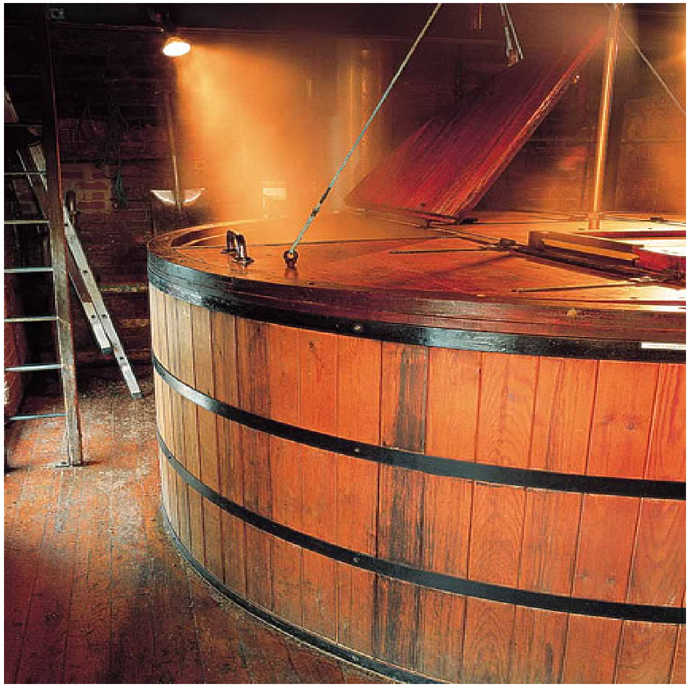
# Barley for Brewing



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# Outline of Presentation

- Barley quality for malting and brewing
- Effects of breeding (especially since 1970s) on barley phenotype
- Implications of current breeding strategies for marker assisted selection
- Future developments

# Why Barley?

- Many cereals used in brewing – wheat, maize, oats, sorghum
- Generally used as unmalted adjuncts
- Barley malts readily, producing enzymes for starch breakdown
- Husk also useful to protect embryo, ensure more even germination during malting and facilitate wort filtration during brewing
- Traditional/historical association between barley and brewing

# Quality for Malting

- Low post-harvest dormancy – avoid precocious germination but not delay malting
- High starch content – increases alcohol yield
- Low/Medium protein content – yeast nutrition, enzyme production, but barrier to starch accessibility
- Low β-glucan content – barrier to starch accessibility
- Potential for adequate enzyme production during malting – enable modification without excess malting loss

# Influences of Malted Barley on Brewing Quality

Desirable

- Good extract of fermentable material
- Proteins for head retention
- Flavour components, from different types of malt
- Diastatic activity – for brews utilising starch-based adjuncts

Undesirable

- High viscosity – from soluble $\beta$-glucans
- Haze – from pro-anthocyanins and proteins
- Off-flavours e.g. DMS and products of lipoxigenase action

# Progress in Selection Methods

| | | |
|---|---|---|
| 1950s | Micro-malting | Only applicable to later generations of breeding programmes |
| 1970s | Small-scale grain testing | Only assessed endosperm properties |
| 1980s | Automated and small-scale malting | Enabled earlier selection, but still required replicated trials |
| 1990s | Marker-assisted selection | Needed statistical techniques to select for quantitative traits |

# Development of Spring Malting Barleys

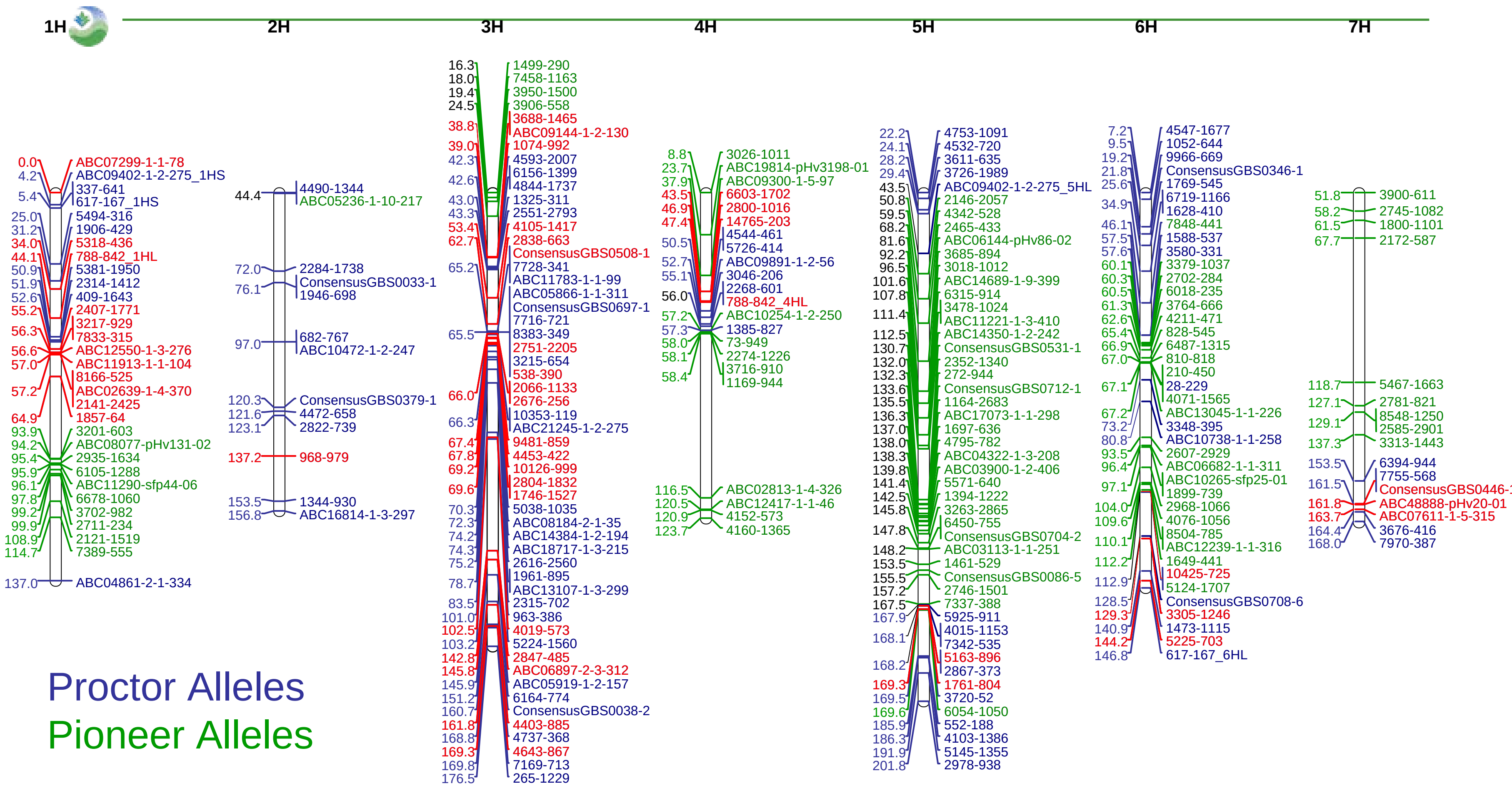
| YEAR | No. of spring barley vars. on NIAB Rec. List (Full or Provisional) | No. of varieties with score of 8 or 9 for malting quality |
|---|---|---|
| 1969 | 10 | 2 |
| 1979 | 16 | 2 |
| 1989 | 12 | 6 |

# Characteristics of Contemporary Malting Varieties

Since the advent of cv. Triumph and its derivatives in the 1980s, malting varieties have been:

- Short (with stiff straw) – derived from *sdw1* gene
- High yielding
- Derived from crosses between elite cultivars
- Major effect genes for quality may be present in both parents

# Patterns of Inheritance in Winter Barley




Proctor Alleles

Pioneer Alleles

Proctor alleles found in Halcyon, Pipkin, Puffin, Fanfare and Pearl

# Location of QTLs for Grain β-glucan

- 3 QTLs in Steptoe x Morex (Han et al.)
- 2 on Chromosome 2H – Morex providing allele with increasing value for both
- 1 on Chromosome 1H – Steptoe providing allele with increasing value
- Largest effect associated with centromeric QTL on Chromosome 2H

# Identification of Candidate Gene (work of Australian group)

- Markers flanking QTL on Chrom.2H used
- Syntenic region of rice genome identified
- Rice genome sequence revealed group of 6 cellulose synthase-like (*CslF*) genes
- Rice *CslF* genes inserted into *Arabidopsis*
- $\beta$-glucan detected in cell walls of transgenic plants
- Demonstrates the utility of genomic approaches to identify and confirm candidate genes

# QTLs for β-glucan in Beka x Logan

| | chrom | Closest marker | LOD[a] | Position[b] (cM) | Additive effect[c] | Allelic effect[d] | Variance explained[e] |
|---|---|---|---|---|---|---|---|
| **Spain** | 1H | Ctig8484 | 3.64 | 183 | -0.10 | 36(L) | 15.2 |
| | 5H | Bmag337 | 3.17 | 22 | 0.10 | 36(B) | 13.3 |
| | 7H | Bmag516 | 5.33 | 77 | 0.13 | 47(B) | 21.4 |
| **Scotland** | 1H | Ctig8484 | 1.77 | 183 | -0.04 | 20(L) | 7.7 |
| | 5H | Bmag337 | 2.23 | 22 | 0.04 | 20(B) | 9.6 |
| | 7H | Bmag516 | 2.41 | 77 | 0.05 | 25(B) | 10.3 |

# Location of largest effect QTLs for β-glucan

| POPULATION | LOCATION OF TRIALS | LOCATION OF LARGEST QTL |
|---|---|---|
| Steptoe x Morex | USA | Chrom. 2H* |
| Derkado x B83 | UK | Chrom. 3H |
| Beka x Logan | Spain/Scotland | Chrom. 7H |

* QTL not detected in other studies

# Limited Relevance of Steptoe x Morex QTLs

MALTING QUALITY MODEL

- Morex not low β-glucan
- Had most increasing alleles for enzyme activity
- Bred to meet N.American brewing specs.
- European malting quality more reliant on endosperm properties

CROSS PHILOSOPHY

- 1970s High Yield Feed x High Quality
- Highly polymorphic with phenotypic differences
- Does not reflect contemporary breeding
- Illustrates what breeders have already achieved by phenotypic selection

# Does Marker Assisted Selection have a future?

Yes, but sometimes we need to look at technology a little bit differently

# Future Application of QTLs

Relevance for Breeding and Genetic Studies

- Need to focus on type of cross relevant to breeders
- Work with QTLs of low effect
- Look for QTLs that are applicable across a number of populations – small cross mapping
- Exploit knowledge of syntenic regions of genome between cereal species to locate candidate genes
- Also look for co-location of QTLs and ESTs

# Future Developments

- Phenotypic measurements often consider start (grain) or end (malt) points of process
- DNA polymorphisms (within known genes) can be linked to function e.g. more sulphur rich amino acids promoting bridging within molecule
- Malting is dynamic process with several (many) simultaneous pathways
- Need to use contemporary tools to study the process – spatial and temporal gene expression, proteomics etc.

# Conclusions

- Breeding barley for malting and brewing has been very successful in combining yield and quality
- Marker assisted selection has had limited application, but may have been based on inappropriate germplasm
- Contemporary technology offers potential to greatly improve understanding of the genetic control of the malting process
- Quality may not be the driver of future breeding (climate change, reduced inputs etc.) but it will remain a key attribute of future varieties

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