

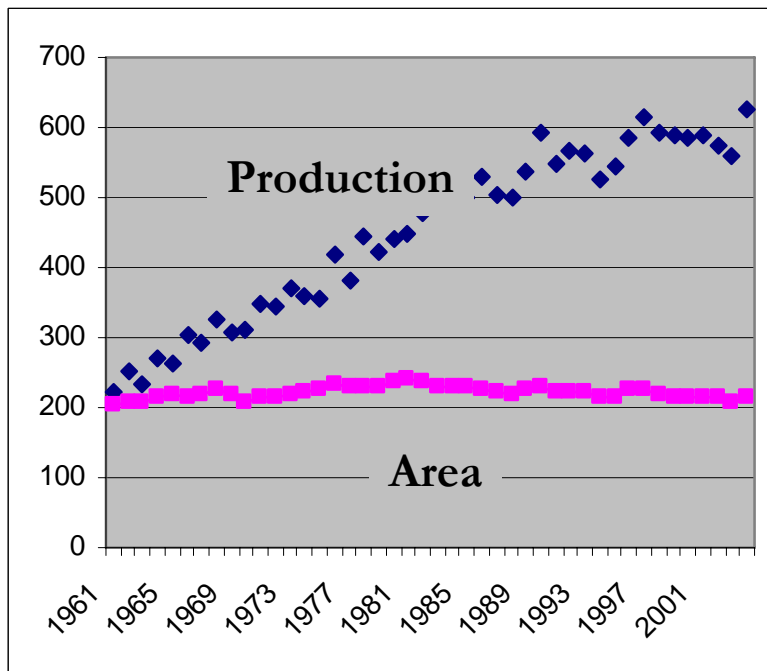


Wheat and Barley

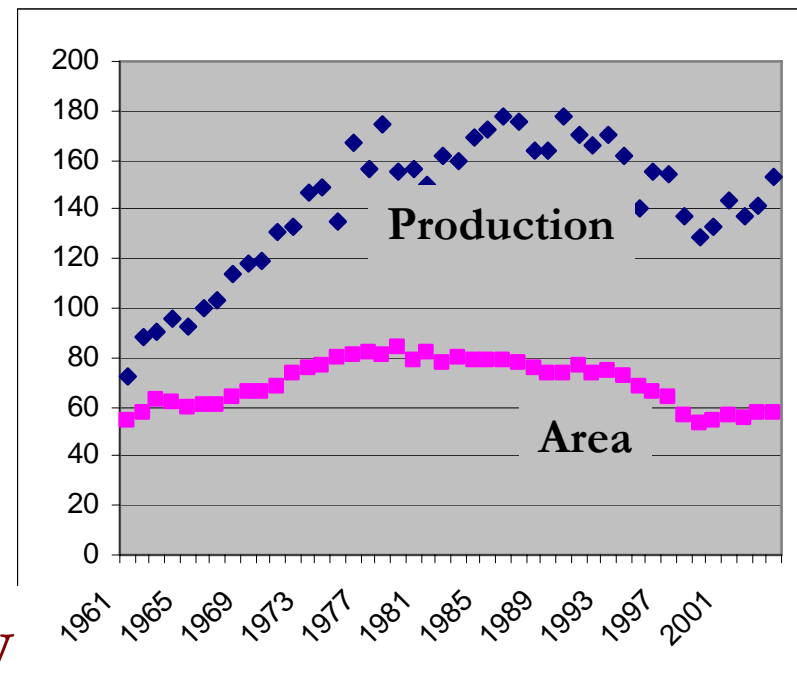


Wheat and barley production

Wheat



2004	Production (Mt)	Area (Mha)	Yield (t/ha)
Maize	721	147	4.9
Wheat	627	216	2.9
Rice	606	151	4.0
Barley	154	57	2.6



Barley

International Triticeae Mapping Initiative

Aims

- ensure data and information on the Triticeae is readily available to all researchers
- help avoid duplication of research efforts
- provide a framework for accessing International collaboration
- keep Triticeae research at the cutting edge of genetic research

Barley and wheat genome sequencing consortia



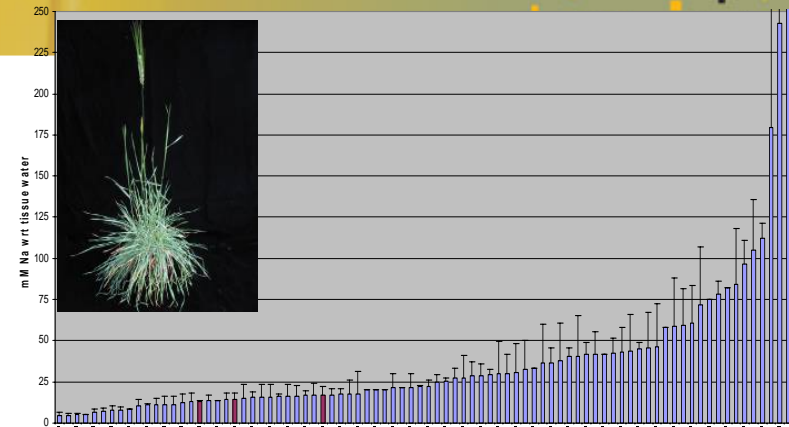
Resources - Barley

- **Forward genetics**
 - Consensus genetic maps
 - SNP platforms
 - Full map by late 2008
 - BAC libraries
- **Reverse genetics**
 - Microarray platforms
 - Metabolite profiles
- **Functional genomics tools**
 - TILLING populations – UK, Italy, Germany, Australia
 - Ac/Ds Tagged populations – Germany, Australia, (USA)



Wheat

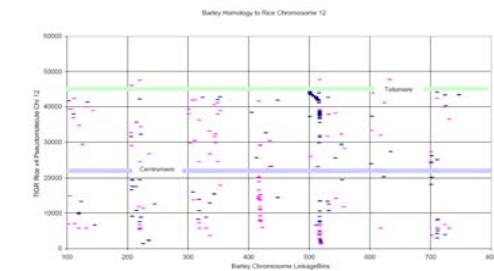
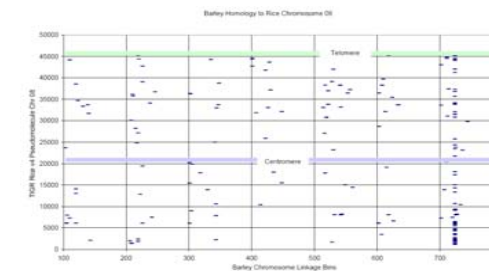
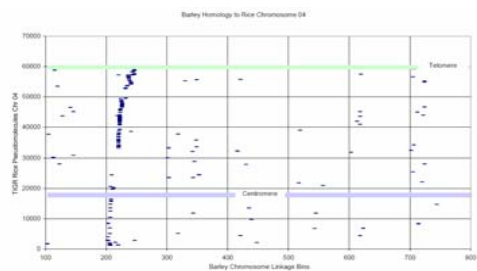
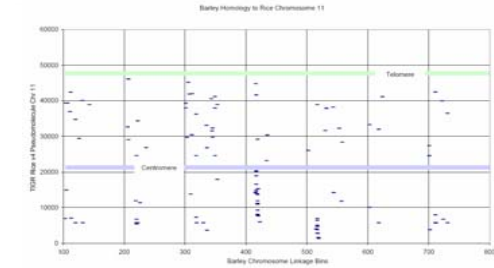
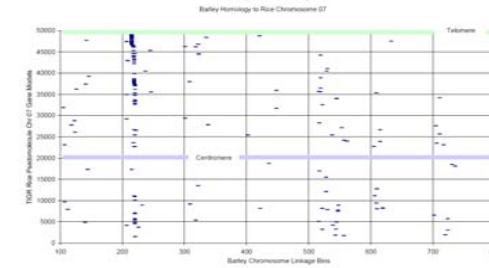
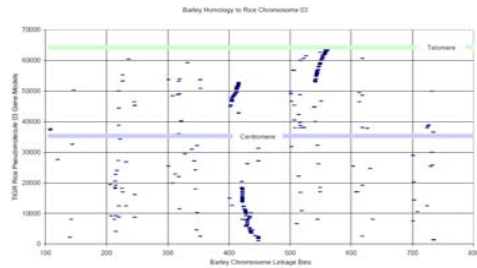
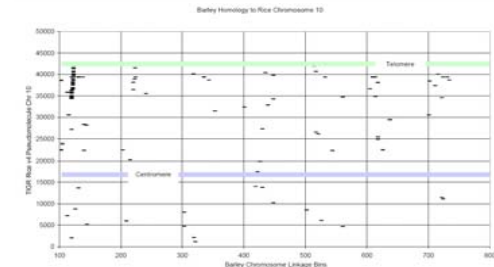
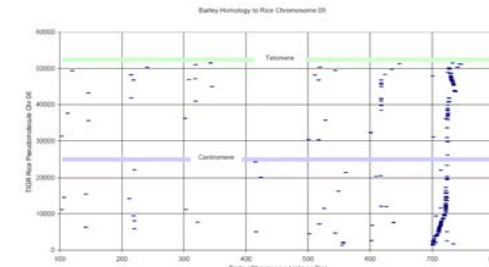
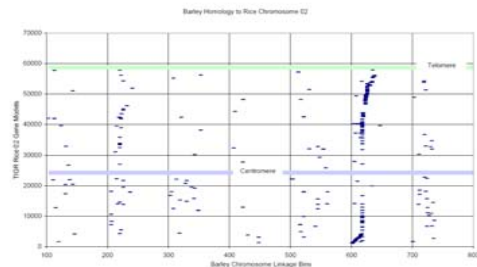
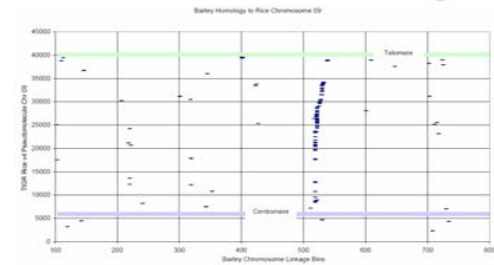
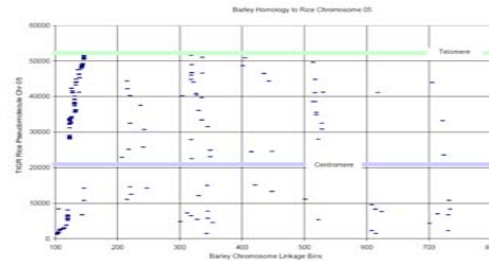
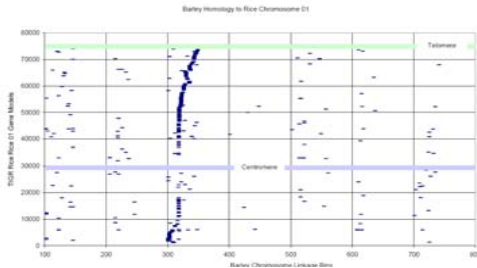
- Forward genetics
 - Consensus genetic maps
 - SNP platforms under development
 - Partial physical map of D genome
 - BAC libraries
 - diploid, tetraploid and hexaploid
 - Chromosome specific
- Reverse genetics
 - Microarray platforms
 - Metabolite profiles
- Functional genomics tools
 - TILLING populations – UK, USA, Australia



>50-fold variation in [Na⁺] in
T. monococcum accessions



Rice/Barley co-linearity

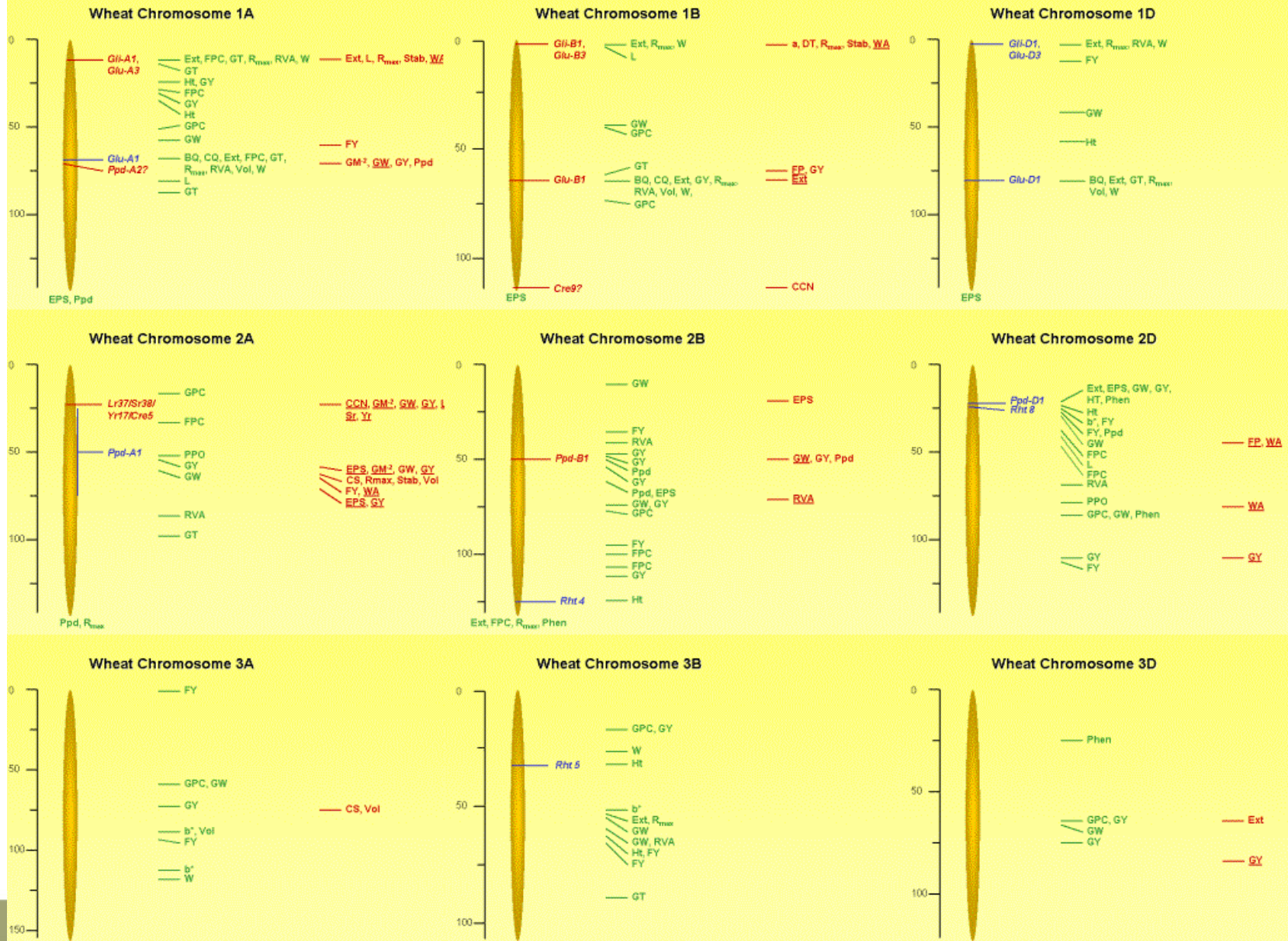


Pathways to delivery

Loci currently being tracked with markers

		Number of loci
<u>Barley</u>	Disease	11
	Abiotic stress	6
	Quality	7
	Other	3
	<i>Total</i>	<i>27 (18 Traits)</i>
<u>Wheat</u>	Disease	12
	Abiotic stress	4
	Quality	10
	<i>Total</i>	<i>26 (20 Traits)</i>

Many high quality linkage and QTL maps



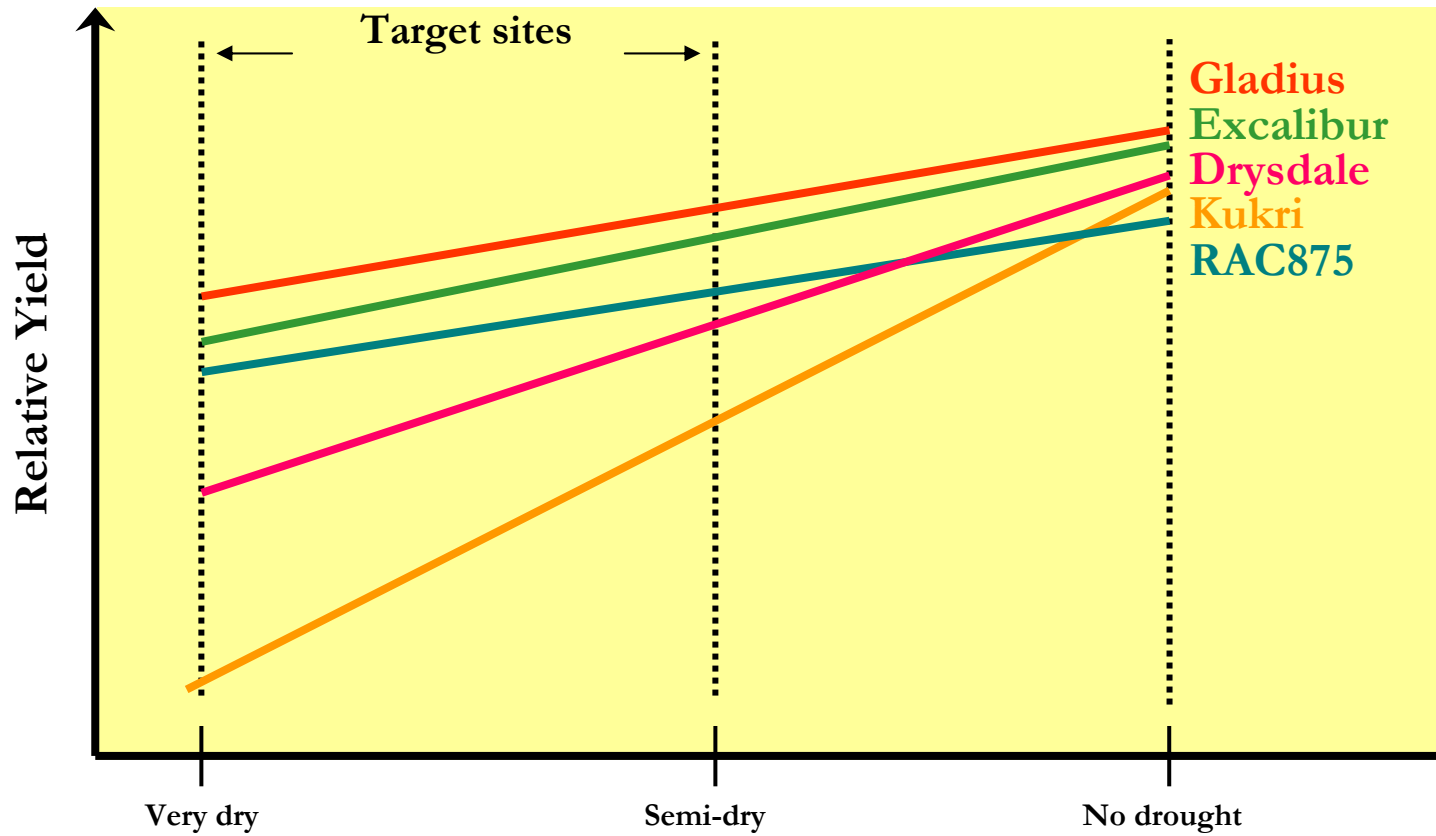


Example - Drought at ACPFG

- **Forward genetics**
 - Large mapping populations and extensive phenotyping
- **Reverse genetics and resources**
 - Transcript, metabolite and protein profiles
- **Candidates**
 - Transcription regulatory pathway
 - Stress recovery – oxidative stress tolerance



Drought tolerant Germplasm



Drought Tolerant Germplasm

Drought tolerant Germplasm

Resources:

Drought Mapping Populations

- Kukri x Excalibur, 233 DHs & 3'000 RILs
- Kukri x RAC875, 368 DHs & 3'000 RILs
- Drysdale x Gladius, 5,000 RILs

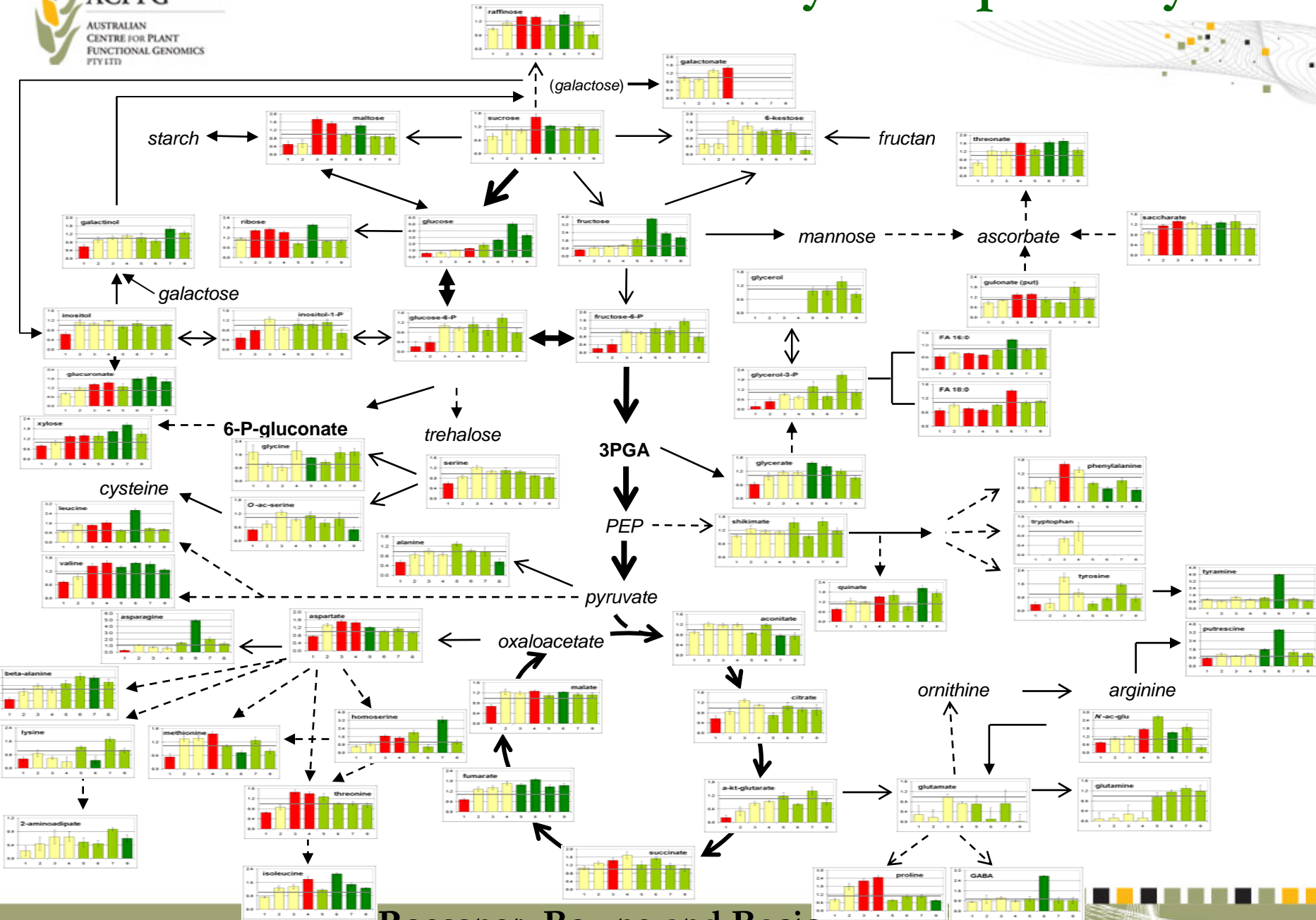
All parents with Rht2 and similar maturity

Traits	RAC875	Kukri	Excalibur
Boron (B) uptake	low	intermediate	very high
Sodium (Na) uptake	low – intermediate	intermediate	low
Micro nutrients: - Zn efficiency	low	low	high-intermediate
Nematodes: - CCN - Root lesion	? susceptible	susceptible susceptible	susceptible moderately resistant
High pH (pH 8.7-9.1)	intolerant	moderately tolerant	intolerant

Example - Drought at ACPFG

- Forward genetics
 - Large mapping populations and extensive phenotyping
- Reverse genetics and resources
 - Transcript, metabolite and protein profiles
- Candidates
 - Transcription regulatory pathway
 - Stress recovery – oxidative stress tolerance

Metabolomics - Analysis of pathways



Building stress comparative data resources

Transcripts, proteins and metabolites

Metabolite profiles

Stress type

independent responses

- Raffinose (↑mineral deficiency; ↓mineral toxicity (carbon transport, osmoprotectant)
- Sucrose (major carbon source)
- Galactinol (osmoprotectant)
- Aromatic amino acids (precursors for secondary metabolism)
- Putrescine (amine, stress marker)

Stress type

specific responses

- proline (osmoprotectant)

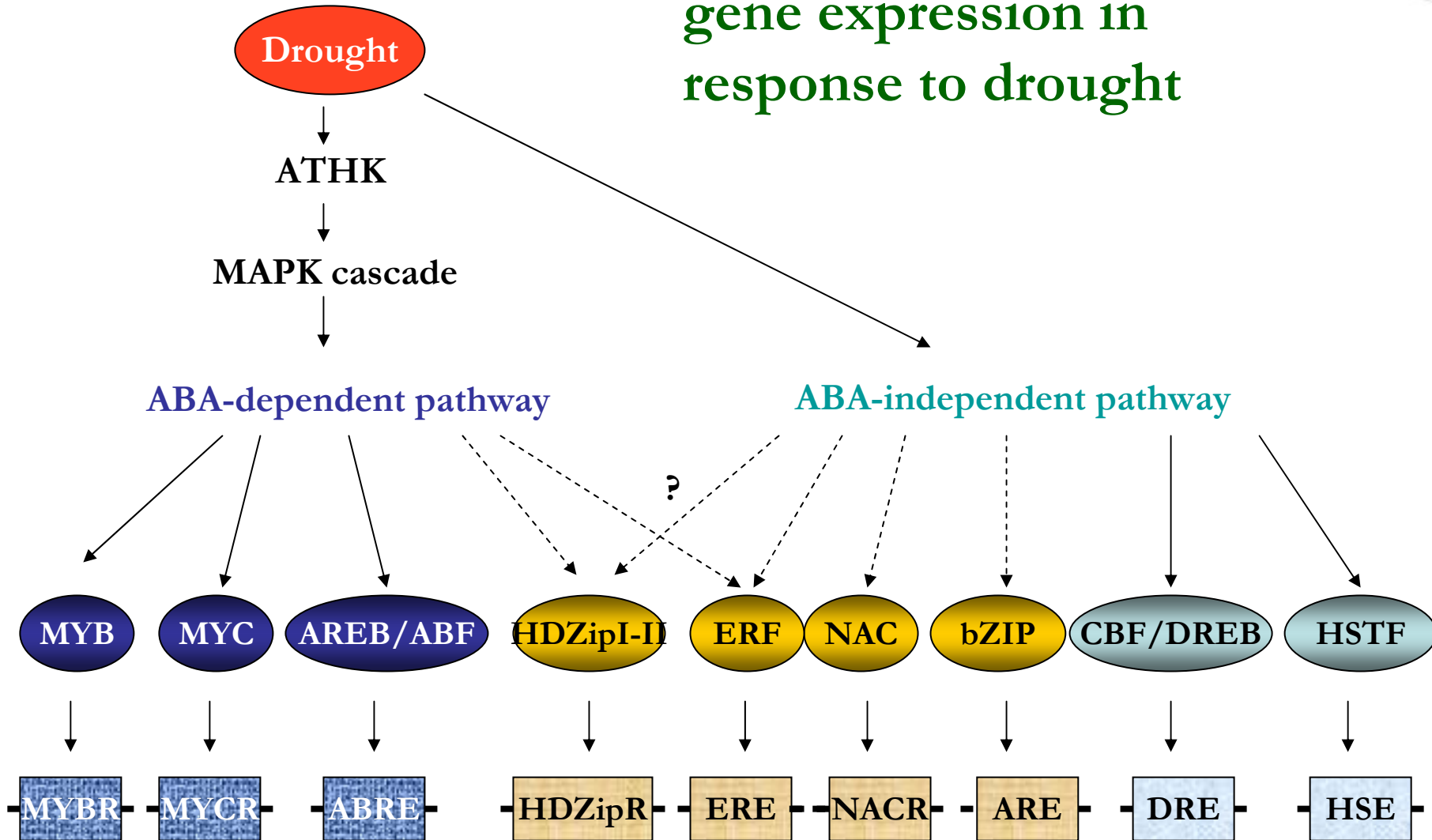
Tissue, cultivar etc. dependent responses

- 6-kestose (fructan synthesis & degradation)
- Maltose (starch degradation)

Example - Drought at ACPFG

- Forward genetics
 - Large mapping populations and extensive phenotyping
- Reverse genetics and resources
 - Transcript, metabolite and protein profiles
- **Candidates**
 - **Transcription regulatory pathway**
 - **Stress recovery – oxidative stress tolerance**

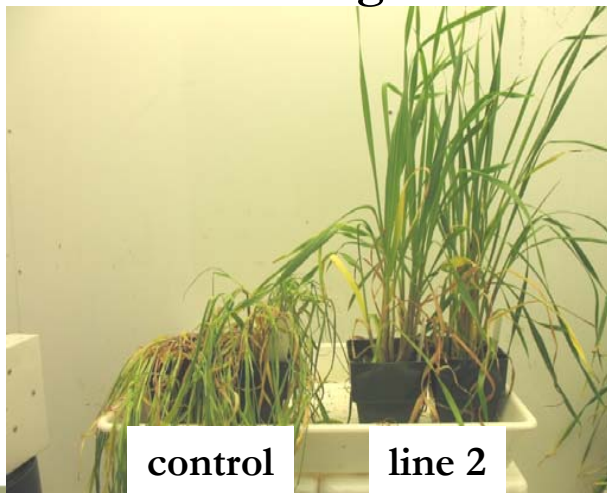
Regulatory network of gene expression in response to drought



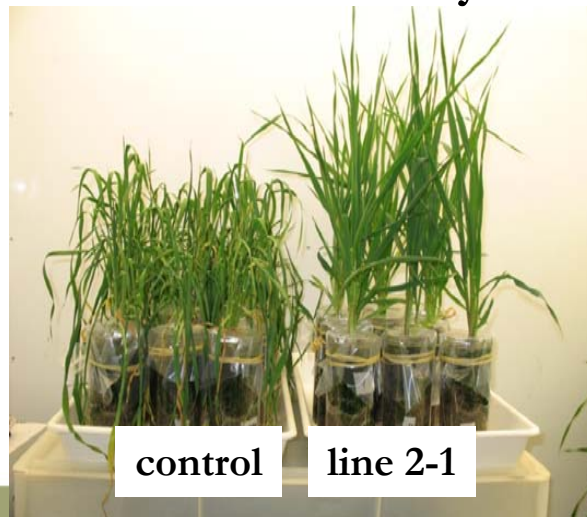
Isolation and functional analysis

- Systematic isolation of transcription factors from developing grain
- Isolation of interacting partners
- Functional analysis
 - Up and down regulation in transgenic wheat and barley
 - Glasshouse and growth room evaluation
 - Field evaluation

Killer drought



Water use efficiency



Grain yield





Conclusions

- Extensive resources available and expanding
- Many key abiotic stress tolerance loci and alleles may be species and variety specific
- Interactions between stresses can be critical in developing tolerant lines
- For intensively bred species, significant improvements in yield stability require complex and novel breeding solutions
- GM approach is looking increasingly attractive and manageable

Collaborators



**Tony Condon,
Plant Industry, Canberra**



**Ken Chalmers,
Matt Hayden, Adelaide**



**Alan Mackay,
Adelaide**



**Jason Eglinton
Tony Rathjen,
Alison Millar**



Matthew Reynolds, El Batan, Mexico



Zoran Ristic, Kansas State University, USA



**Steve Jefferies,
Haydn Kuchel**



**Scott Tingey
Shoba Sivasankar**



