Mapping and analysis of loci controlling quality traits in broccoli

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Aims of the project

1. Identify and map additional QTL linked to a range of quality traits
   a. Shelf life (turgor); QTL for yellowing already identified
   b. Nutrient content (different components)
   c. Stability of nutrients during storage
   d. Head morphology

2. Analyse nutrients and potential flavour attributes
   a. Global metabalome analysis
   b. Key nutrients (antioxidants, glucosinolates, flavanoids, vitamins)

3. Fine scale mapping of QTL, potential gene identification
   a. Backcross selected lines for fine scale mapping
   b. Microarray analysis
   c. Candidate gene nomination

Introduction – Broccoli shelf life

'short' and unpredictable shelf life

Determined by Genotype

Head remains green For longer

Yellowing of head

Firm and attractive
Increased storage potential
Slower deterioration of nutrients
Flavour
Crunch

Soft - unattractive
Prone to impact damage
Reduced nutrients
Reduced Flavour
Unfit for retail

Broccoli x Broccoli Double Haploid (DH) lines

P1 Mar 34

DH line from the F_1 cv Marathon.
Yellowing >4 days at RT

Mar 34 x GD33

↓

F_1
Microspore culture

↓

72 unique DH lines

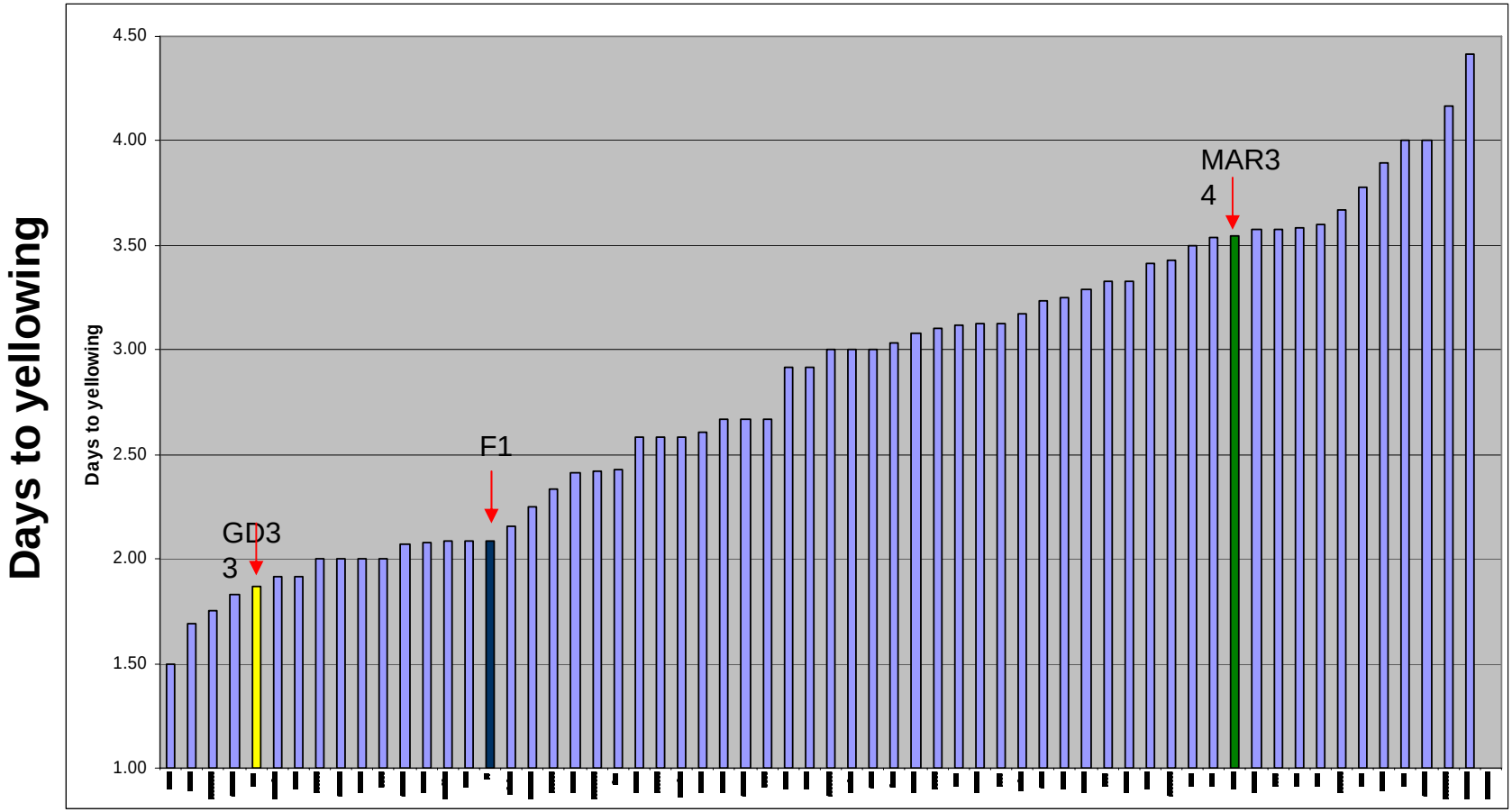
Fixed mapping resource

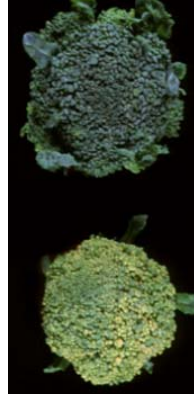
P2 GD33

DH line from Green Duke.
Yellowing >2 days at RT

Variation in shelf life

Distribution of head yellowing for a broccoli x broccoli DH population





DH line head morphology

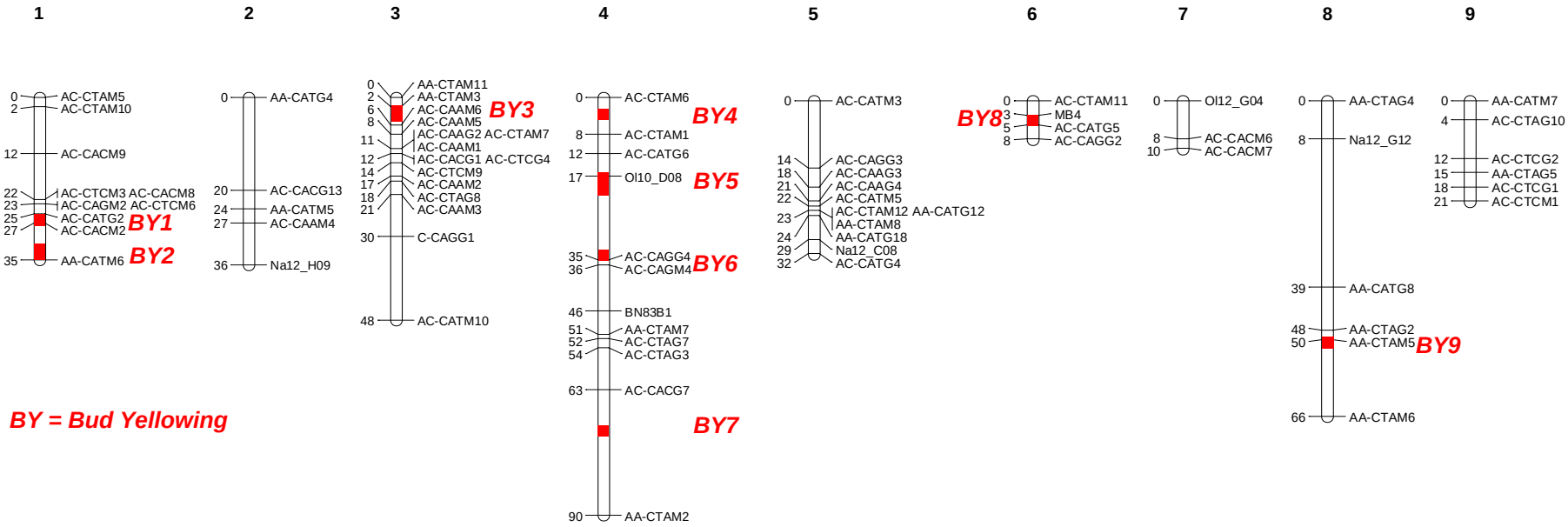
Head size and colour variation: (a, c)
Head shape variation: b (bracted and loose); e (domed and flat); f (flat)
Leaf shape and size (a, c, e)

Phenotype data

- Field trial 2007 – All lines grown together
- Improved assessment of shelf life quality components
- Metabolite analysis - QTL linked to quantity and relative composition
  - Metabolite loss during storage
- Global metabolome variation
- Lines identified for backcross programme

Linkage map

- Linkage analysis resulted in a *B. oleracea* map
- Based on 94 loci derived from AFLP and SSR marker data.
- The nine linkage groups identified cover 346 cM (total length)
- Corresponds to 38.3 % of the *B. oleracea* genome



BY = Bud Yellowing

Improved Linkage map

- Skeleton linkage map

- New linkage map
- Greater AFLP, SSR coverage

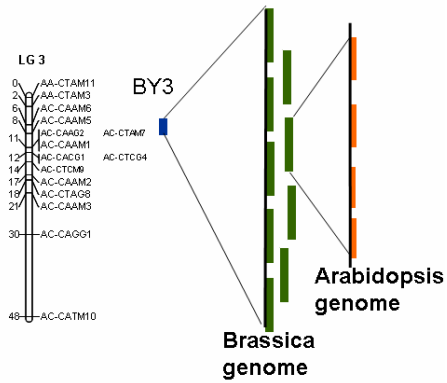
Mapped SSRs – anchor map to N x G; A x G maps

Improved AFLP marker coverage – comparative mapping

- Syngenta SSR platform

- Significant QTLs – Postharvest Yellowing

- Improved QTL analyses
  Multi –trait analyses



Future direction

- BC F_1 DH lines – fine mapping of QTL
- Metabolome variation
- Microarray analysis
- Functional role of candidate gene (s)
- Markers developed for breeding programme
- QTL transferred to elite breeding lines
- Happy consumers

Acknowledgements

Team Members

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