WGIN Diversity and Double Haploid Trials: possibilities for improving N use

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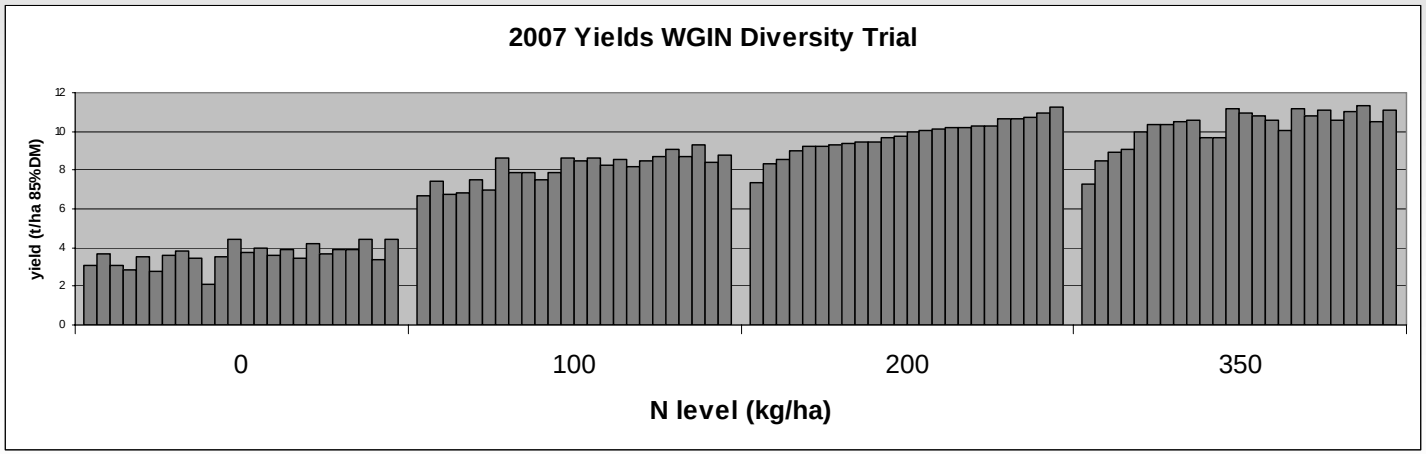
ROTHAMSTED RESEARCH

Rothamsted WGIN field trials and nitrogen

- WGIN Rothamsted Diversity Trial and mapping population
- Summary of acquired data on Diversity Trial (2004-07)
- The Avalon x Cadenza trial (2007)
- 2008 trials (final year?)
- Gene based approaches
- Why nitrogen? (yield, N, cost, environment)



Overview

- Current varieties have been selected under high-inputs
- Surprisingly little information in the public domain on UK cultivars
- Is there any variation in N-efficiency in wheat cultivars?
- Need for good basic data on the complex trait of N-efficiency
- Need to identify good performers and the traits responsible to aid breeding programmes
- Need to de-convolute traits and identify contributing genes

WGIN Diversity Trial
2004-08

WGIN Diversity Trial summary

Diversity trial

- 2004: 0, 50, 200 & 350N, 32 varieties*
- 2005: 0 & 200N, 20 varieties*
- 2006: 0, 100 & 200 N, 24 varieties*
- 2007: 0, 100, 200 & 350N, 24 varieties*
- 2008: 0, 100, 200 & 350N, 24 varieties*

*Varieties varied with core set identical. 2007 and 2008 will be identical.

N usually 0, 100, 200 and 350 kg/ha.

2007: randomised block design, 3 replicates, 18 x 3 m plot size

WGIN-06 Varieties

WGIN-06

24 Varieties x 3 N x 3 Reps

1.	Avalon	HEreward	MErcia	SAvannah
2.	BAtis	HURley	MOnopol	SHamrock
3.	Beaver	ISTabraq	NApier	SoiSsons
4.	CadenZa	LYnx	PAragon	SoKrates
5.	CLaire	Malacca	RIband	SoLstice
6.	COrdiale	Maris Widgeon*	ROBigus	XI19

Underlined = parent of public DH mapping population

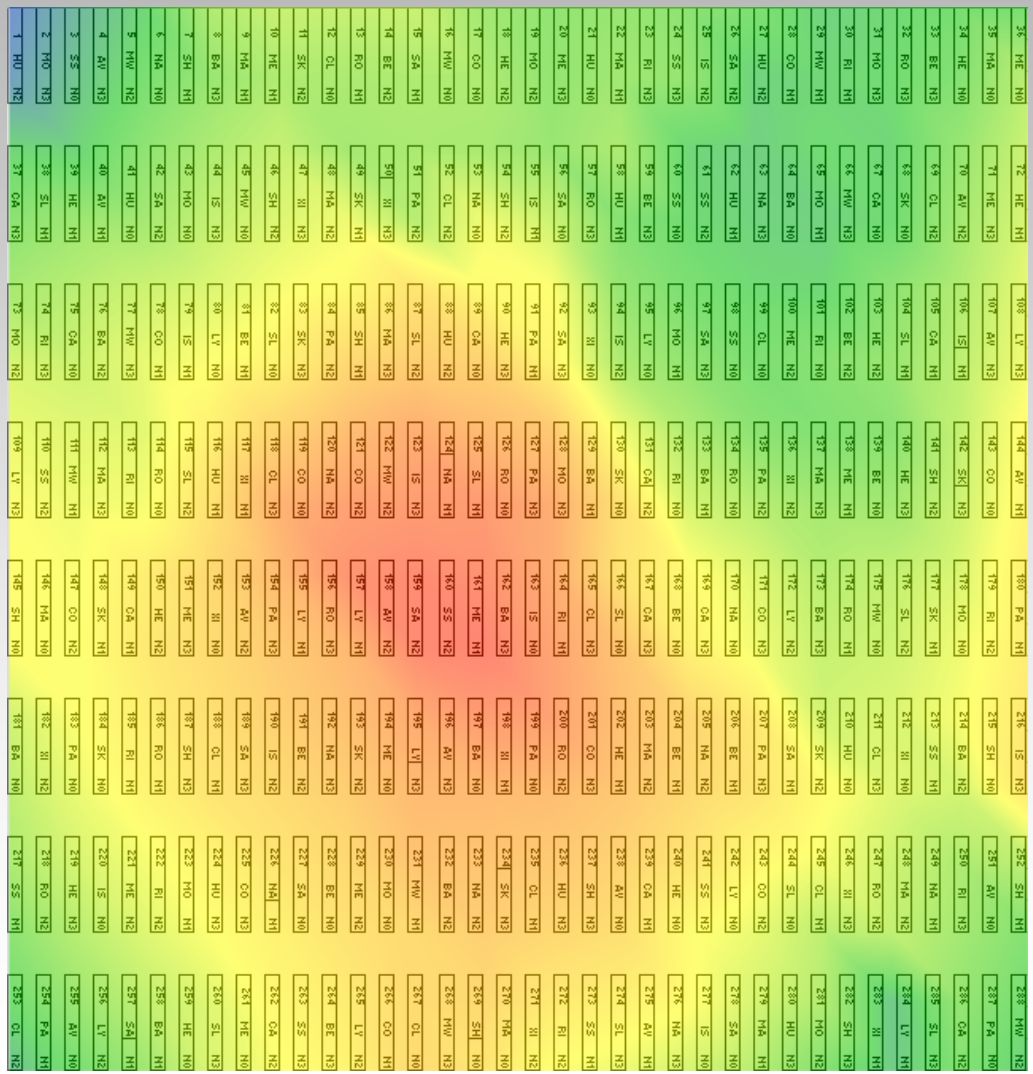
Blue = public molecular data available

Green = Broadbalk @ RRes

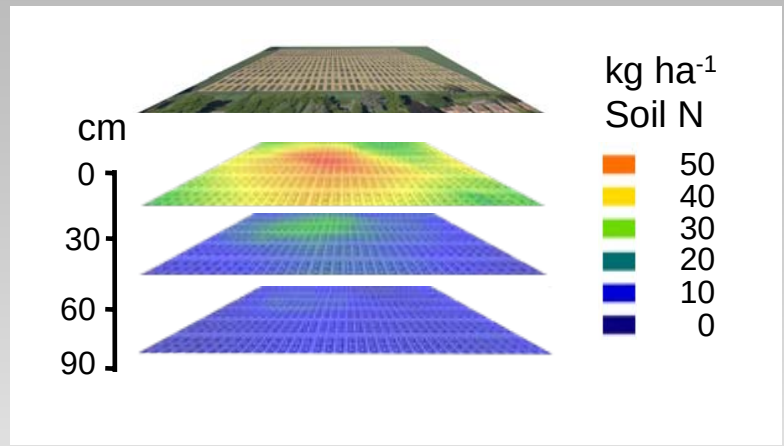
Purple = spring variety

***Tall variety**

Soil N measurements: WGIN Diversity Trial, 2007



Depth 0-30 cm

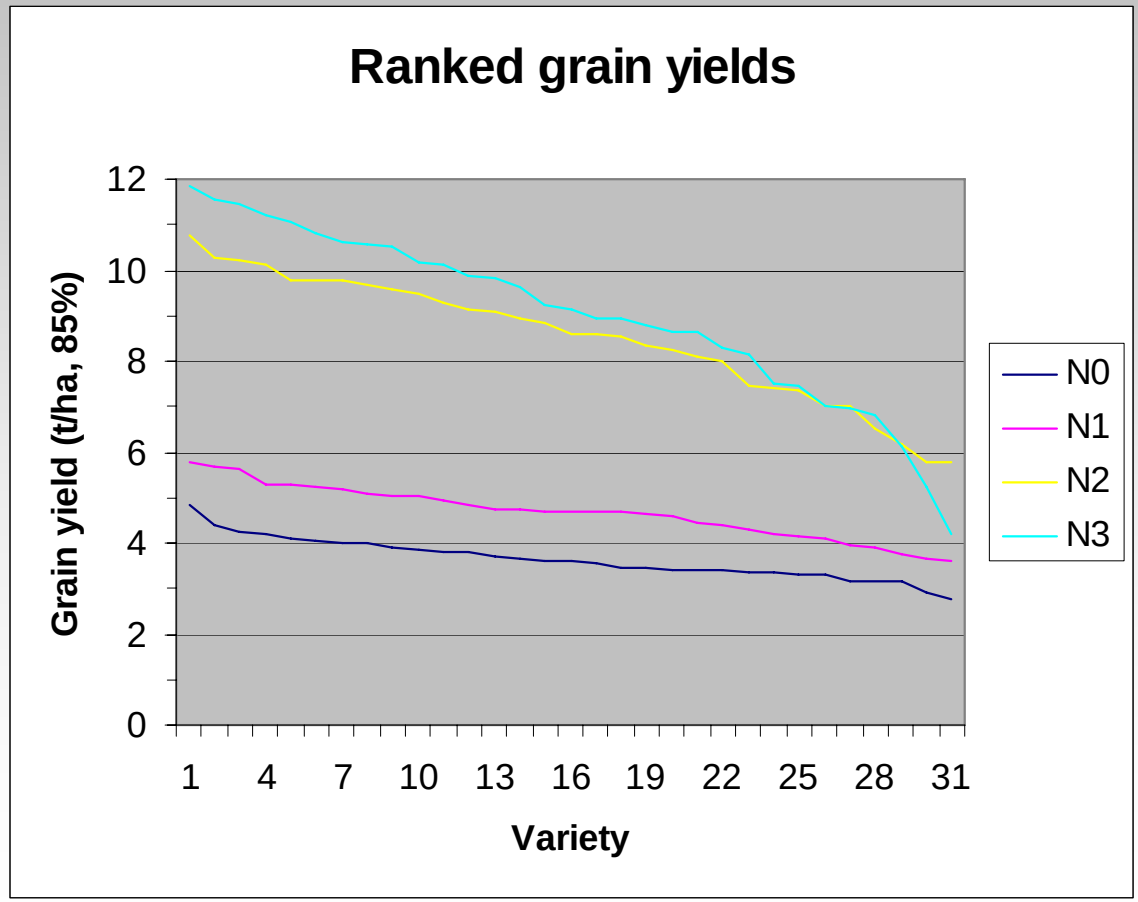


Diversity trial, 6th July, 2007

Yield: WGIN studies indicate genetic diversity

Data collected from WGIN trials 2004-2007 and being analysed

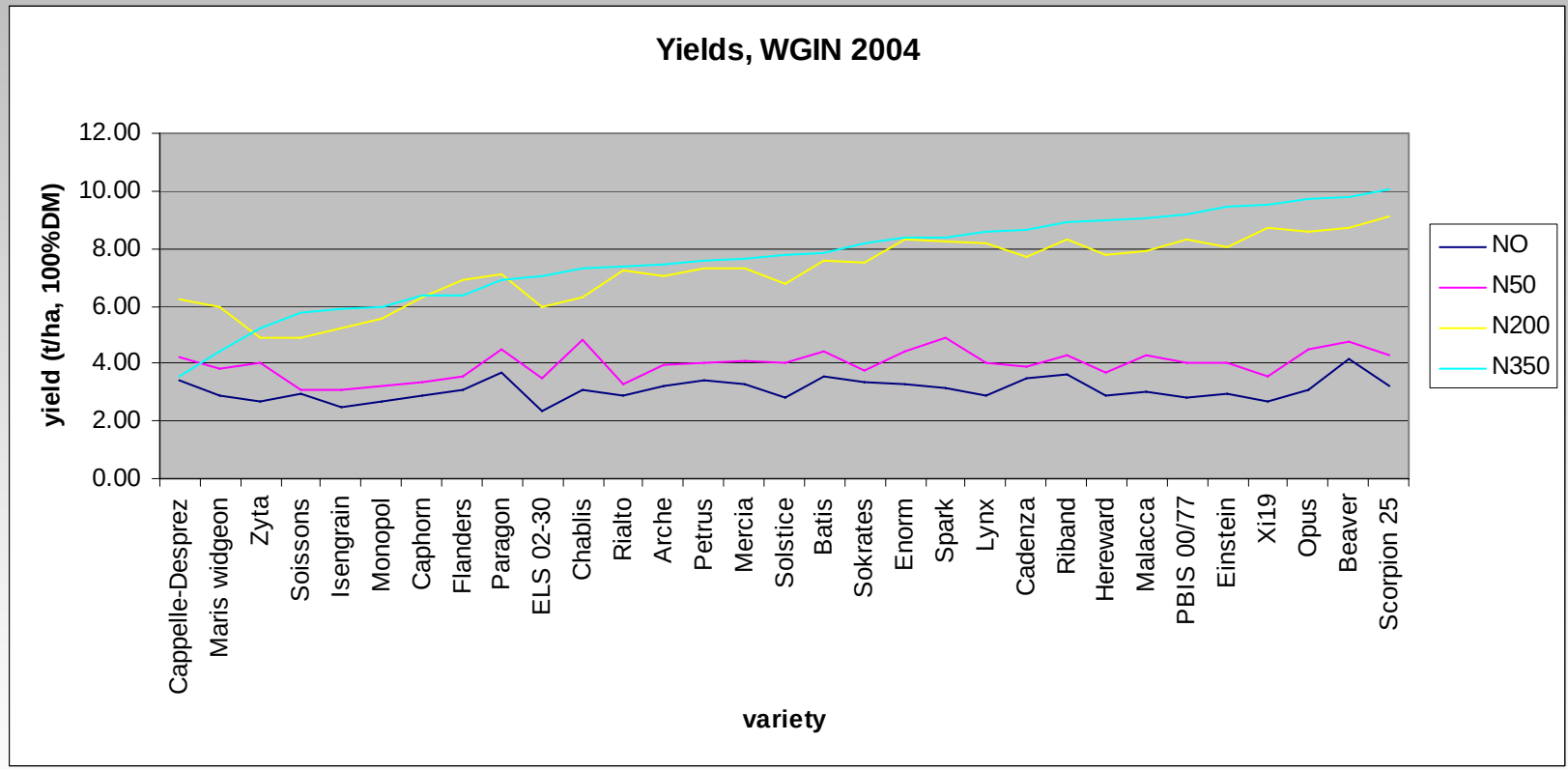
Considerable variation in yield and NUE parameters



LSD (5%) = 1.313

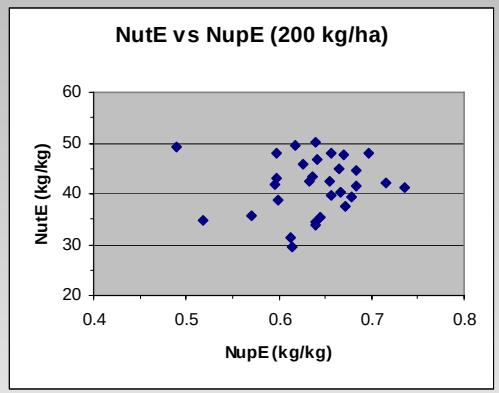
Note: varieties ranked independently for each N rate

Varieties do not perform in same rank order at different N inputs



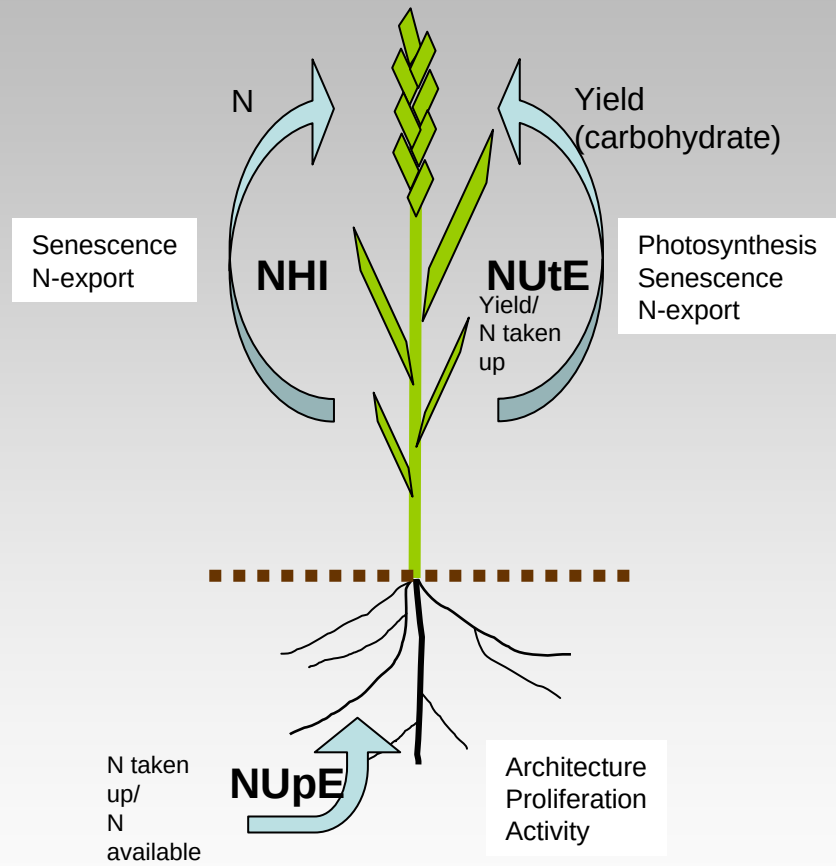
NUE, NUpE and NUtE

- NUE has two **independent** components: uptake efficiency and utilisation efficiency

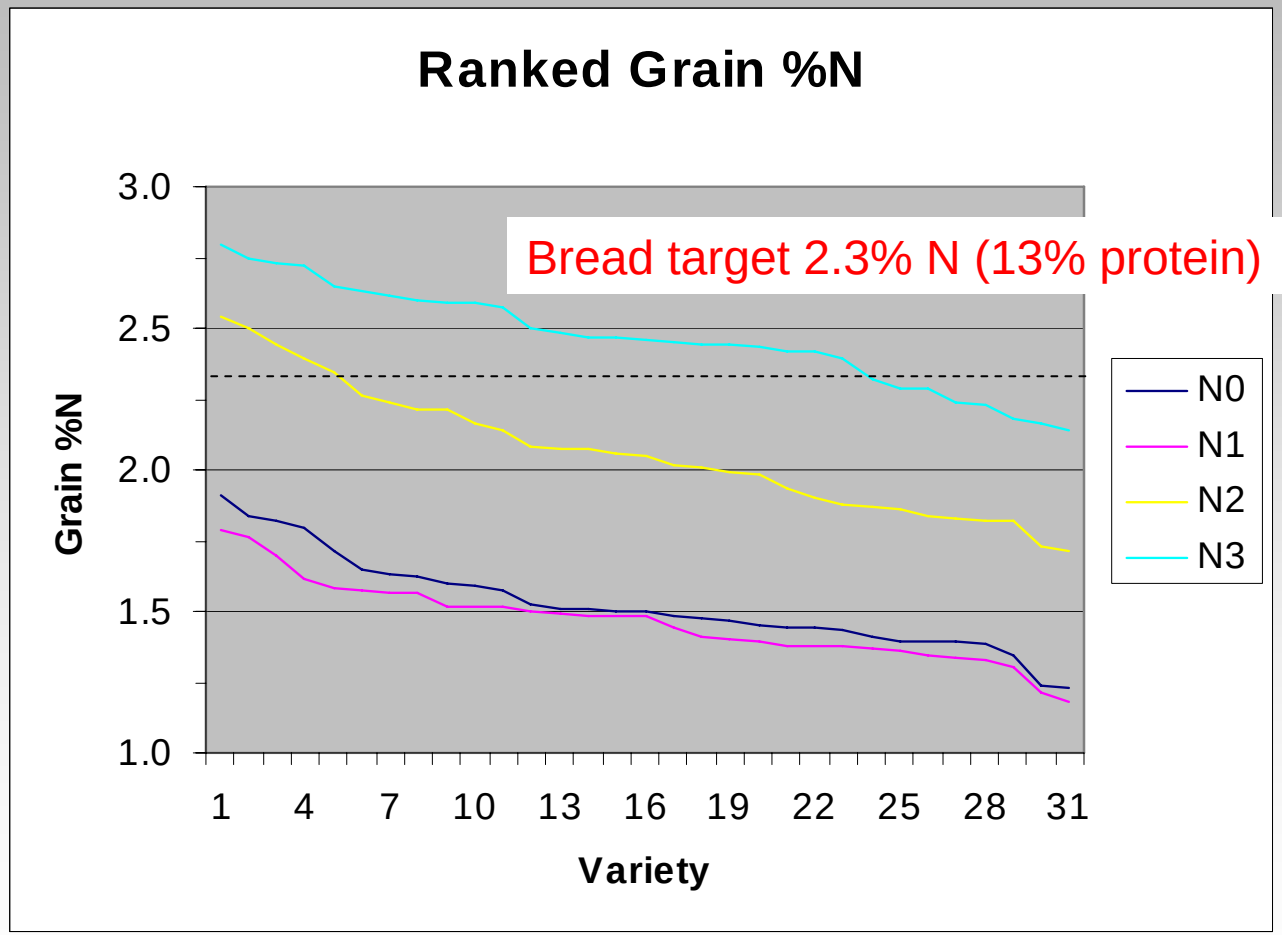


- N-uptake efficiency (**NUpE**) is total crop uptake divided by N supply from soil and fertilizer (uptake/supply) – root trait?
- N-utilisation efficiency (**NUtE**) is grain yield (100%DM) divided by total N uptake (yield/uptake)
- Overall N-use efficiency, **NUE = NUpE x NUtE** (=yield/supply)

- **How much variation in grain N and NUE parameters?**
- For all component traits, multiple pathways, enzymes, genes and control sites/forms of regulation involved



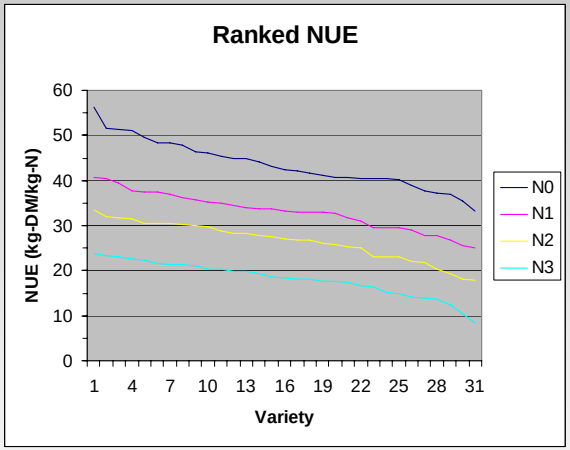
Grain %N: N-rate dependent and genetic diversity



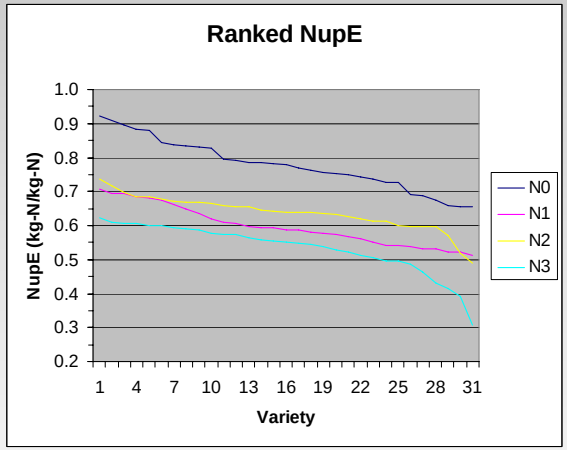
LSD (5%) = 0.218

Evidence for genetic diversity: variation in NUE and components

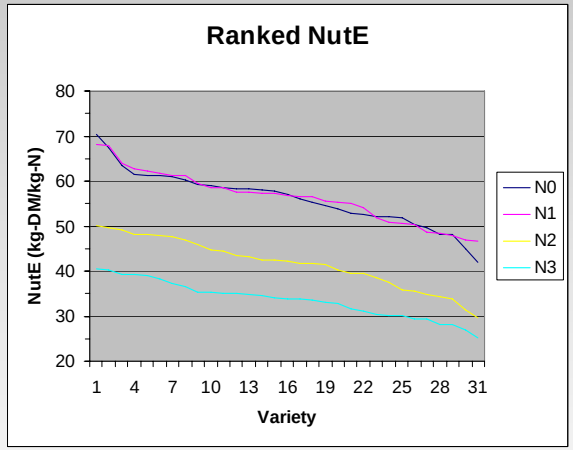
(2004 data)



LSD (5%) = 5.6 (10.7)

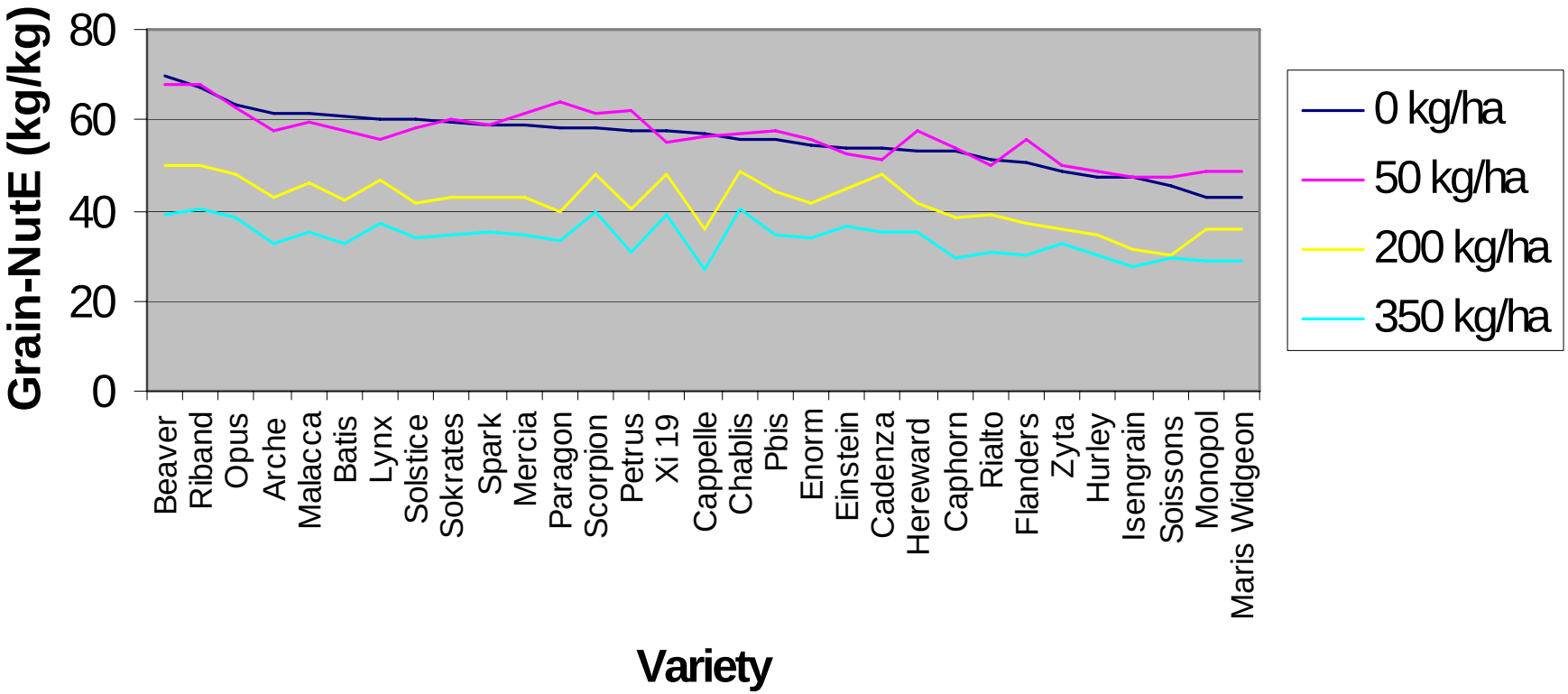


LSD (5%) = 0.197



LSD (5%) = 6.33

Rothamsted WGIN-04
Combine Grain-NutE



Ranked on performance at 0 kg/ha

Multiple year comparisons

- Data presented from WGIN year 1, 2004
- Data also analysed 2005 and 2006, 2007 in preparation and 2008 in ground
- Some year to year variation in varieties tested and in experimental design
- Comparison of 2004-6 indicates similar year to year results with some exceptions

Double haploid trial

Avalon x Cadenza

Working on DH population, 19th June

WGIN Mapping Population Trial summary

DH (Avalon x Cadenza)

- 2007:2 sites (3 + 2 reps)
- 2008: 2 sites (3 + 3 reps) + seed

204 lines + parents.

Sites: Rothamsted and Woburn

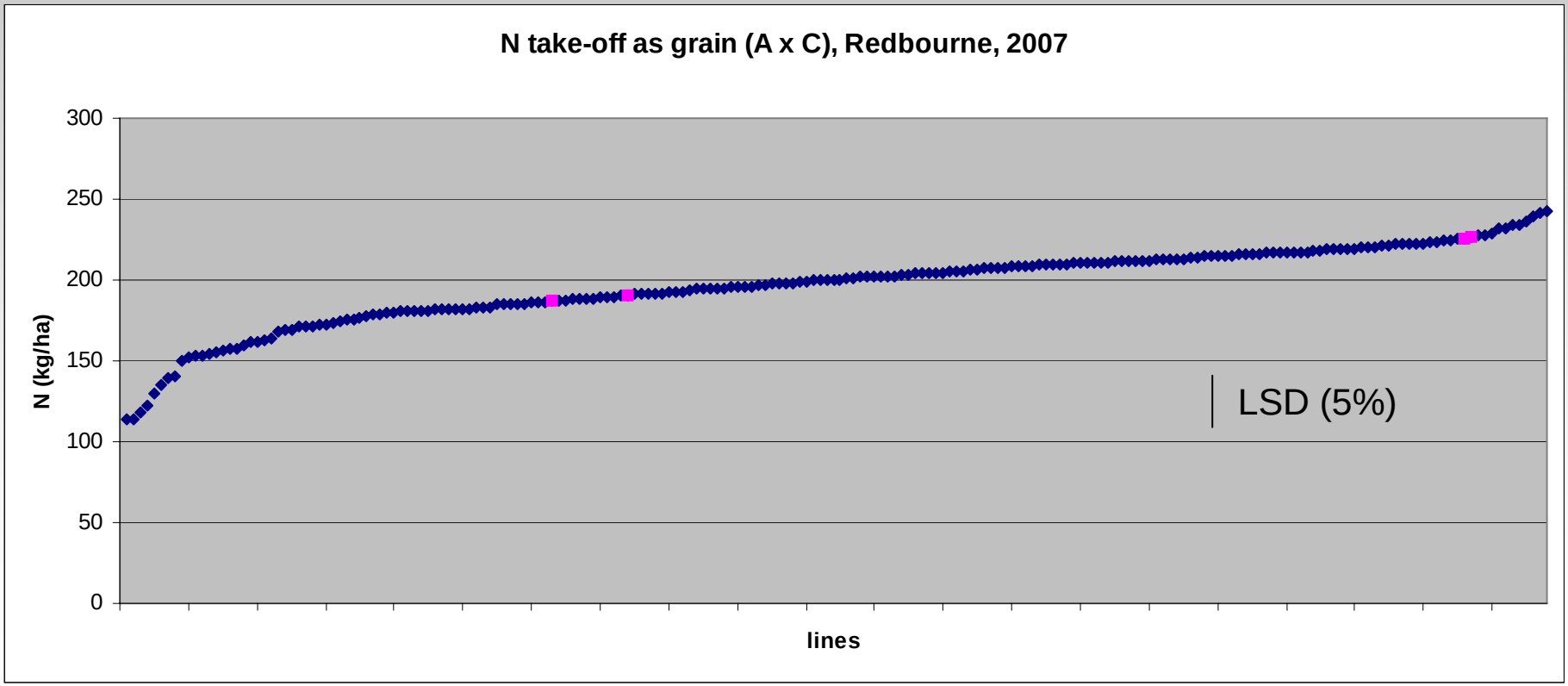
Randomised block, 3 reps, plot size was 8 x 2 m

N was 200 kg/ha in 2007 and will be 100 kg/ha in 2008.

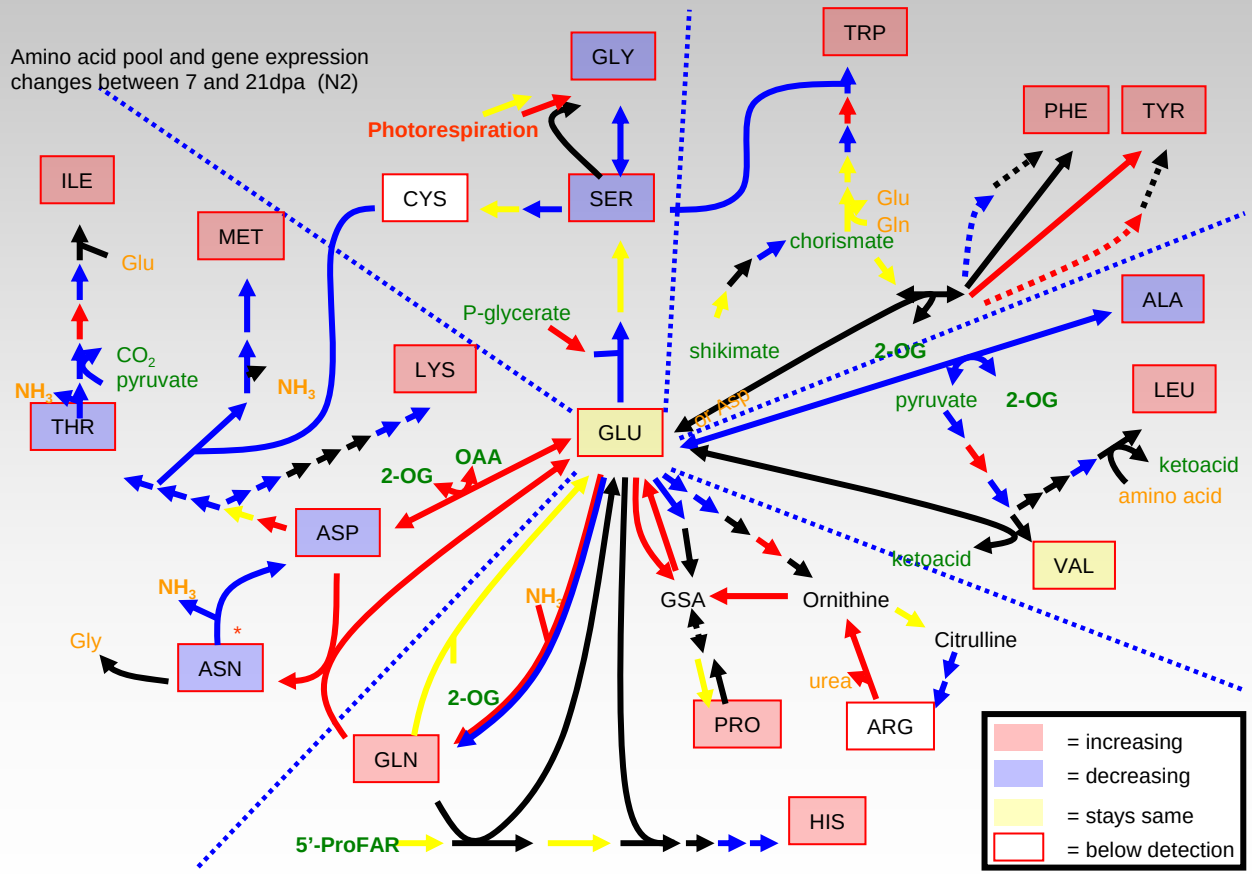
Measuring yield, flowering time, N parameters, candidate gene expression

WGIN DH trial at Rothamsted, 2007

Yield (4.6-11.1 t/ha)
Grain %N (2-3%)
Leaf 2 %N (3.4-5%)



Gene based approaches :
identifying pathways and genes involved in NUE



Gene discovery approaches - tools and resources

Aim: link pathways/genes to traits

Small scale variety N trials (Hereward, Istabraq, Maris Wigeon, Riband, Soissons, Welford

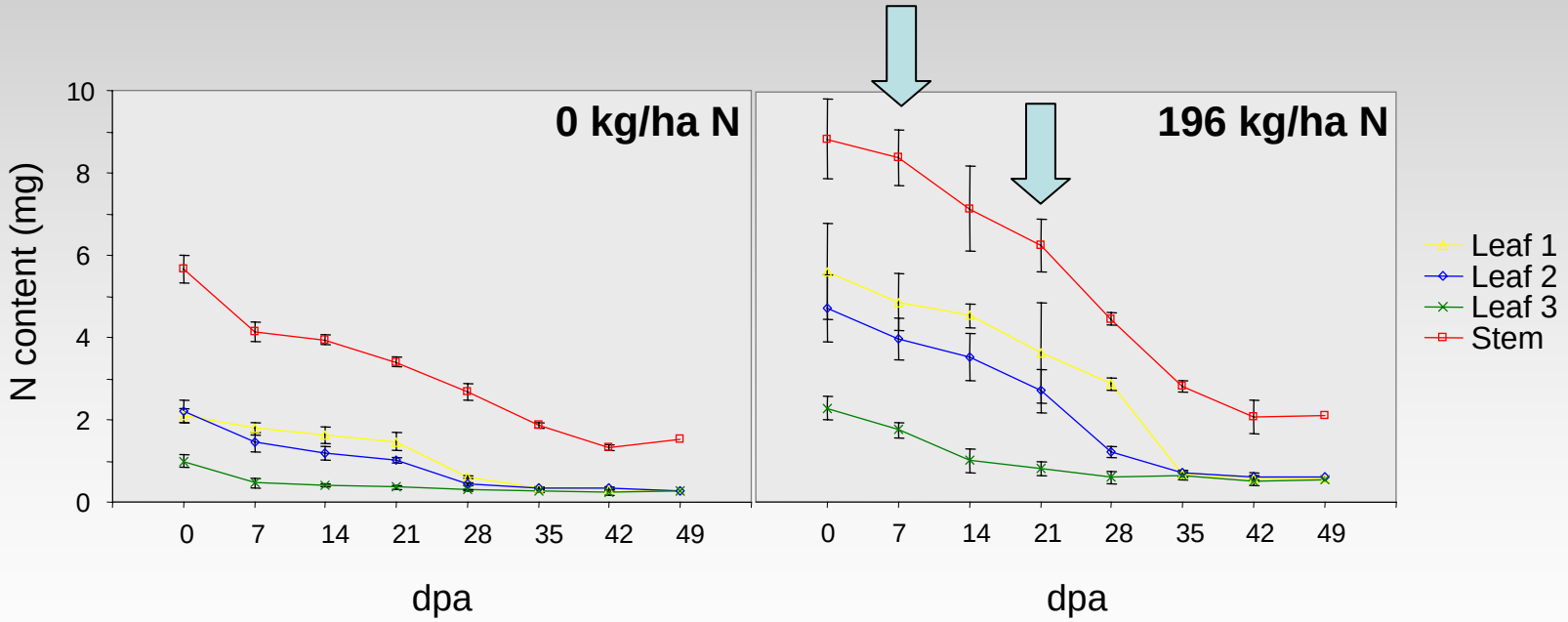
Candidate genes

Validation on WGIN diversity trial

AFFYMETRIX

Post anthesis N remobilisation is a key component of NUE

- N is exported from the leaf
- Timing and degree of N re-mobilisation depend upon:
  - N-input
  - Genotype
- Use this variation to identifying genes involved



Changes in N content of leaf2/3 post anthesis (Hereward)

What next?

- Publication of full Diversity trial datasets
- Collection of year 5 data
- Analysis Avalon x Cadenza population
- Validating candidate genes using diversity trial + A x C trial

Contributors

- Peter Barraclough
- Jonathan Howarth
- RRes Farm staff
- WGIN team at RRes
- Group and field team: Peter Buchner, Mark Durenkamp, Saroj Parmar, Janina Jones, Dan Godfrey, Emmanuelle Cabannes, Guillaume N'guyen, Claire Marescal

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