

# Hagberg and pre-harvest sprouting

## 1. What do we know?

- Physiology
- Genetics
- Developmental biology

## 2. PHS vs. PMAA

## 3. Where do we need to go?

- Physiology
- Genetics
- Developmental biology



*Red & white isolines  
for the R genes*

Nottingham

Mike Holdsworth

John Foulkes

Harper-Adams

Peter Kettlewell

John Innes

John Flintham

Bristol

John Lenton

Rothamsted

Andy Phillips

Peter Hedden

**+ input from colleagues at the 10th International Symposium on  
Pre-Harvest Sprouting in Cereals (XISPHSC)**

**(still going on....)**

## **HFN: *Meetings and consultation:***

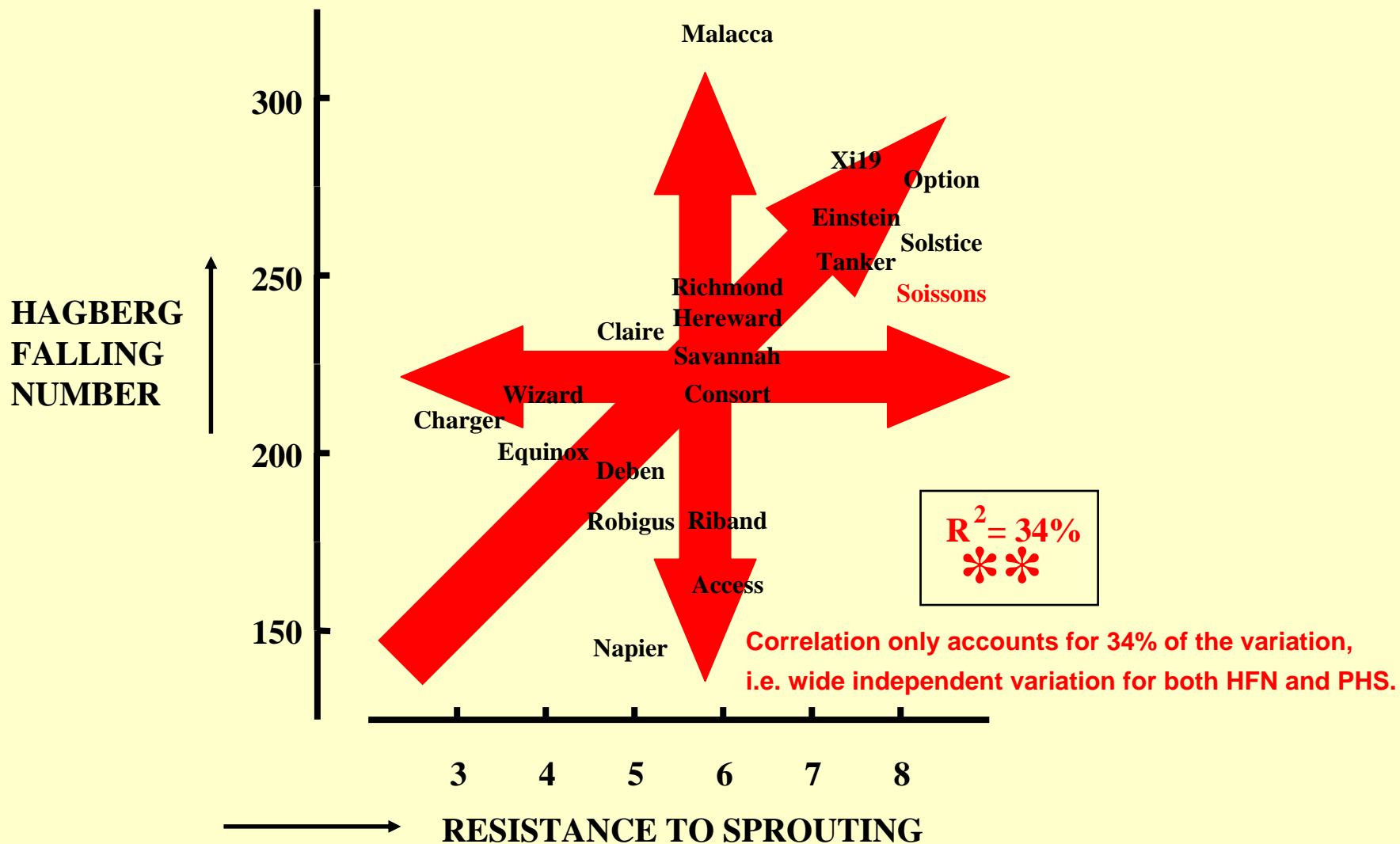
1. JIC, 21 January, meeting of scientists and representatives of breeding companies

**Main feedback: more reliable physiological and molecular tests for sprouting/PMA**

2. UoN, 12 March, follow up meeting of scientists to discuss output from (1).

*Genetics:*

# UK RECOMMENDED WINTER WHEATS 2004/05



*From JF*

Data from HGCA National List trials (Hagberg mean over trials, sprouting from artificial rainfall on ripe plots).

*Lunn et al J. Cereal Sci. 33 (2001) 313-329*

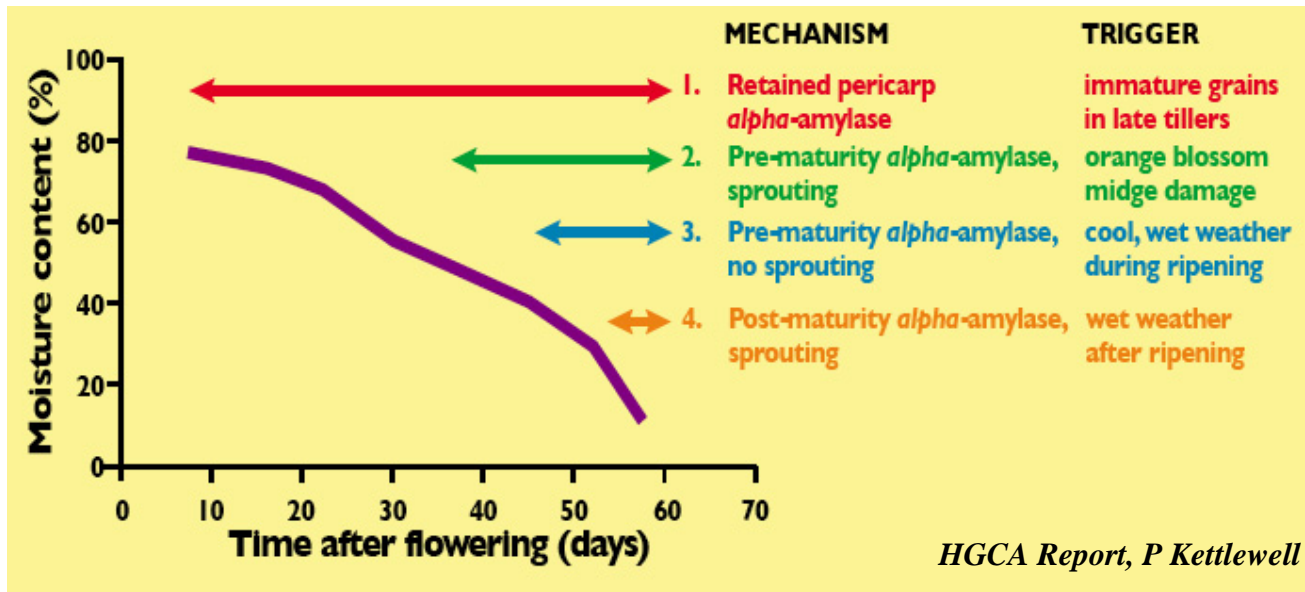
4 modes of accumulation of alpha-amylase in UK wheat:

1. Retained pericarp alpha-amylase activity (RPAA)
  2. Pre-maturity alpha-amylase activity (PMAA)
  3. Pre maturity sprouting (PrMS)
  4. Post maturity sprouting (PoMS)
- A. Developmental switch 'PHS'
- B. Inappropriate enzyme expression 'PMA'

*Levels of importance:*

PoMS > PMAA > PrMS > RPAA

*Lunn et al J. Cereal Sci. 33 (2001) 313-329*



# What do we know?

*Timings of enzyme activities:*

Normally:

*pericarp*  $\alpha$ -AMY-2  
*embryo*

$\alpha$ -AMY-1  $\alpha$ -AMY-2

fertilization..Cell proliferation.....Maturation.. ...Desiccation..

..Imbibition ..Early Germination Late..

*pericarp*  $\alpha$ -AMY-2 RPAA

*embryo*

$\alpha$ -AMY-1PMAA

$\alpha$ -AMY-1/2 PoMS

High Amylase conditions

# What do we know?

## **PHS vs. PMA:**

- Both can cause quality problems associated with increased Levels of amylase production
- These do not appear to be the same phenomena
- Some underlying developmental mechanisms may be regulated in the same way
- Both have specific different environmental triggers

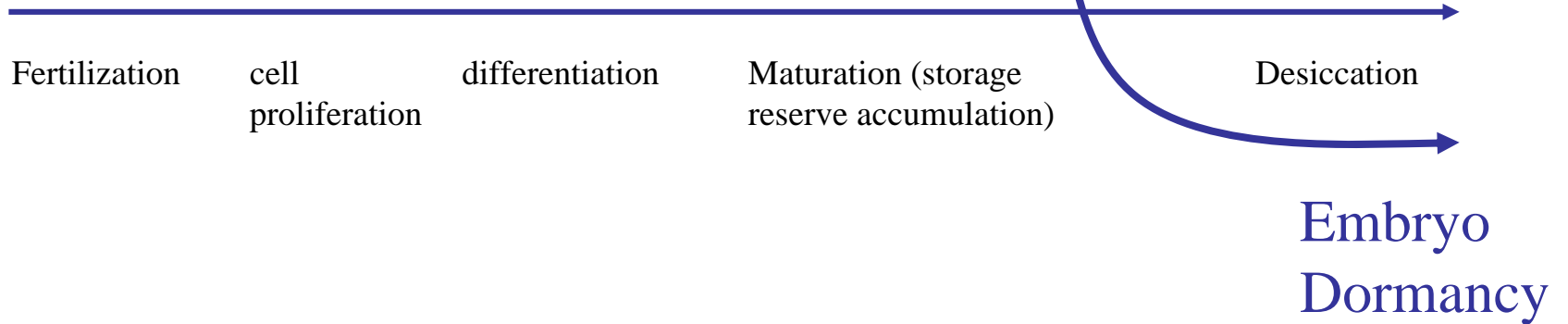
# Sprouting

*Physiology:*

Net water loss

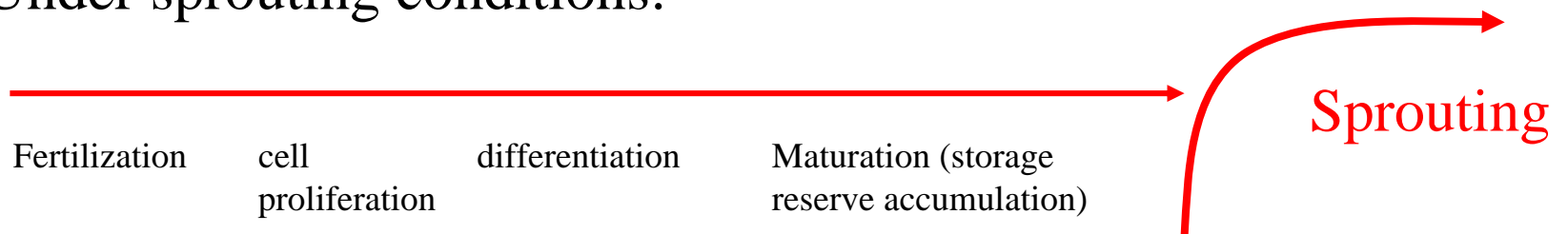
[Abscisic Acid  
(ABA)]

Normally:



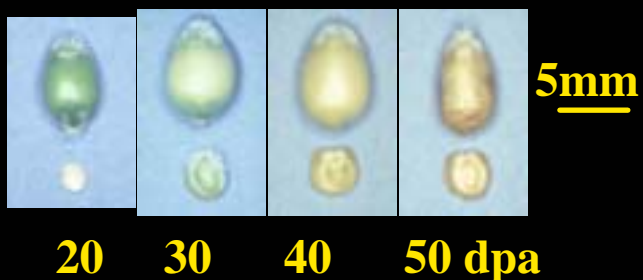
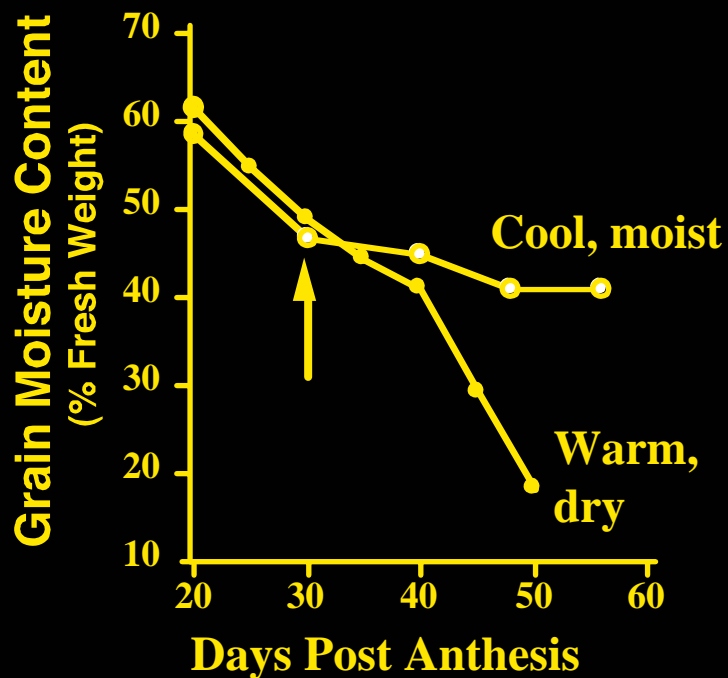
Under sprouting conditions:

Gibberellins?



# Physiology:

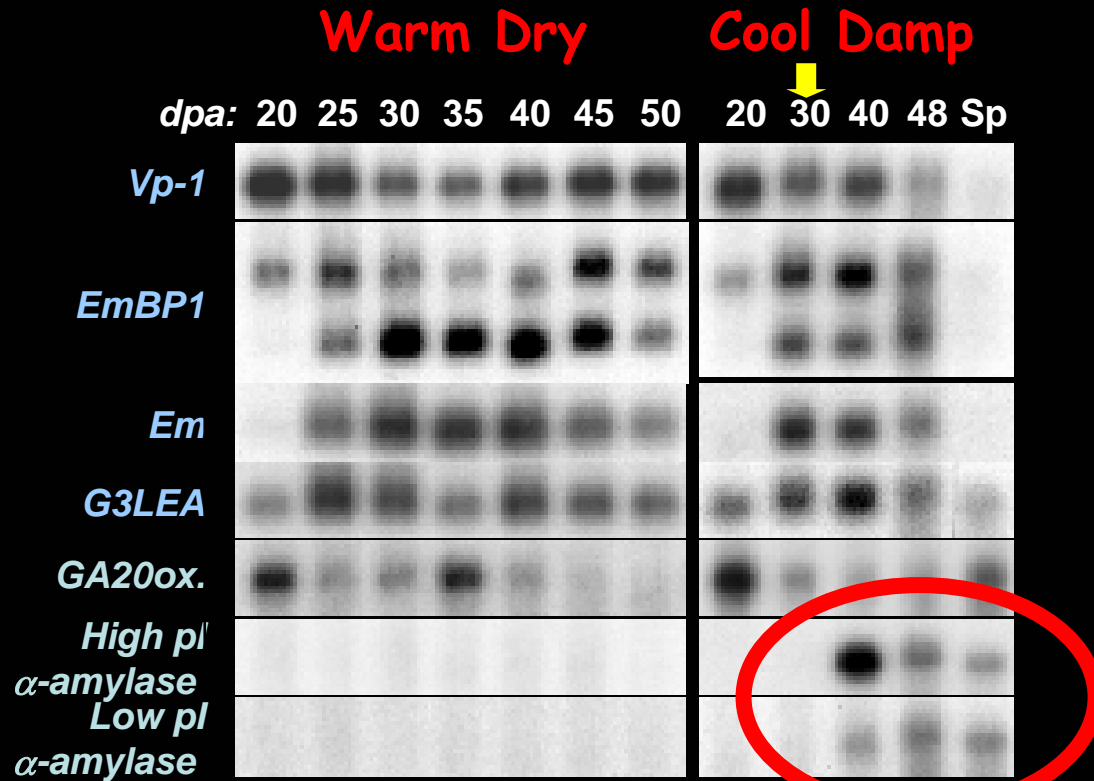
## Cool Moist Conditions Delay Seed Development, and Induce Pre Harvest Sprouting



- Stochastic
- Non-coordinated

# Developmental biology

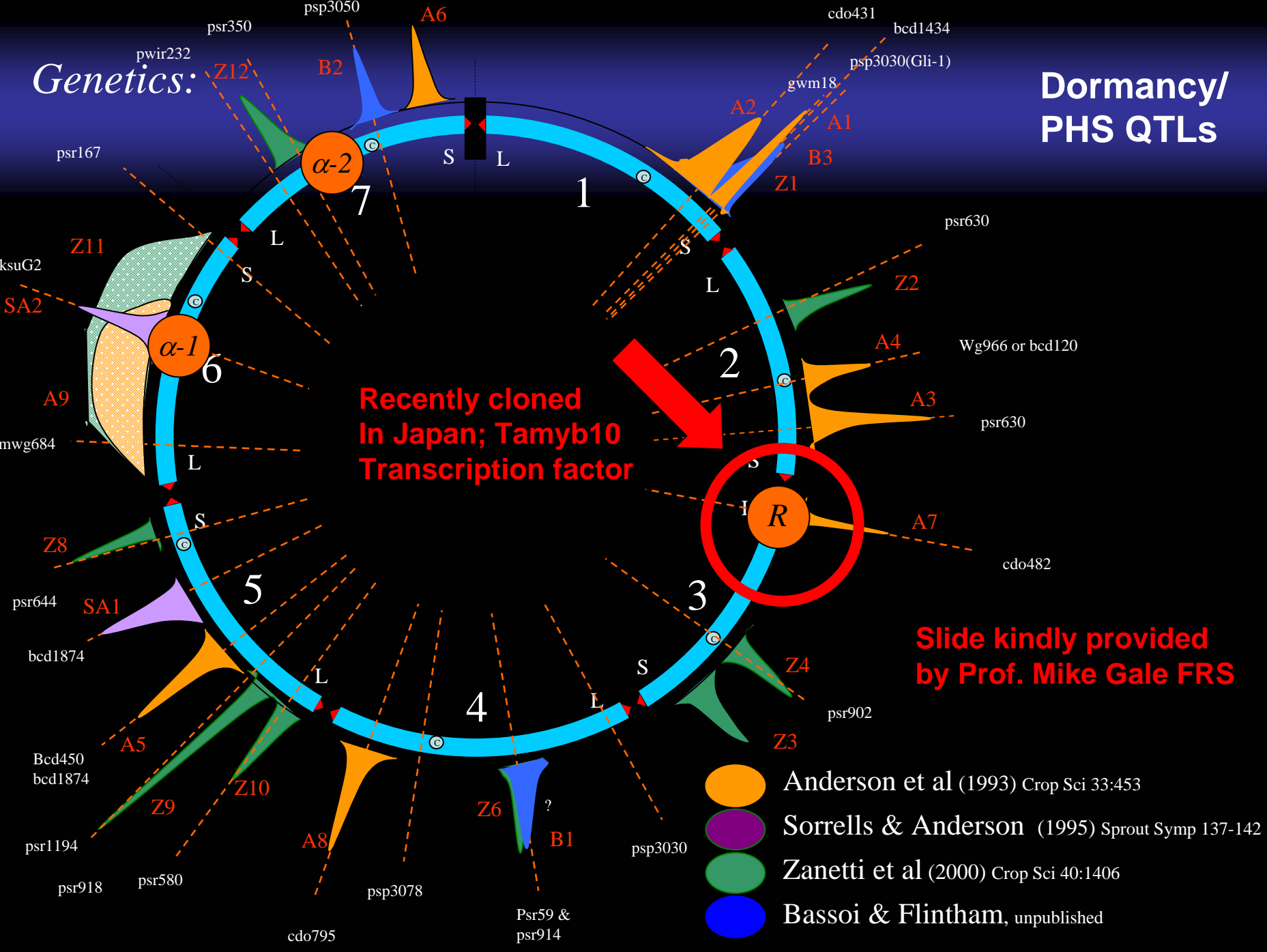
## Gene Expression Before the Visible Onset of PHS



↓ Transfer to cool damp conditions  
Sp; sprouted seedlings

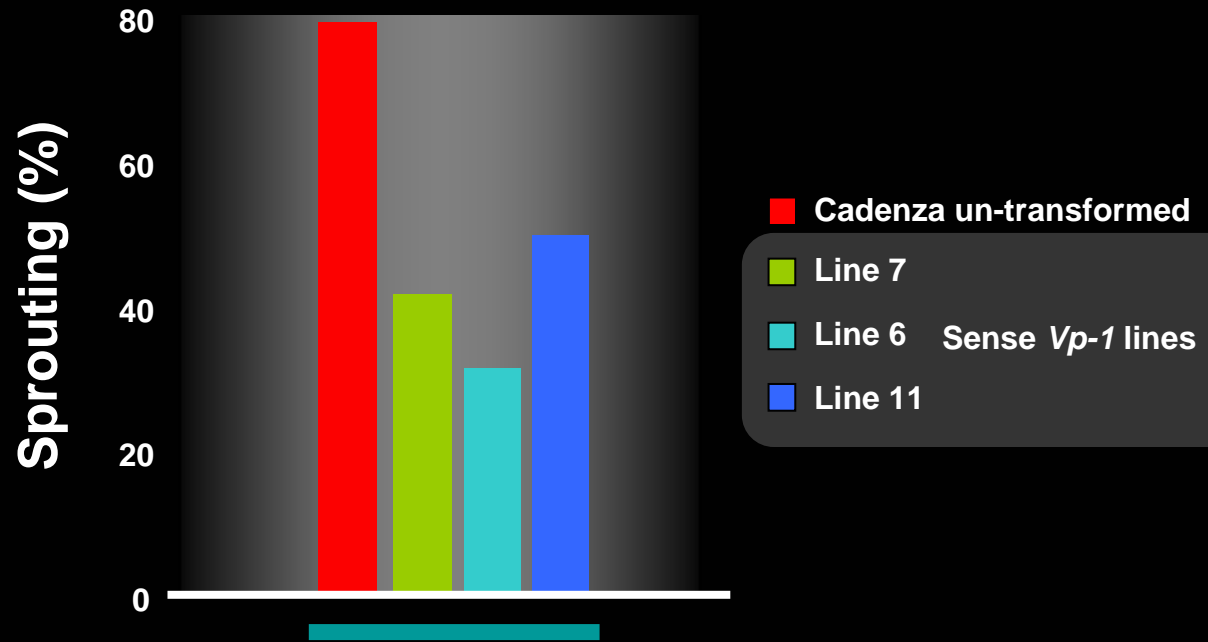
Genetics:

Dormancy/  
PHS QTLs



*An example using comparative genetics to influence sprouting resistance:*

## Effect of Introducing Fully Spliced Vp-1 Into Wheat



**Therefore Wheat does not produce enough functional Vp-1 protein to repress sprouting**

# Key PMAA Studies

1990's - study of origin of high alpha-amylase activity at Harper Adams University College (Bernard Major and Peter Kettlewell) and University of Nottingham (Gavin Lunn and Keith Scott) with University of Aberdeen (Bob Naylor) and ADAS Bridgets (Martin Froment)

- Lunn et al., 2001. *J. Cer. Sci.* **33**:313-329.

2000-2004 Determining the PMAA status of Rialto; further controlled environment transfer experiments; initial development of a PMAA screen at Harper Adams (Andro Tjin and Peter Kettlewell) and Monsanto (Richard Summers)

– Tjin (2004). PhD Thesis (Open University) submitted.

# Key PMAA Findings

- Controlled environment experiments showed that **transfer of plants to higher temperature** for three days before 45% grain moisture, followed by slow grain-drying conditions led to greater PMAA in some cultivars
- **Transfer to cool temperature gave fewer responses**
- Equipment constructed for detached tiller screen

[ELISA test exists to screen for PMAA]

Where do we need to go?

- Physiology
- Genetics
- Developmental biology

# *Physiology*

## ***Drivers:***

At present there is not a good understanding of the physiology of PHS/PMA, or a generally accepted robust physiological test to define variety responses.

In order to provide strategies for the development of resistant wheat types, we require greater understanding of both:

- *physiological **competence** of seeds for the development of PHS/PMA*
- *physiological changes associated with **developmental response** to environmental conditions*

## ***Opportunities:***

**Development of physiologically-relevant plant-based screens to categorise PHS/PMA susceptibility of varieties.**

- *Example of what can be done,  
Australia: Univ. Melbourne screening centre*

## *Developmental Biology:*

### *Drivers:*

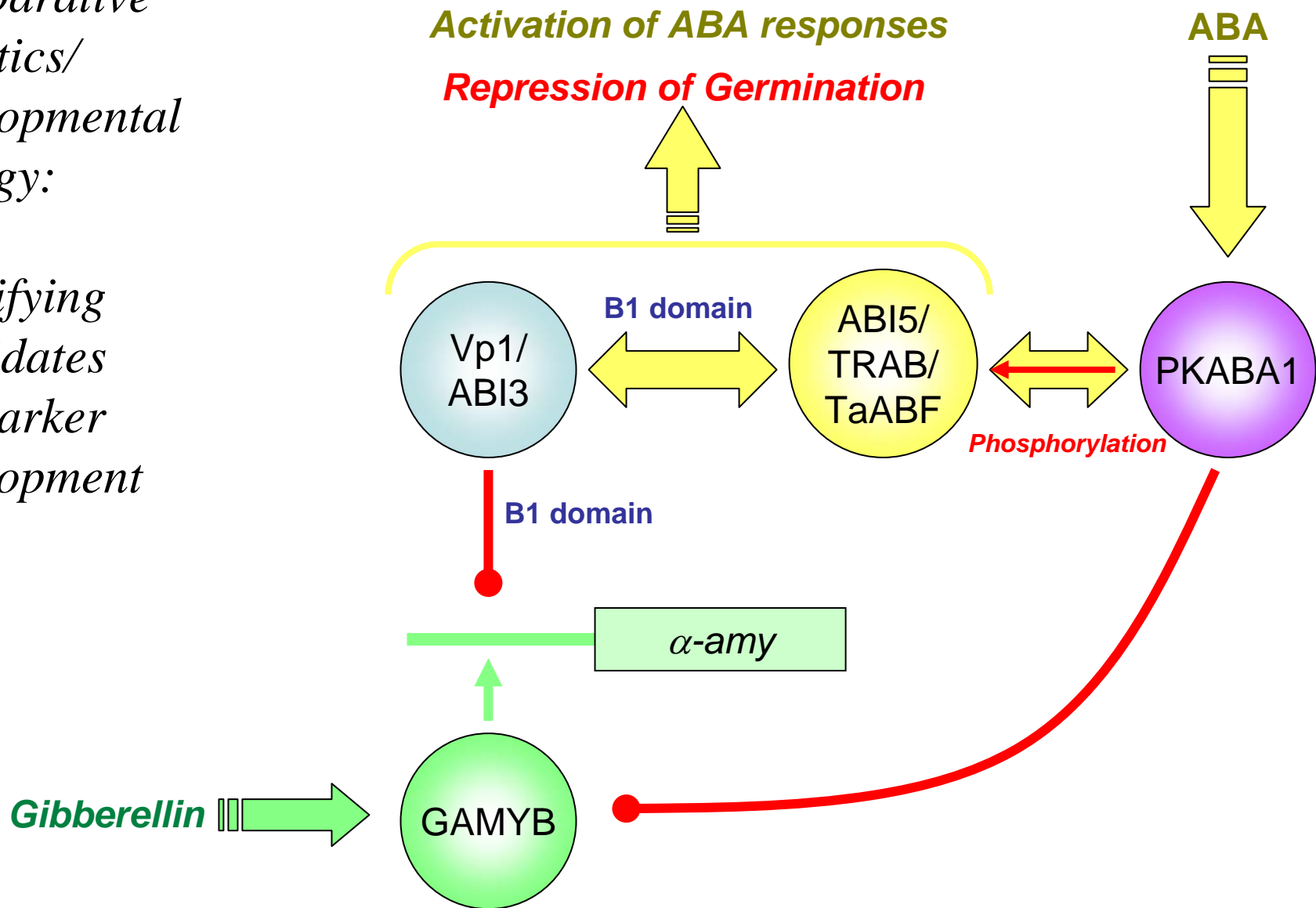
- Need to understand the genetic basis for *susceptibility* to PHS/PMA.
- Need to understand the molecular basis for PHS/PMA *development*.

### *Opportunities:*

- 1. Analysis of the precise gene expression and metabolism changes associated with PHS/PMA.**
  - **Transcriptomics/ targeted analysis of ‘key’ candidate genes**
  - **Developmental timing and tissue specificity of candidate gene expression**
  - **Metabolomic analysis eg. GA precursor/ABA catabolite levels**
- 2. Characterization of elite and exotic germplasm for variation in responsiveness at the molecular level.**

*Comparative  
Genetics/  
developmental  
biology:*

*Identifying  
candidates  
for marker  
development*



## *Genetics:*

### *Drivers:*

- To identify new lines resistant to PHS/PMA over a *range of environments*.  
[physiology opportunities]
- Requirement for DNA diagnostics, linked to *useful QTLs*, for efficient marker-aided selection from small samples.
- Gaps in our understanding of *genes controlling development* of resistance /susceptibility to PHS/PMA. [developmental biology opportunities]

### *Opportunities:*

- **QTL analysis of genetic variation in modern UK germplasm:**
  - **Mapping populations representing PHS/PMA genetic diversity**
    - **Reliable PHS and PMA scores for mapped WGIN populations.**
    - **Genomic linkage maps of DNA polymorphisms**
- **Identification and analysis of *candidate genes* from QTLs, models, new research.**

*Genetics:*

WGIN mapping population parents:  
Variation in HFN characters

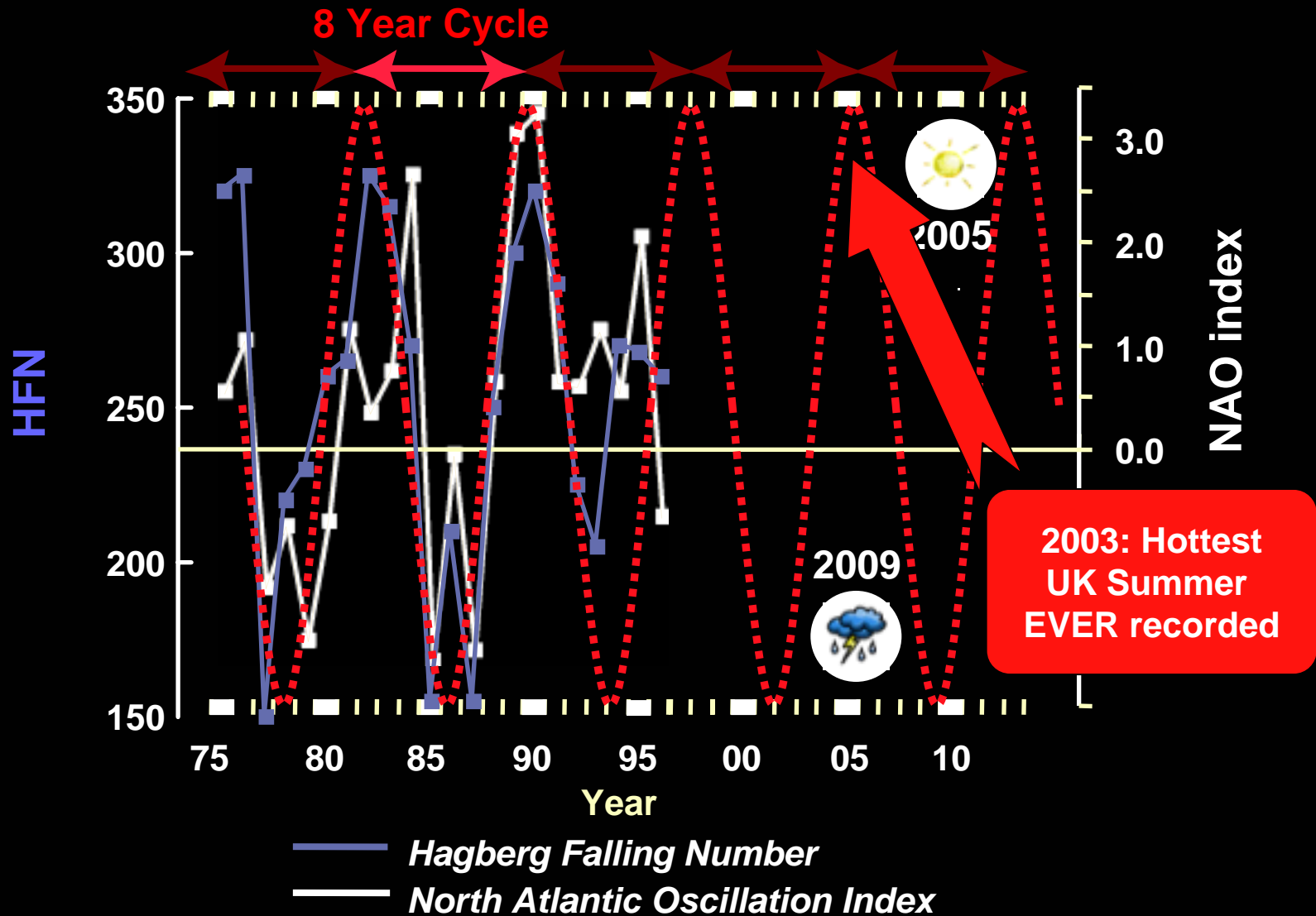
Avalon      *high*  
Cadenza      300

Beaver      *low*      *HFN being done;*  
Soissons      258      *BBSRC ExGen project*

Spark      322 <i>HFN on 60 lines</i>
Rialto      220 <i>ExGen project</i>

Cadenza      300  
Lynx      172

# Wheat Sprouting; Needs continued research for resistance



Adapted from Kettlewell et al, *J. Cereal Science* 29; 205-209 (1999)

NAO winter readings from [http://www.cgd.ucar.edu/cas/catalog/climind/nao\\_monthly.html](http://www.cgd.ucar.edu/cas/catalog/climind/nao_monthly.html)

