Discovering QTL controlling yield and yield components in wheat

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Simon Griffiths, M. John Foulkes
Dissecting gene x environmental adaptation

For predictive plant breeding move from a description of
‘genotype x environment’ interaction
to
‘gene x environment’ interaction

Howard Eagles, 2006

Identify those genes and gene combinations providing increased yield potential within and over environments
Macro and micro environmental adaptation

Macro:
Latitude - length of growing season
Climate - winter & summer temperatures
Water availability

Micro:
Soils
Water availability
Disease and pest profile
The UK is one of the best places in the World for growing wheat

Long growing season, mild winters, low summer temps
Good soils (few toxicities or deficiencies)
Generally adequate moisture (but 20% soils ‘drought prone’)
Mechanized agriculture
High inputs
Sophisticated agronomy
Average UK Wheat yields 1892-2002

GB Wheat Yields, 1892 -2002

Harvest year

Landrace selection
Knowledge development: Pedigree selection
‘Scientific’ Breeding & agronomy

0.00 1.00 2.00 3.00 4.00 5.00 6.00 7.00 8.00 9.00

0.00 1.00 2.00 3.00 4.00 5.00 6.00 7.00 8.00 9.00

tonnes/ha

Yield
Wheat Yields UK

UK Wheat Yield Production 1975 - 2005

Yield increase = 0.1 tonne per year

Data Source: DEFRA

y = 0.1114x + 4.9611

R² = 0.7767
Wheat Yields UK

UK Wheat Yield Production 1995 - 2005

y = 0.0122x + 7.6987
R² = 0.0162
Breeding advance for yield potential in UK

Mainly by phenotypic selection through trialing

No apparent yield plateau?

Significant genetic variation in yield trials within and between different breeding programmes

Significant varietal interaction with season and region

Genetical knowledge has made little impact on yield potential and environmental adaptation (apart from disease and pest resistance)
Can we understand the genetic variation for yield variability and yield stability?
Our approach: combining physiology with genetics

Use precise genetic stocks to locate and understand genetical variation for yield and yield stability and its environmental interaction and use this information predictively.

- Understand the physiological consequences of specific genetic variation - Rht genes, Ppd, 1B/1R, EPS
- Find genes controlling uncharacterized variation in yield and yield components by genetic mapping & QTL approaches for MAS
- Understand mechanisms of genes controlling yield components through a combined genetic, physiological and molecular approach
Strategy

• Gene discovery
• Gene validation
• Understanding of variation
• Gene transfer (MAS)
• Gene cloning
Large scale QTL 'searching': experimental approaches

• Study many recombinant doubled haploid mapping populations based on crosses between adapted key European winter wheat varieties

• Molecular mapping of these populations

• Field experiments to evaluate performance in sites with diverse environments

• Field experiments under defined environments - water limitation, low nitrogen

• QTL analysis from combining maps with field data
<table>
<thead>
<tr>
<th>Population</th>
<th>DH Lines</th>
</tr>
</thead>
<tbody>
<tr>
<td>Beaver x Soissons</td>
<td>65</td>
</tr>
<tr>
<td>Spark x Rialto</td>
<td>144</td>
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<tr>
<td>Charger x Badger</td>
<td>99</td>
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<tr>
<td>Renesansa x Savannah</td>
<td>177</td>
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<tr>
<td>Trintella x Piko</td>
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<tr>
<td>Rialto x Savannah</td>
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<tr>
<td>Avalon x Cadenza</td>
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<tr>
<td>(Lynx x Cadenza)</td>
<td>107</td>
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<tr>
<td>Buster x Charger</td>
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<tr>
<td>Weevil x Bacannora</td>
<td>106</td>
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<tr>
<td>Milan x Catbird</td>
<td>98</td>
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</table>
Genetic Mapping

Use all available public wheat SSRs: 800 core set of microsatellites tested, 36-43% polymorphic

Use DArT extensively to fill gaps and extend maps
Avalon x Cadenza map with DArT

DArT fills gaps

DArT extends maps

Approx 250 extra markers per adapted cross
Yield trials over several years, several sites

High Potential sites:
Drought limited sites
N limited sites

To date ~60 genotype x environment datasets
Analysis of source traits influencing yield potential and environmental interactions

- Growth stage
- Accumulation of remobilisable stem carbohydrate reserves
- Green canopy area persistence
Current conclusions concerning stem soluble carbohydrate effects

• Shows genetical variation between varieties and within recombinant populations
• Positively correlated with yield
• Appears independent of water availability
• Component of greater yield stability?
Correlation between stem soluble carbohydrate on grain yield for lines of Beaver x Soissons DH mapping population in 2002 at Gleadthorpe, in irrigated and unirrigated treatments.

\[ y = 0.39x + 6.36 \]
\[ R^2 = 0.16 \]

\[ y = 0.48x + 4.72 \]
\[ R^2 = 0.25 \]
The loss of assimilatory capacity as leaf senescence progresses contributes to limiting grain yield.

Delayed leaf senescence, particularly of the flag leaf, could help to increase grain yield.

Can we exploit genetic variation for this trait?
Beaver x Soissons DH population: Plot yield vs duration of flag leaf senescence JIC 2004

Length Degree Days 0-5 (04) vs Plot yield (04)

\[ y = 1.6229x + 4547.8 \]

\[ R^2 = 0.3924 \]
Senescence scoring

Flag leaf senescence was measured by an overall visual assessment (once per week) of the percentage of flag leaf area turned to yellow. An arbitrary scale from 0 to 10 was utilised for scoring senescence.

Beaver x Soissons DH population

Matteo Ciavarrella, Marie-Curie PhD student
Analysis of leaf senescence scores

- Duration of flag leaf senescence (degree days)

- Rate of flag leaf senescence:
  
  Slope of regression of flag leaf senescence scores against cumulative degree days
  
  - linear analysis
  - quadratic analysis
Linear Regression Analysis 2004
Each individual DH line

Line 24

y = 0.019x - 27.307
R^2 = 0.9381
Polynomial Regression Analysis 2004

Line 24

\[ y = 1 \times 10^{-5} x^2 - 0.0292 x + 12.875 \]

\[ R^2 = 0.9523 \]
Linear Regression Analysis 2004

DH 36

\[ y = 0.0106x - 14.722 \]
\[ R^2 = 0.9805 \]

DH 28

\[ y = 0.0211x - 31.154 \]
\[ R^2 = 0.8046 \]
Correlations between senescence data for 2004-05

= $P < 0.05$

<table>
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<tr>
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<th>Slopes LRA 04</th>
<th>Slopes 0.5 04</th>
<th>Slopes 5.10 04</th>
<th>LDDays LRA Analysis 04</th>
<th>LDDays 0.5 04</th>
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B x S: Most significant QTLs for senescence, plot yield and 1000 grain weight

2D

Length Degree Days 0-5 (04) $\uparrow$ B (P=0.03)
Slopes 5-10 (05) $\uparrow$ B (P=0)

Length Degree Days 0-5 (04) $\uparrow$ B (P=0.012)
Slopes 5-10 (05) $\uparrow$ B (P=0.003)
LDDLRA (05) $\uparrow$ S (P=0.005)
Plot yield (04) $\uparrow$ B (P=0.007)

1000 grain weight (04) $\uparrow$ S (P=0.035)

3A

Length Degree Days 0-5 $\uparrow$ S (P=0.041)

1000 grain weight (04-05) $\uparrow$ B (P=0)
LDDLRA (05) $\uparrow$ S (P=0.039)
LDDPRA 0-5 (05) $\uparrow$ S (P=0.019)

SPRA 5-10 (05) $\uparrow$ B (P=0.005)

SPRA 5-10 (05) $\uparrow$ B (P=0.033)
LDDPRA 0-5 (05) $\uparrow$ S (P=0.035)
LDDPRA 5-10 $\uparrow$ B (P=0.022)
Summary of senescence QTLs in Beaver x Soissons population 2004/05 studies

• Heritable trait

• Duration of senescence stages 1-5 most important for yield

• QTLs related to senescence on chromosome 2D and 3A

• Also QTLs related to flowering time on chromosomes 2D and 3A (2004 and 2005): Senescence a pleiotropic effect?
What about yield ‘per se’ QTL and unknown gene x environmental interactions?

Detection of:
QTL stable over years & environments
QTL specific to years or environments
QTL detected in different crosses
QTL analysis of the Charger x Badger DH cross

Charger (High yield, group 2 quality : PBI bred) X
Badger (High yield, feed quality : Advanta bred)

Very similar (and high) yield potential

3 years trials, 2-5 environments/year
= 12 data sets
Charger x Badger: yield QTL detected

2-3g increase in 1000 gw ~ 4-6%  
420g increase in yield/plot ~ 8%
Charger x Badger: yield QTL detected

5A

1000GW

B↑ 3.57g

gwm293

6A

B↑ Crop Height
gwm518

C↑ 2.65g 1000GW

C↑ Grain Fill Period

wmc32

= 30cM

3.5g increase in 1000 gw ~ 8%

<table>
<thead>
<tr>
<th>Charger x Badger (Church Farm 2001)</th>
<th>Charger x Badger (Sandringham 2001)</th>
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<tr>
<td>Charger x Badger (Scotland 2003)</td>
<td>Charger x Badger (Germany 2003)</td>
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Yield QTLs: Future yield advancement & yield stability

- QTL for yield performance with specific and general environmental adaptation identifiable

- Further advances are possible by selecting QTL alleles for:
  - increasing grain filling period
  - increasing stem carbohydrate reserves
  - recombining grain size QTL
  - increasing spike fertility to increase sink capacity
Future studies

- Development of backcross NILs for more detailed genetic and physiological studies of identified QTL.
- Study relationship between leaf area duration and nitrogen economy
- Greater molecular characterization of processes.
- TILLING in mutant populations to identify mutants for specific genes in photosynthesis, nitrogen economy and water use efficiency
**QTL Validation: development of backcross inbred lines**

*Graphical genotypes for chromosome 6A*

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<tr>
<th>6A</th>
<th>SR 4</th>
<th>SR 30</th>
<th>SR 56</th>
<th>SR 103</th>
<th>SR 136</th>
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<td>-</td>
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<td>2A/psp3029</td>
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</table>

- **Selection SSRs**
  - psp 3071
  - gwm 570

- **Yield**
  - 1000GW
- **Grain Fill Period**
  - 2.2g Yield
- **Spike Yield**
  - 2.3 days
  - 1000GW

**Graphical genotypes for chromosome 6A**

![Graphical genotypes for chromosome 6A](image-url)
Acknowledgements

JIC
Matteo Ciavarrella
Lesley Fish
James Simmonds
Michelle Leverington
Yingkun Wang
Liz Sayers
Leodie Alibert
Simon Orford
Simon Griffiths

JIC Field trials team

University of Nottingham
John Foulkes

ADAS
Roger Sylvester-Bradley

Nickerson-Advanta
John Barrett

Syngenta
Andy Greenland