

HFN LINK Proposal

Peter Jack

WGIN Stakeholders Meeting
29/11/04



Overview

- What is HFN & why is it so important to UK Wheat
- What research has been done before & why has it not helped?
- What is the structure of the current HFN proposal?
- Next Steps

HFN = Hagberg Falling Number

- Name of the Industry assay used to measure starch integrity
- Inappropriate expression alpha amylase > starch breakdown > sticky dough > low value
- “The final results of the HGCA Quality Survey show that in some areas Hagberg falling numbers were the lowest for 10 years”.

Main UK Causes Poor HFN?

- Pre-harvest sprouting
 - Inadequate depth of dormancy or failed maintenance of dormancy
 - Promoted by damp harvest conditions
- Pre-Maturity Alpha amylase (PMA or LMA)
 - Elevated alpha amylase in absence of sprouting
 - Temperature stress during development can promote it; other factors??
- Genetically independent

Why Can't Breeders Select for it?

- PHS assay eg mist irrigated plots
 - Expensive (in breeding terms) to run,
 - Wrong time of year for labour;
 - Inconsistent results;
 - Not high throughput
- PMA Assay
 - Environmental triggers poorly understood
 - No validated assay for UK
 - If phenotype-based, would suffer same problems as PHS in terms of cost, throughput *etc*

Variation for PHS & PMA

- Some UK elites do perform well even in poor years
- Thus adequate levels of genetic resistance in elite pool
 - Cultivars well characterised and genes are already dispersed in elite pool
 - Just need a high throughput, cheap, reliable means of selection
 - Probably a DNA marker
- What about utilising Exotic sources?
 - Discovery cost
 - Very high introgression cost
 - Uncertain behaviour once introgressed
- Start with Elites!!

QTL Analysis

- Studies in US; Aus; Jap; Fra; Can *etc*
 - **27** chromosome arms implicated!
 - Statistical Noise; Environment; Germplasm
 - Some particularly interesting regions
 - Independent studies > same region
 - Some QTLs line up on/near known genes
 - Amy 1; Amy2; Rht; Red genes
- How about UK germplasm/environment?
- Only 1 published QTL study.....

UK Study – Flintham et al (JI)

- Soleil x Boxer (both triple red)
 - '98 artificial sprouting conditions > major QTL on 4AL
 - 2 other wheat QTL studies > 4AL (& rice Dor gene)
 - GA biosynthesis gene maps in similar region
- QTL Validation
 - Introgressed into range white backgrounds > no effect
 - '99 **field** conditions > no 4AL QTL!
- Stresses need to use validated phenotyping methods
- Also demonstrates difficulty of utilising Global QTL data (very different environments/germplasm)

Conclusions on Previous Work

- None of this has provided UK breeders with something they can use – even indirectly!
- Need properly coordinated UK programme to look at both PMA & PHS
- Phenotyping screens **MUST** be validated against actual field conditions
- This is a not a 3 year x 1 scientist project!!

Research Discussions

- WGIN Stakeholders Meeting Nov 03
 - Breeders & end users identified HFN as major problem
 - No WGIN core projects relate to HFN specifically – would require specific initiative
- Many Subsequent Meetings including:
 - Cambridge Oct 04 –
JI/Rothamsted/Nottingham/HAdams/
Advanta/Nickerson/RAGT
 - Agreement of outline research programme as follows

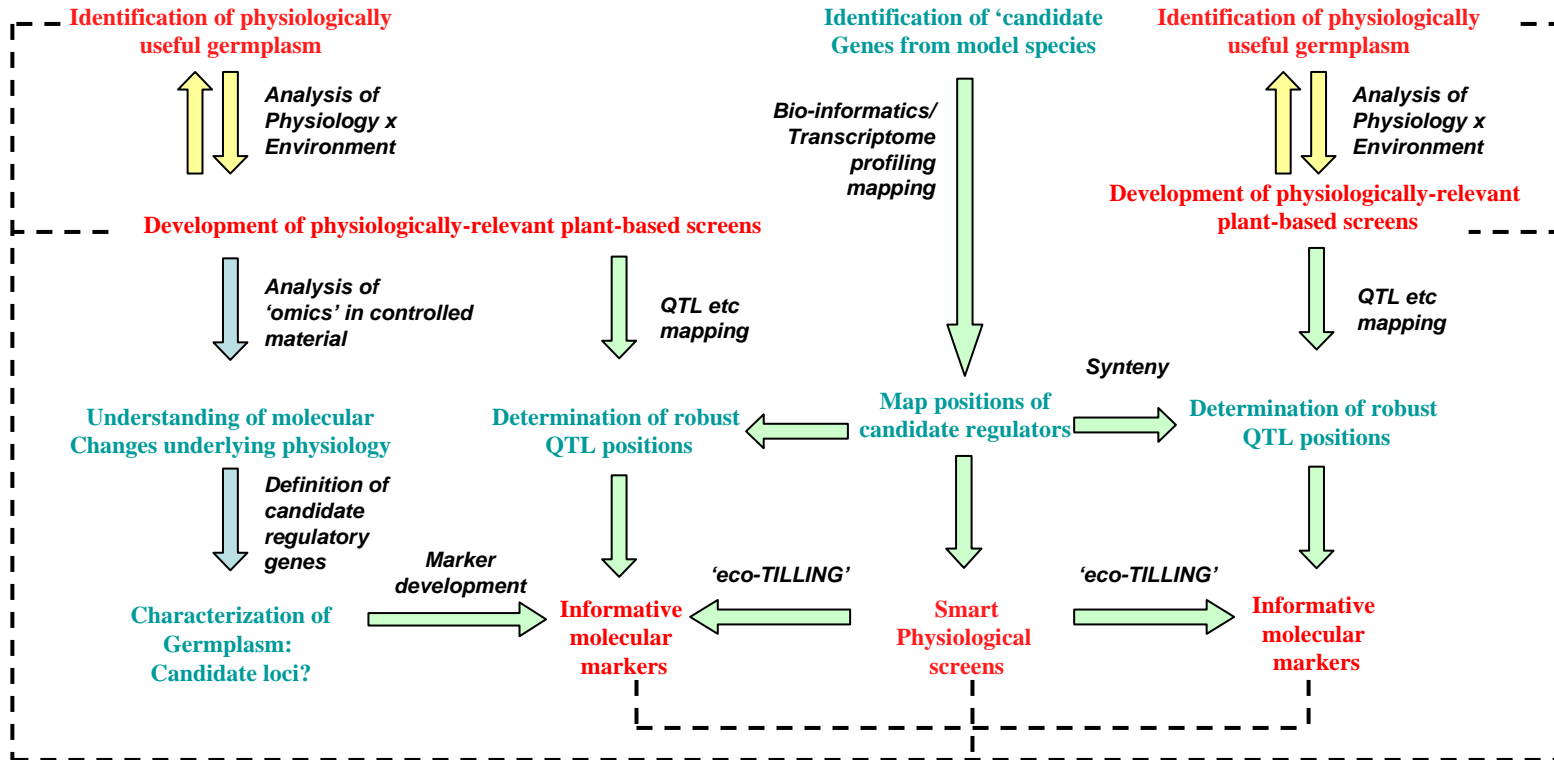
Convergent Germplasm-based & Gene-based approach

- Germplasm-based (QTLs; Association genetics)
 - Need to develop reliable Phenotyping systems for PHS & PMA using well characterised UK **elite** cultivars
 - Phenotype **elite** populations (breeders) > QTLs
- Gene-based
 - Candidate genes from literature & from expression studies (PMA)
 - Identify wheat homologues, fine map & look for overlap with elite QTLs
- Validate best candidates using Association Genetics
 - advanced breeding lines & additional cultivars
- End-point = Validated, high throughput marker system

INTEGRATING A PMA AND PHS RESEARCH PROGRAMME

PMA

PHS



Objectives	Physiology
Exploitation Outputs	Developmental biology
Approaches	Genetics

**Project Output:
High throughput
breeding screens**

Courtesy Mike Holdsworth



Key Components & Coordinators

1. PMA Phenotype Development
 - Peter Kettlewell (Harper Adams)
2. PHS Phenotype Development
 - Mike Holdsworth (Nottingham)
3. Population Phenotyping, Mapping & QTLs
 - John Flintham (JI)
4. PMA Gene Expression
 - Peter Shewry (Rothamsted)
5. Candidate Gene Characterisation
 - Mike Holdsworth (Nottingham)

LINK Proposer:

- Peter Jack (RAGT) representing Breeding Community



Key Features

- Target is HFN improvement – not basic science
– but it will involve interesting science along the way!
- Multidisciplinary – good lab-lab coordination vital
- Development of Phenotypic methods is Essential
– its not sexy but without it all else fails!
- Focus on elite materials & breeder involvement at ALL stages

Status

- Oct 21st – Agreement Project Outline
- Oct 27th – WGIN Management Meeting
 - Details outlined
 - Coordinating team met for 1st time – main objective = Concept Note
- Nov 21st – Concept Note to DEFRA LINK
 - and breeders; HGCA; CCFRA – others?
- Nov 29th – Funding strategy meeting
 - Peter Street (Sustainable LINK)
-

Outstanding Issue

- How to get end user involvement (millers; baking industry etc)
 - CCFRA
 - HGCA
 - NABIM?
 - Individual Companies – if so who?
 - WGIN Stakeholders
- Ideas & suggestions to: peter.jack@ragt.fr