

Gene Discovery For UK Wheat Farming

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WGIN Stakeholder Meeting

RRes 22nd November 2011

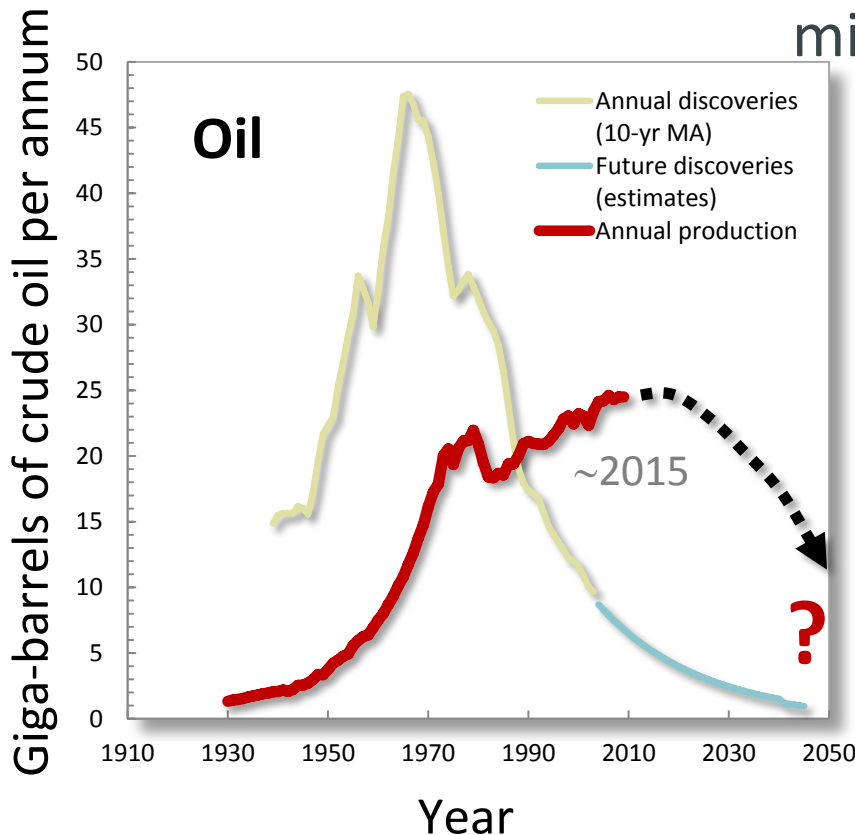
Overview

- Long term challenges to UK wheat farming
- The potential contribution of genetics
- Quantitative Traits (QT) and Quantitative Trait Loci (QTL)
- WGIN strategy
- Examples based on height and heading
- Genetic dissection
- Where next?

Challenges

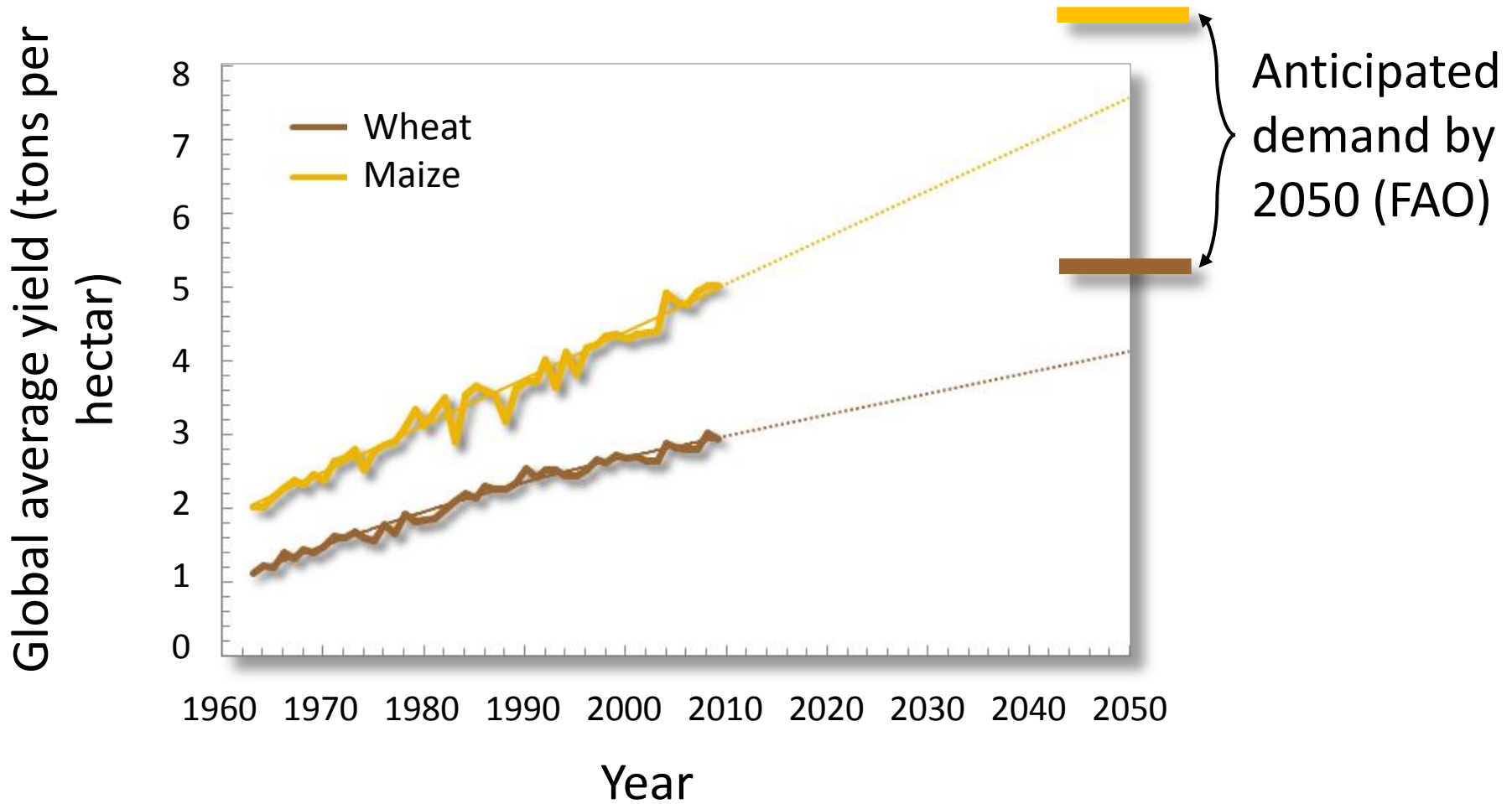
Peak oil and fertilizer production

- ▶ **Peak Oil** is likely in **2015** at the latest: Oxford University, UK Department of Energy, US military, UK Energy Task Force, Kuwait University, Lloyd's of London, German military, ...



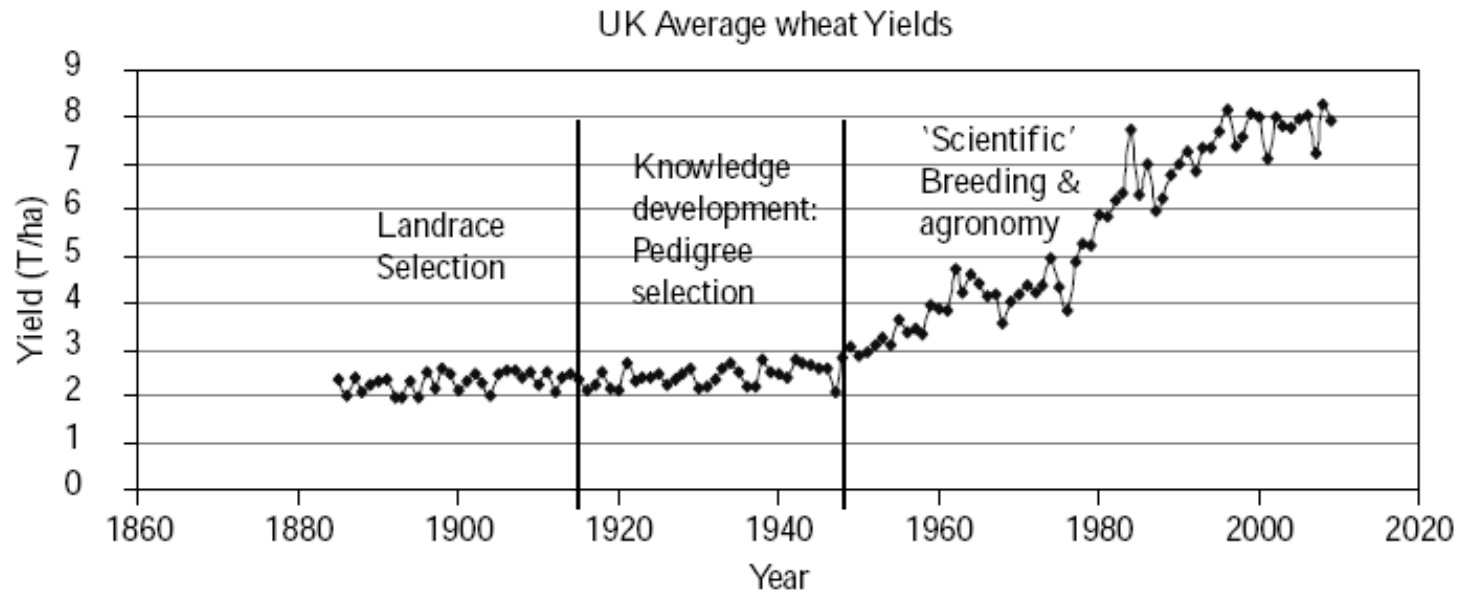
- ▶ **Peak phosphorus** projected to occur by **2030**, but may already have happened (Déry and Anderson 2007; Cordell et al. 2010)

Global Rates of yield increase



[Source: USDA PDS database]

Gains are slowing in the UK too



Climate, heat, and water

- ▶ **Climate change- heat stress, volatility**
- ▶ **Water usage- dropping water table, hard to predict drought**
- ▶ **Both increasingly serious problems for UK**

Potential for Genetics- WGIN strategy

Breeders need the tools to manipulate complex traits

- The genetic control of grain yield, efficient nitrogen use, drought/heat tolerance, and adaptation is COMPLEX
- Each trait is controlled by many genes
- Each gene needs to be identified as a quantitative trait locus (QTL)
- QTL interact with each other and the environment

QTL prioritisation

- Target QTL that are:
 - Strong effects
 - Expressed in most genetic backgrounds
 - Expressed in most environments
- Deliver QTL for breeding by:
 - Validating effect in Near Isogenic Lines
 - Developing close flanking genetic markers
 - Ultimately cloned genes and ‘perfect’ markers

Adapted populations for dissection of genetic gain in breeding programmes

Beaver x Soissons	65 DH lines
Spark x Rialto	144 DH lines
Charger x Badger	99 DH lines
Revensa x Savannah	177 DH lines
Trintella x Piko	158 DH lines
Rialto x Savannah	132 DH lines
Avalon x Cadenza	203 DH lines
Lynx x Cadenza	171 DH lines
Buster x Charger	128 DH lines
Malacca x Charger	98 DH lines
Shamrock x Shango	87 DH lines
Buster x Hereward	49 DH lines
Hobbit `sib x Avalon	84 RIL lines
Mercia x 94-08	91 DH lines
Milan x Catbird	96 DH lines
Weebil x Bacannora	106 DH lines

Majority are crosses between varieties from different breeding programmes

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WGIN population adopted as UK reference	Trintella x Piko	158 DH lines
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Yield trials over several years, several sites, treatments

High Potential sites:



Drought limited sites

N limited sites

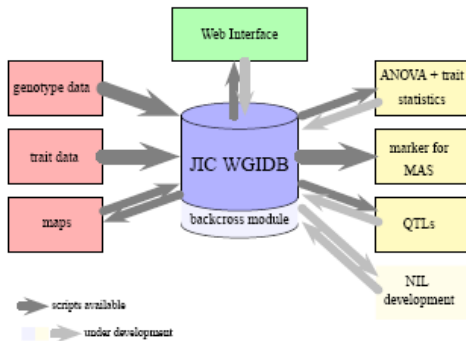


WGIN data collected at RRes, JIC, and University of Nottingham adds to this analysis

Integration of data sets-

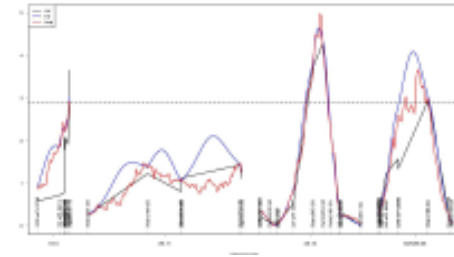
Relational database

- Rapid turnaround- field to gene
- High quality analysis



QTL analysis

- R-QTL
- Meta analysis
- QTL x E interactions
- Selection of lines for BC



Trial data

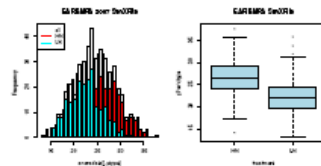
- Standardised formats
- Agreed protocols
- Trait ontologies



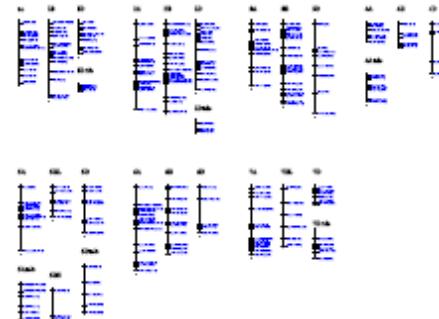
Statistical analysis

- Variance components
- Heritability
- GxE interactions
- Error checking

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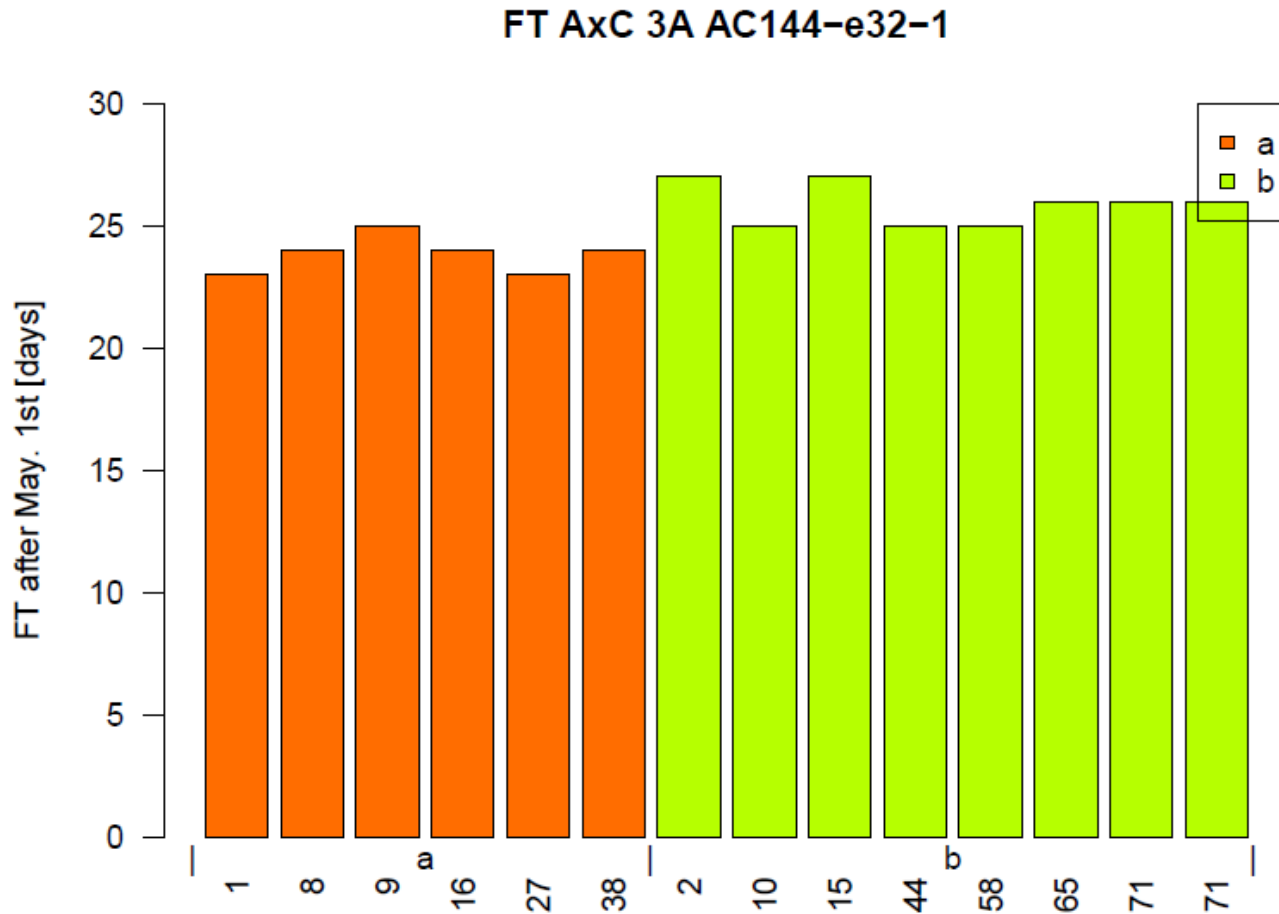
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First examples of WGIN QTL validation

Avalon X Cadenza 3A FT QTL NILs



NIL lines, carrying two different allele at the 3A FT QTL, show a significant difference in flowering time of about 2 days in field trials.

Significant phenotypic differences present in more Avalon X Cadenza NILs

QTL	trait	stream	BCparent	no A	no B	t-stat	df	Ava		p.val	signif	
								mean	Cad mean A>B			
AxC 3A	FT	AC179-e27-8	Ava		3	8	-10.58	7	22	24	FALSE	0 ***
AxC 3A	Ht	AC179-e27-2	Ava		14	5	-7.37	15.8	55.4	62.6	FALSE	0 ***
AxC 3A	Ht	AC144-e32-1	Ava		6	8	-7.64	10.7	55.8	66.1	FALSE	0 ***
AxC 3A	Ht	AC113-e113-10	Ava		19	12	-4.69	25.7	59.6	63.5	FALSE	1.00E-04 ***
AxC 3A	FT	AC144-e32-1	Ava		6	8	-4.79	11.5	23.8	25.9	FALSE	5.00E-04 ***
AxC 3A	Ht	AC179-e27-8	Ava		3	8	-6.07	6.1	53.2	61.8	FALSE	8.00E-04 ***
AxC 3A	FT	AC179-e27-2	Ava		14	5	-5.06	8.1	22.6	23.8	FALSE	9.00E-04 ***
AxC 3A	FT	AC113-e113-10	Ava		20	12	-3.31	28.6	23.6	24.3	FALSE	0.0026 ***
AxC 6A	Ht	AC104-e6-9	Cad		3	3	3.46	3.7	71	62.3	TRUE	0.0297 **
AxC 6A	FT	AC104-e6-8	Cad		3	3	-3.13	2.9	10.3	12.7	FALSE	0.0535 *
AxC 6A	FT	AC89-e5-1	Cad		3	2	-3.12	2.9	14.3	17.5	FALSE	0.0549 *
AxC 2D	Ht	AC162-e21-8	Cad		3	3	-2.81	3.4	62	73.5	FALSE	0.0589 *
AxC 2A	FT	AC174-e8-2	Cad		3	3	2.46	3.9	17.3	13	TRUE	0.0712 *
AxC 6A	yield	AC104-e6-9	Cad		3	3	2.98	2.1	421.3	292.3	TRUE	0.0917 *
AxC 3A	Ht	AC113-e113-8	Ava		13	18	-1.77	17.1	56.8	59.7	FALSE	0.094 *

Height QTL

Multiple Environment Analysis estimates of QTL effects at JIC Church Farm site (WGIN data)

Height effects shown in cm – double for full substitution effect

QTL location	2005	2006	2007	2008
2A	-2.241	-2.241	-2.241	-2.241
2D	4.78	4.415	6.152	4.833
3A	3.925	3.527	5.204	3.991
3B	-2.475	-2.475	-2.475	-2.475
4D (<i>Rht-2</i>)	4.063	4.511	3.015	4.488
6A	-2.849	-2.849	-2.849	-2.849

- sign shows that Avalon carries the height increasing allele

+ sign shows that Cadenza carries the height increasing allele

Rht8 NIL in Paragon

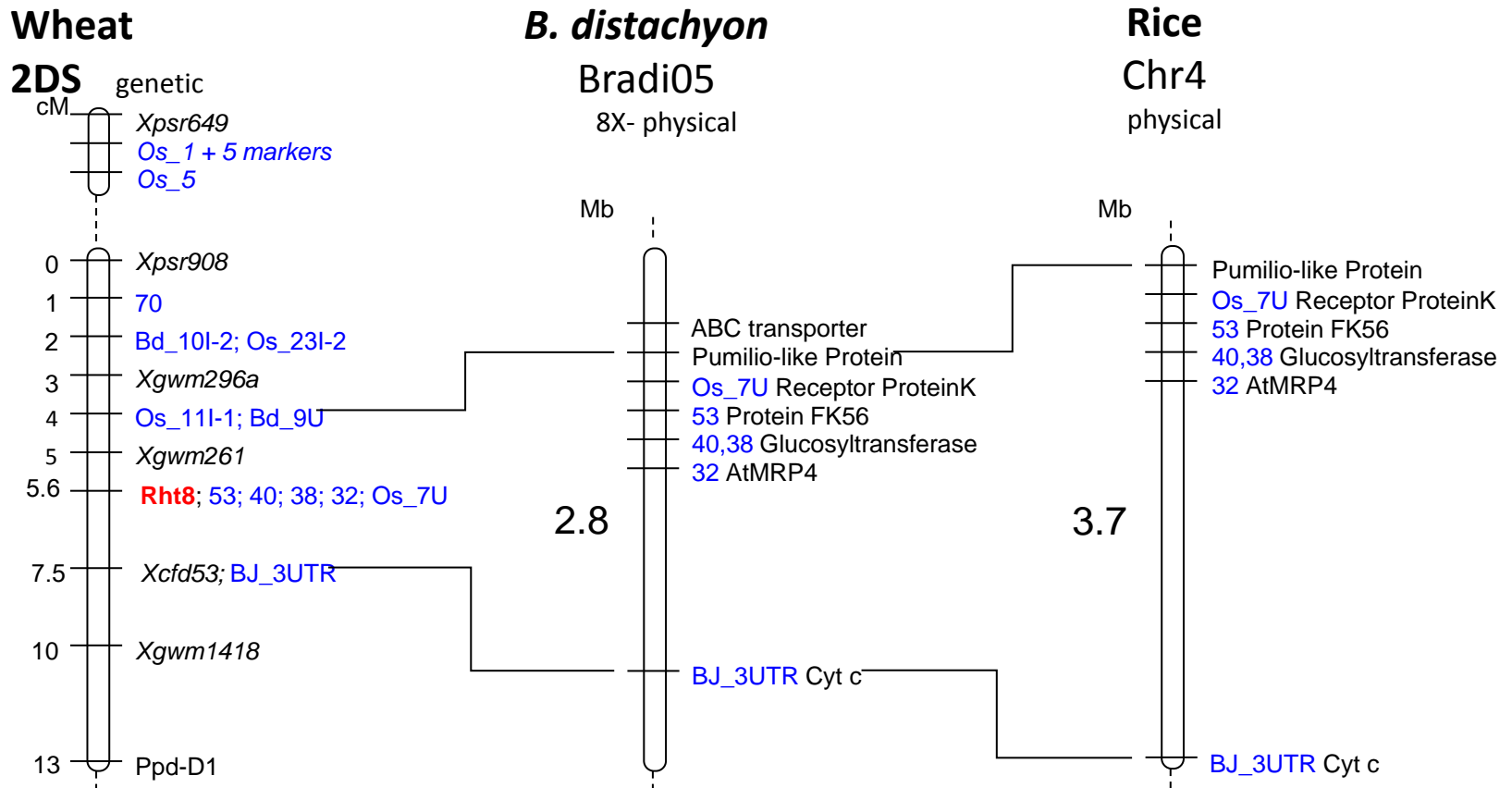
Rht8 BC₃

Paragon



BBSRC, defra, and HGCA funded projects are underway to develop Marker Assisted Selection for these genes

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



Acknowledgement

JIC WGIN team

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