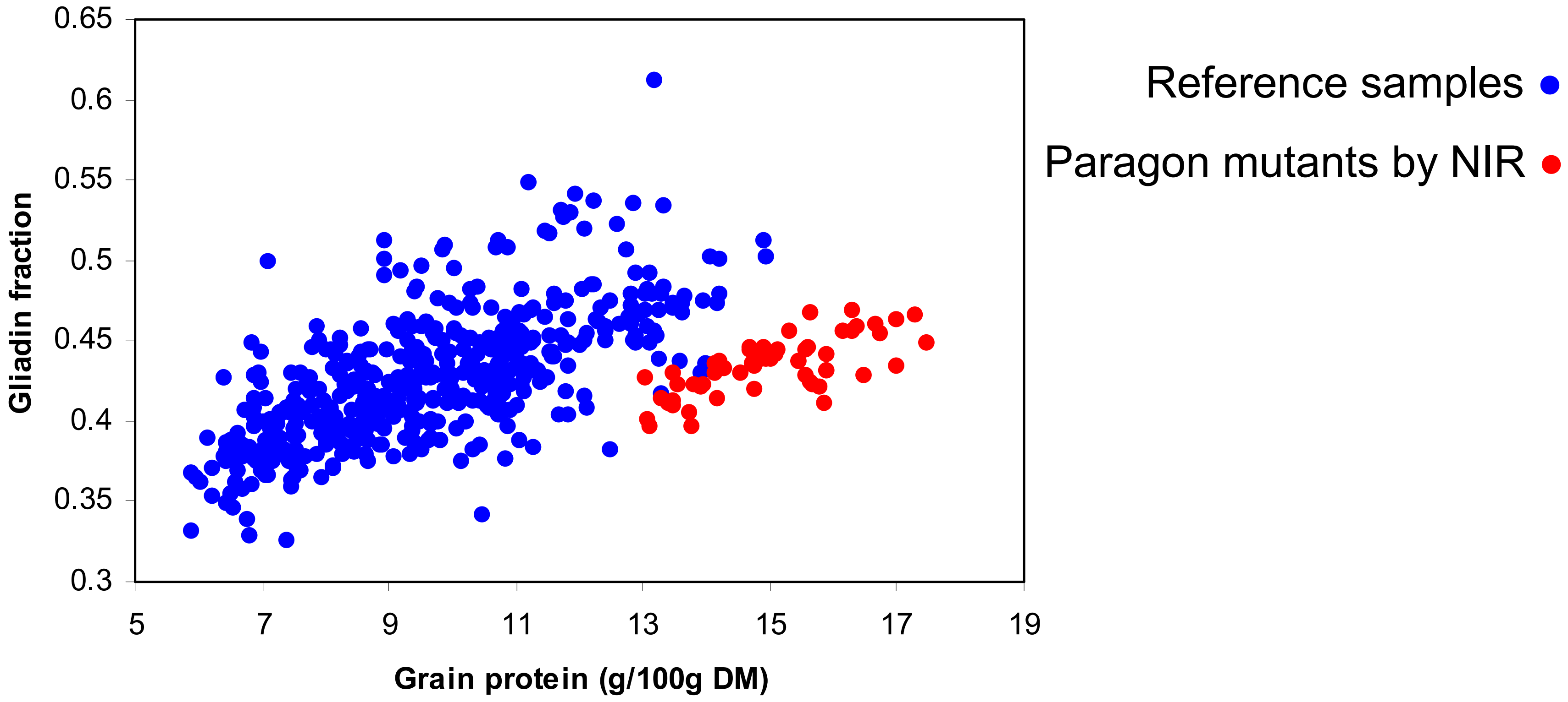
AY and protein – predicted by NIR



Grain storage protein fractions



Grain storage protein fractions



Summary

- Have NIR predictions for a range of parameters
  - 6500 more powerful machine than Infratec
  - >550 samples for main parameters
  - protein and AY cals perform well
  - protein fractions within performance limits of other workers
- Average protein high (15% DM)
- Range of protein low (13-17.5%)
- Low average AY (415 L/t) reflects the high protein content

Summary

- Protein content appears to explain low AY
- Initial samples appear to be low gliadin, relative to their protein content
    - need to do full dataset (55 samples a small subset)
    - Ultimately reference analysis will be required

Summary

- Next steps
  - Need to complete scanning of mutant lines
  - Need to complete other grain parameters (grain size, shape, TGW) at JIC
  - Staffing issues - to discuss
  - Invoicing

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Thank you

richard.weightman@adas.co.uk