

In search of canola phenology genes



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Where this research is heading



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- We want to develop a ‘phenology-by-design’ system whereby canola breeders can manage phenology genes in their breeding programs
- We want to expand AUS phenological diversity by tapping into overseas germplasm more effectively



Background



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- Phenology is controlled by the interaction of genes with environmental cues:
 - Vernalisation, photoperiod & ambient temperature
- Canola has undergone many genetic bottlenecks which reduced genetic and phenological diversity
- Breeders have experienced difficulty in bringing in 'new blood' from overseas due to late flowering

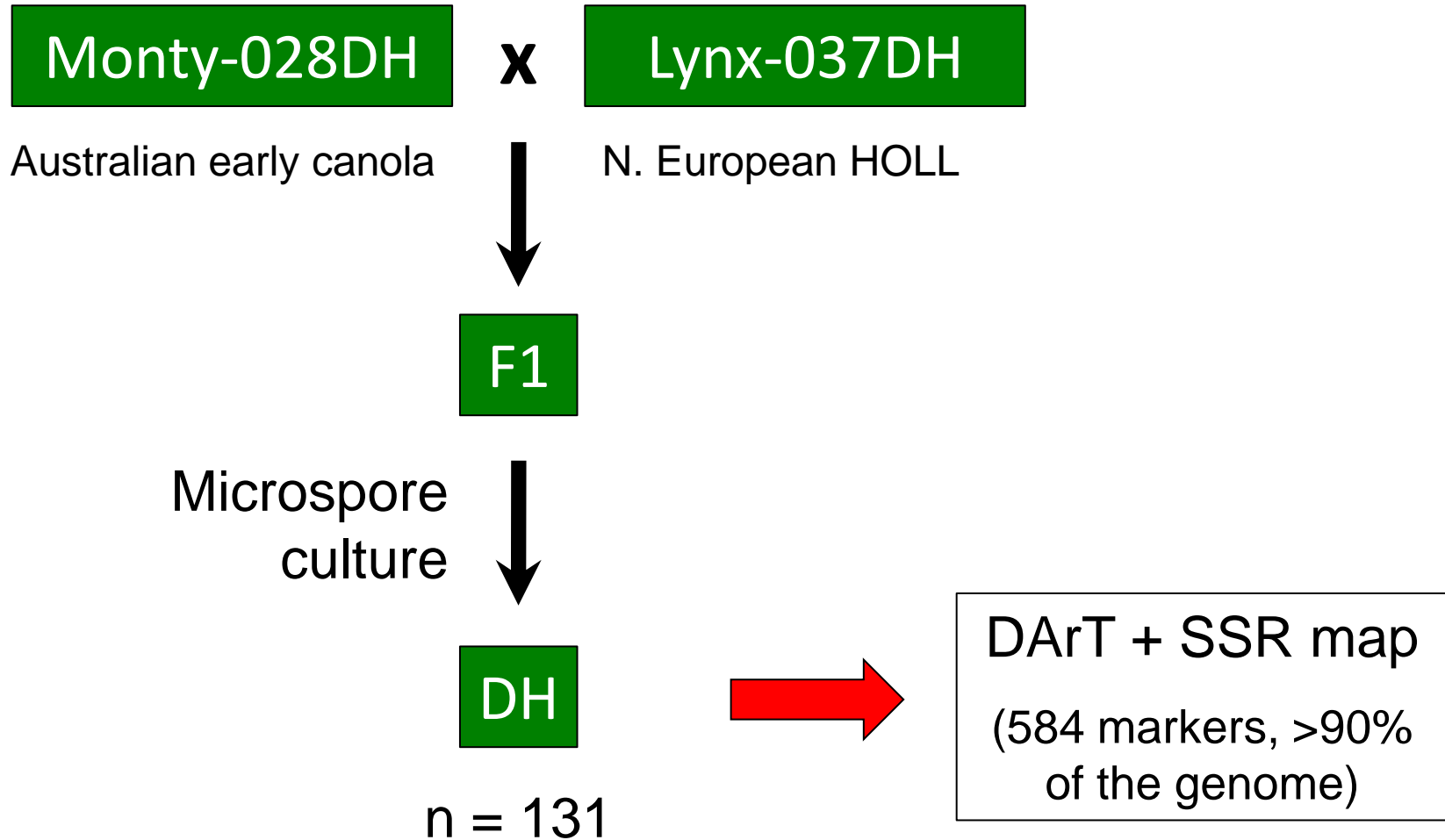
Rationale for this experiment



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- We want to understand how phenology is controlled in Australian and overseas canola
- As a first step, we conducted a QTL study to investigate time of flowering in long day and short day conditions in a cross between AUS and EUR varieties
- We expected the EUR parent to contribute alleles for greater photoperiod responsiveness
- We expected the AUS parent to contribute alleles for greater temperature responsiveness

LMDH population



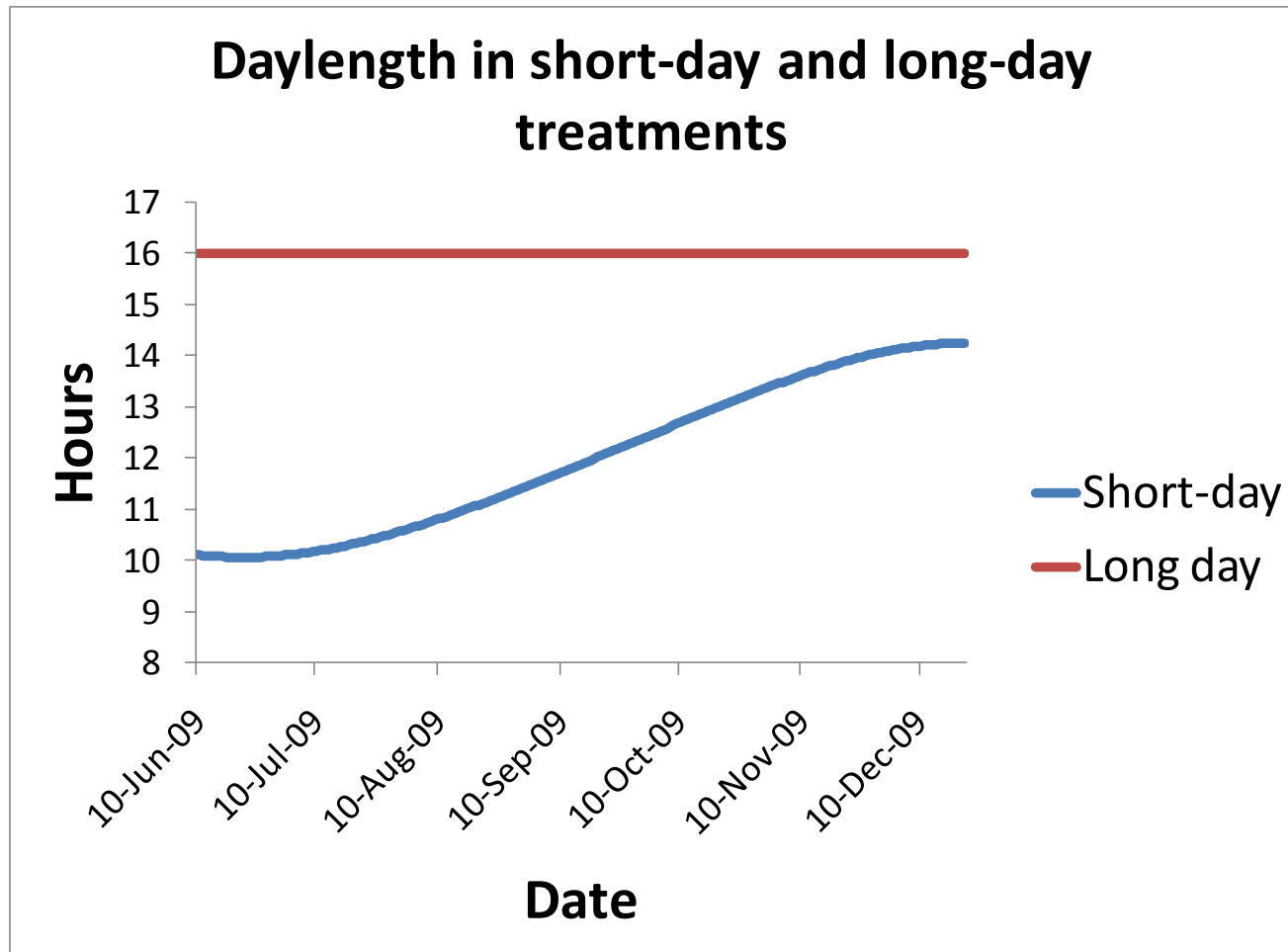
Spatially-optimised p-rep design

- Four benches each contained the LMDH population, parents and variety controls (n=200)



LD was achieved using supplementary lights

- Temperature was measured every 15 minutes



Long-day treatment

- Curtains prevented light reaching SD benches



Trait measurements



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- Days to first open flower (DTF)
- Thermal time to flowering (THERM)
- Number of leaf nodes at first open flower (LNF)

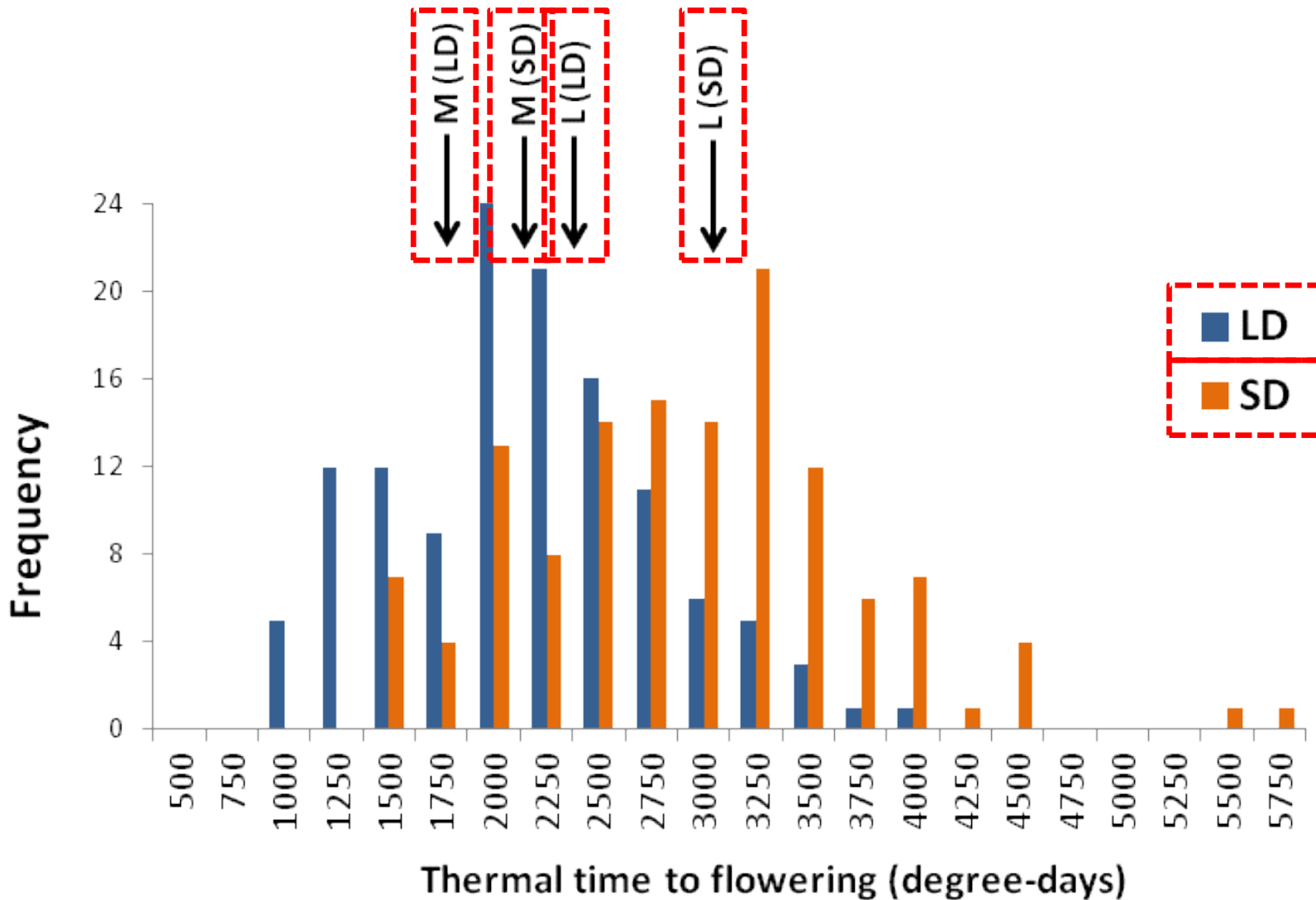
QTL approach



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- One-step, bivariate QTL analysis implemented in ASReml-R (Alison Smith)
- For full details see:
 - Nelson et al. (2014) PLoS ONE 9: e102611

Transgressive segregation in LMDH popn.



Line means and heritability estimates

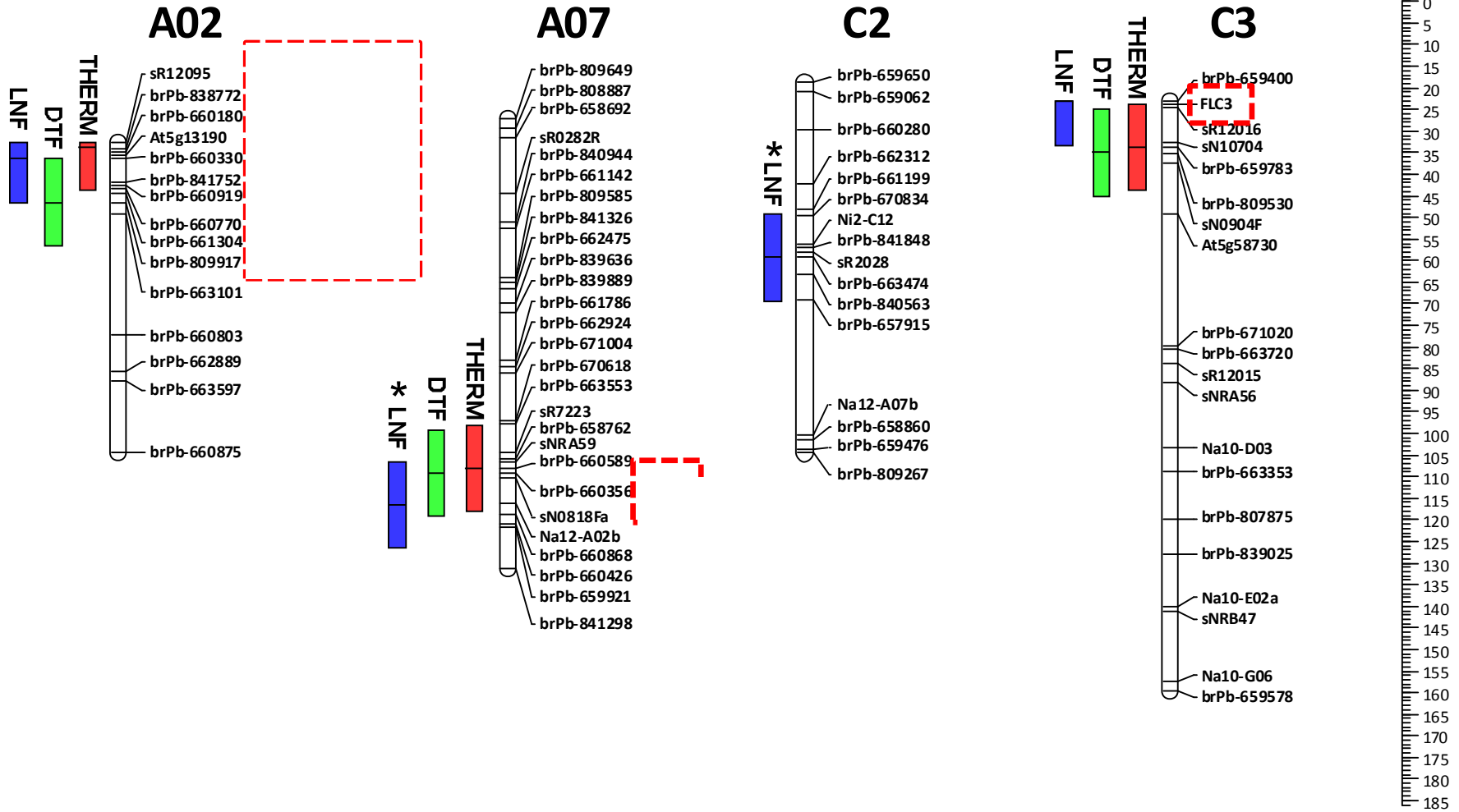
	THERM ¹	DTF ²	LNF ³
LD mean	2029	97.2	14.8
SD mean	2794	128.0	22.6
<i>P</i> -value	< 0.0001	< 0.0001	< 0.0001
LD heritability	0.91	0.91	0.85
SD heritability	0.92	0.93	0.89

¹ THERM = thermal time to flowering (expressed as degree-days)

² DTF = days to flowering

³ LNF = leaf nodes at flowering

QTLs explained ~60% of phenotypic variation



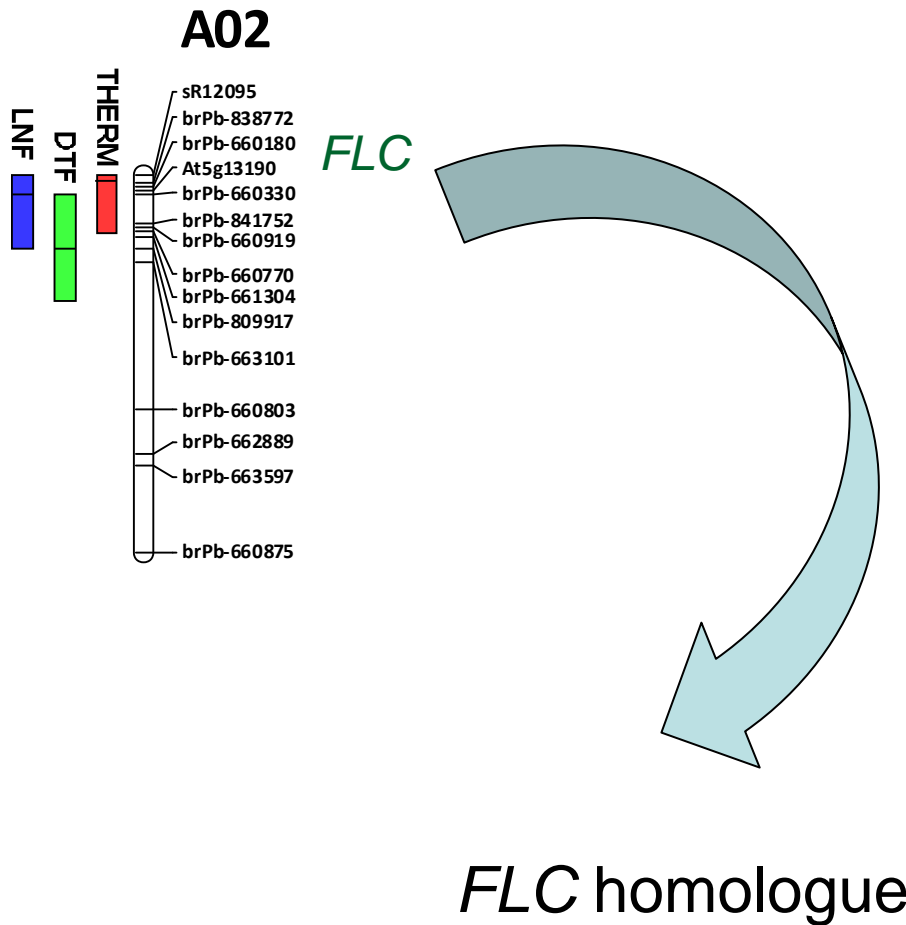
Summary of QTL results



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- Primarily main effect QTLs, meaning the QTLs were observed in both LD and SD treatments
- In other words, both parents had similar alleles for photoperiod responsiveness
- This was unexpected as we thought the EUR parent would have stronger photoperiod effect given that EUR canola is grown in longer days
- Both AUS and EUR parents contributed alleles for earliness, explaining the huge transgressive segregation observed in the LMDH population

Gene discovery



Genome re-sequencing
AUS and EUR parents
(Jacqui Batley & Dave Edwards)



Where next?



- Validate candidate genes that drive phenological adaptation in Australian and overseas canola
- Incorporate these genes into the phenological model being developed in GRDC project led by John Kirkegaard, Penny Riffkin and Mark Seymour
- Develop phenology gene markers to allow breeders:
 1. to predict flowering date of progeny from crosses (including with overseas germplasm)
 2. to mix and match phenology alleles to target particular flowering windows around Australia

Acknowledgements



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- Phenotyping was supported by the UWA Institute of Agriculture
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- MNN & WAC were partially supported by GRDC
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- Jacqui Batley & Dave Edwards for re-sequencing parent lines (UQ-UWA bilateral grant)

Recap: Where this research is heading

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