



Australia's National Science Agency

Genomic strategies for optimising flowering time in canola

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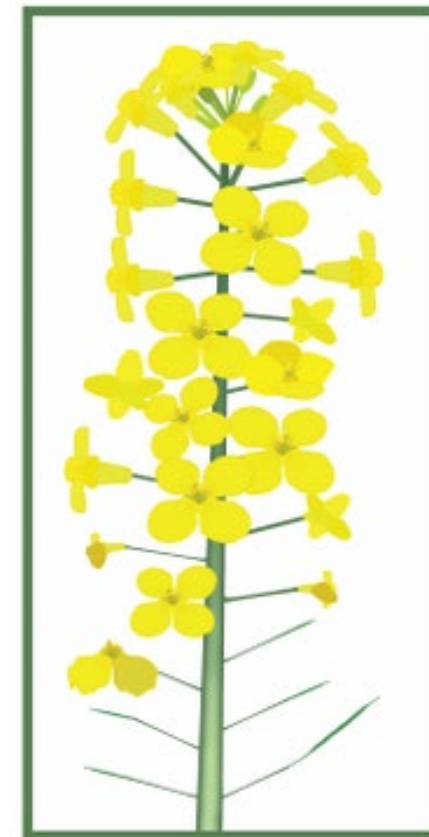
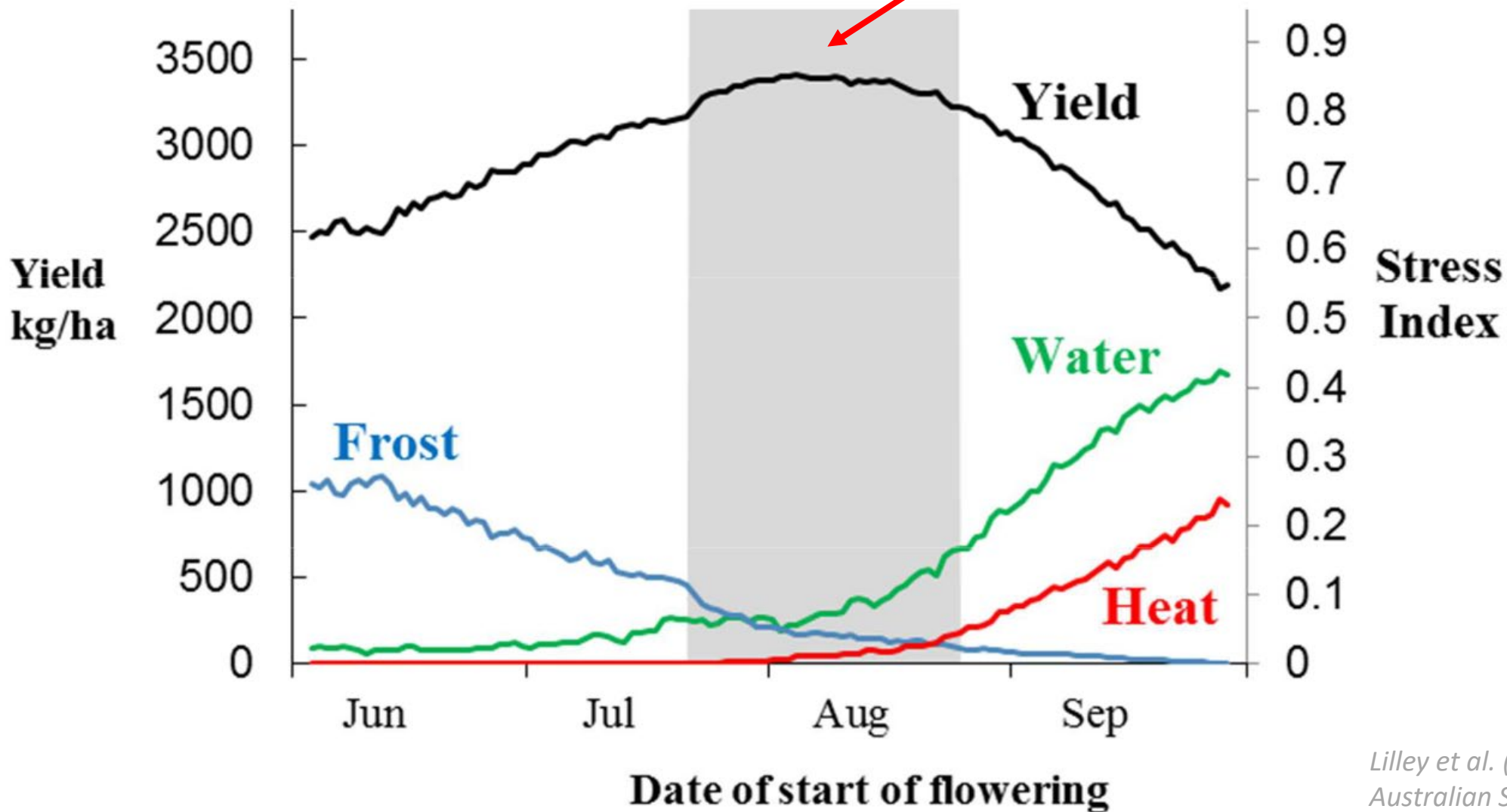
IRC 2023, Sydney | 27 September 2023



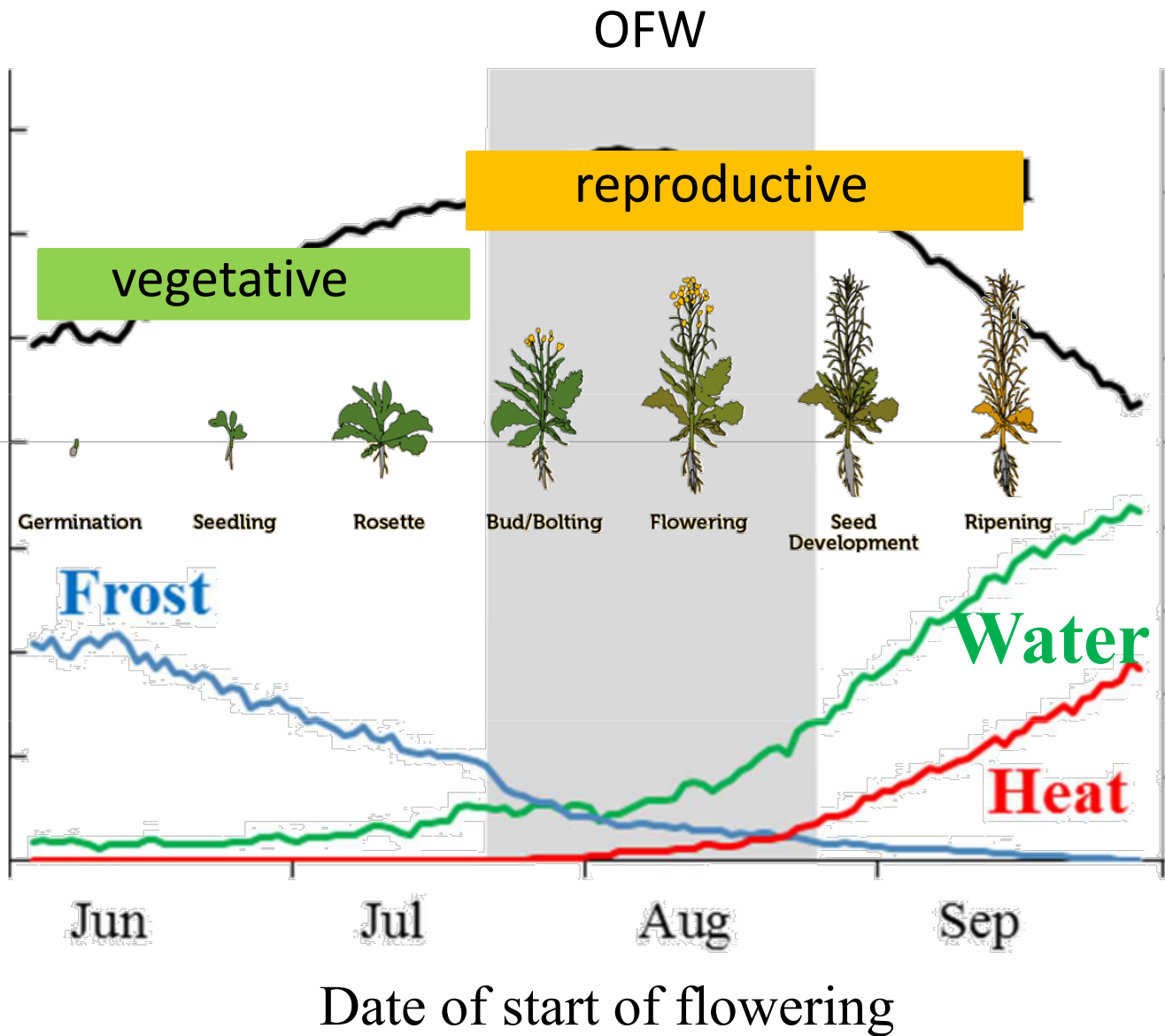


Optimising canola phenology

Optimal Flowering Window



Genetics and environment drive phenology



Genome

- genetic effects
- GxG

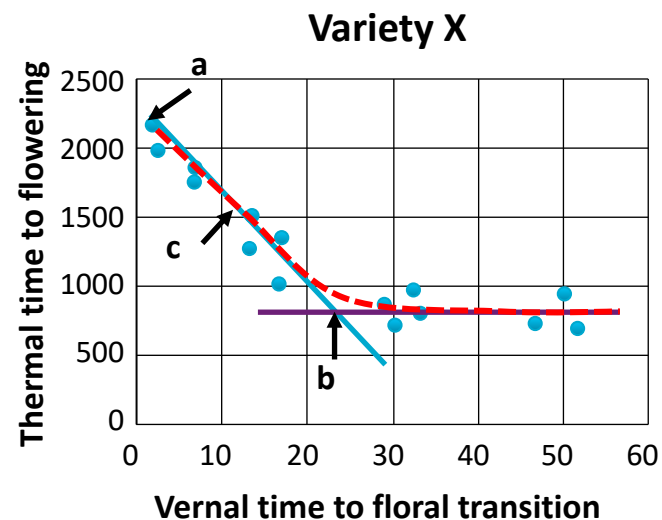
Environment

- plastic responses

Interactions

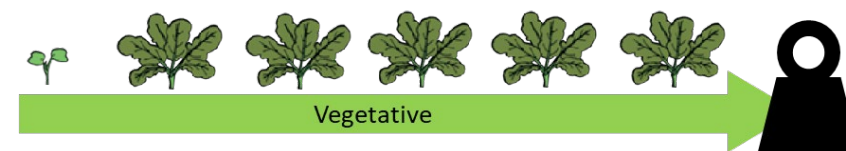
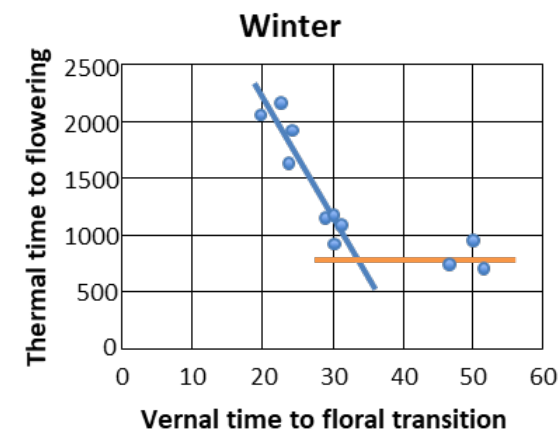
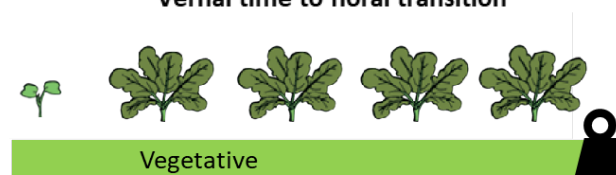
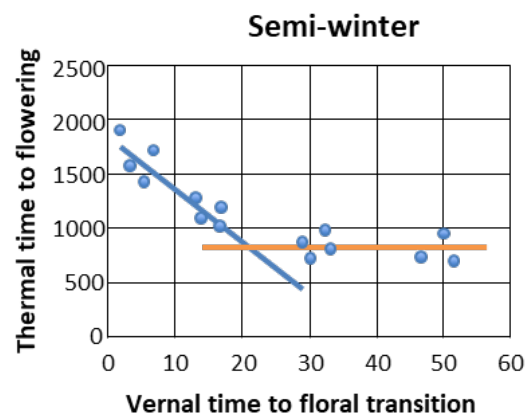
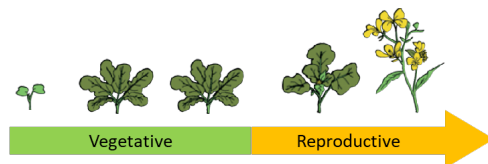
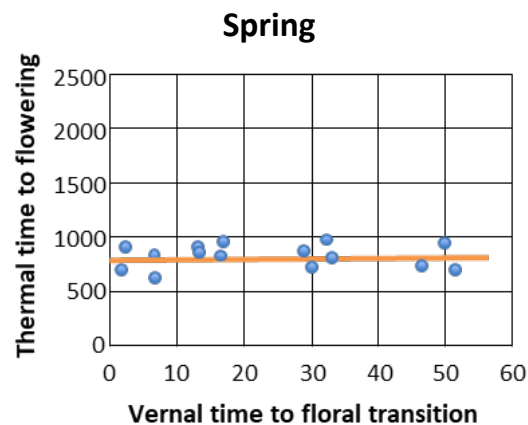
- GxE

Example - phenology response multi-site data



Parameters

- a. TT to flower – no vern
- b. Vern response saturated
- c. Rate of response to vern





The current state

APSIM canola model simulates phenology

Does this accurately

But..

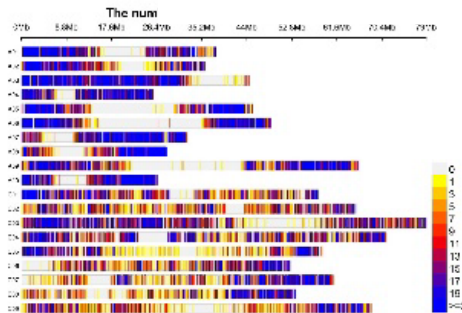
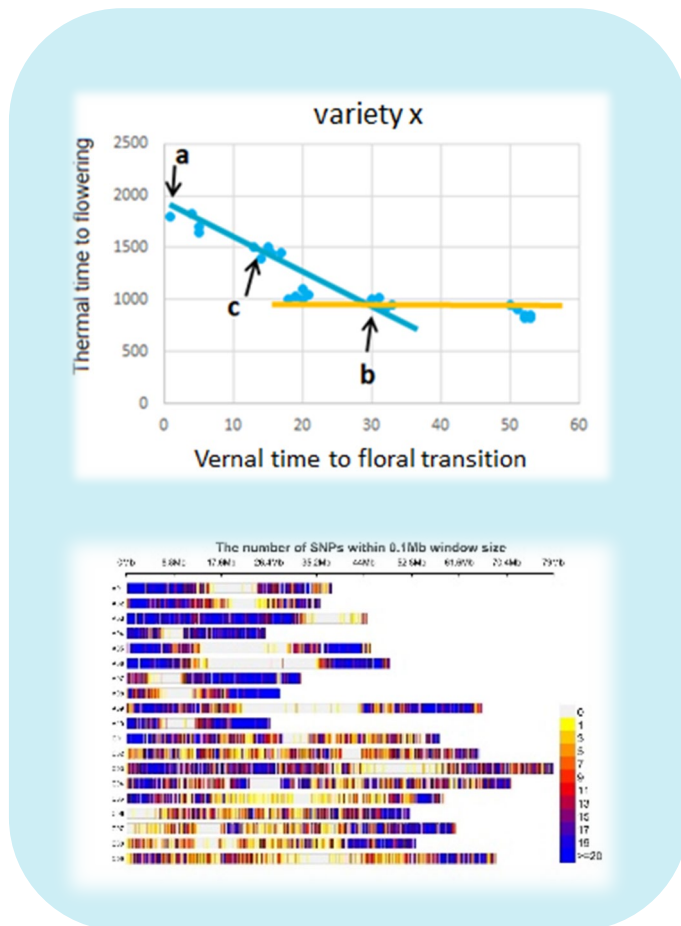
Phenology parameters must be estimated first

Compounded by rapid turn-over of canola varieties



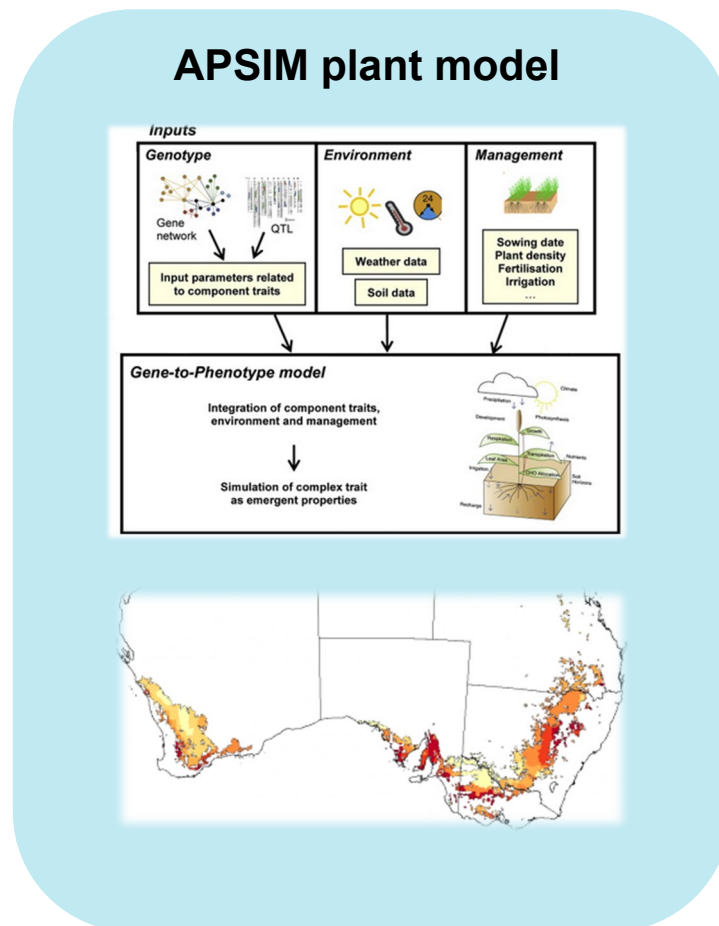
<https://www.canolaflowering.com.au/>

Training data



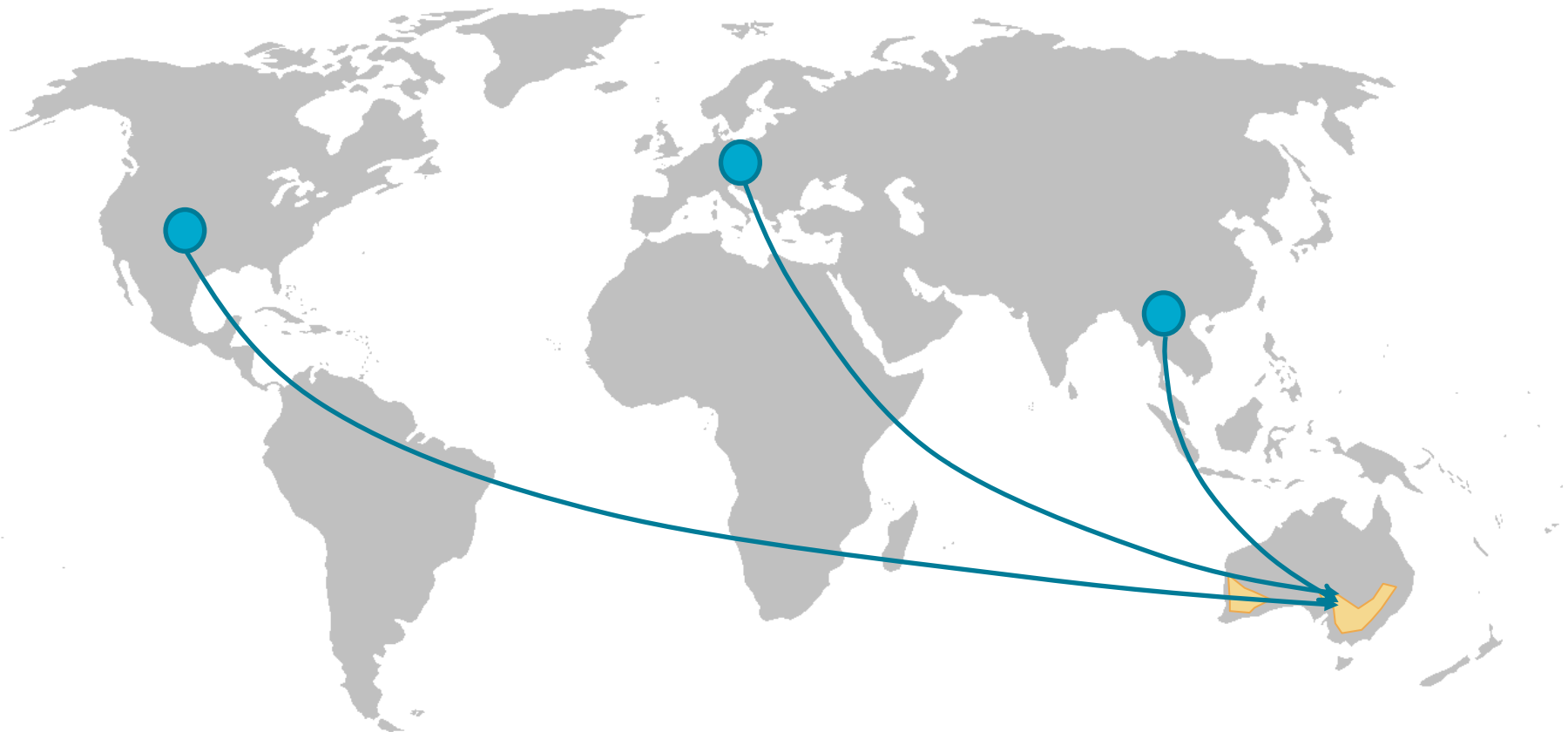
ML prediction
APSIM parameters

Simulate flowering time





Canola Diversity Panel (OzCanola)



690 varieties

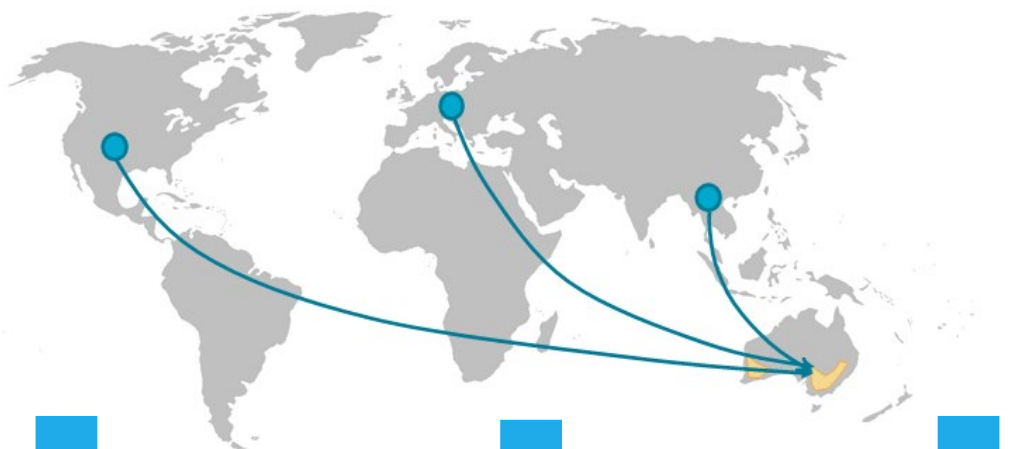
- Modern AUS
- Global:
 - BRAVO
 - ASSYST

Mixed phenology

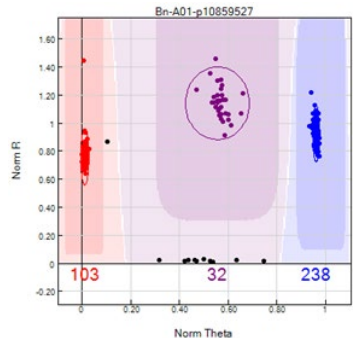
Core set of 350 varieties
underpinned data
collection



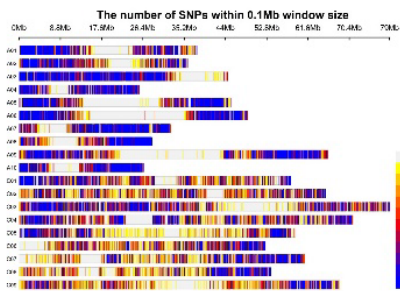
Canola Diversity Panel



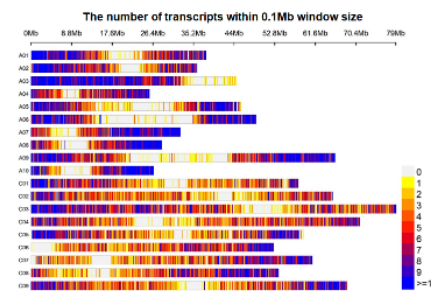
30K SNPs Brassica array



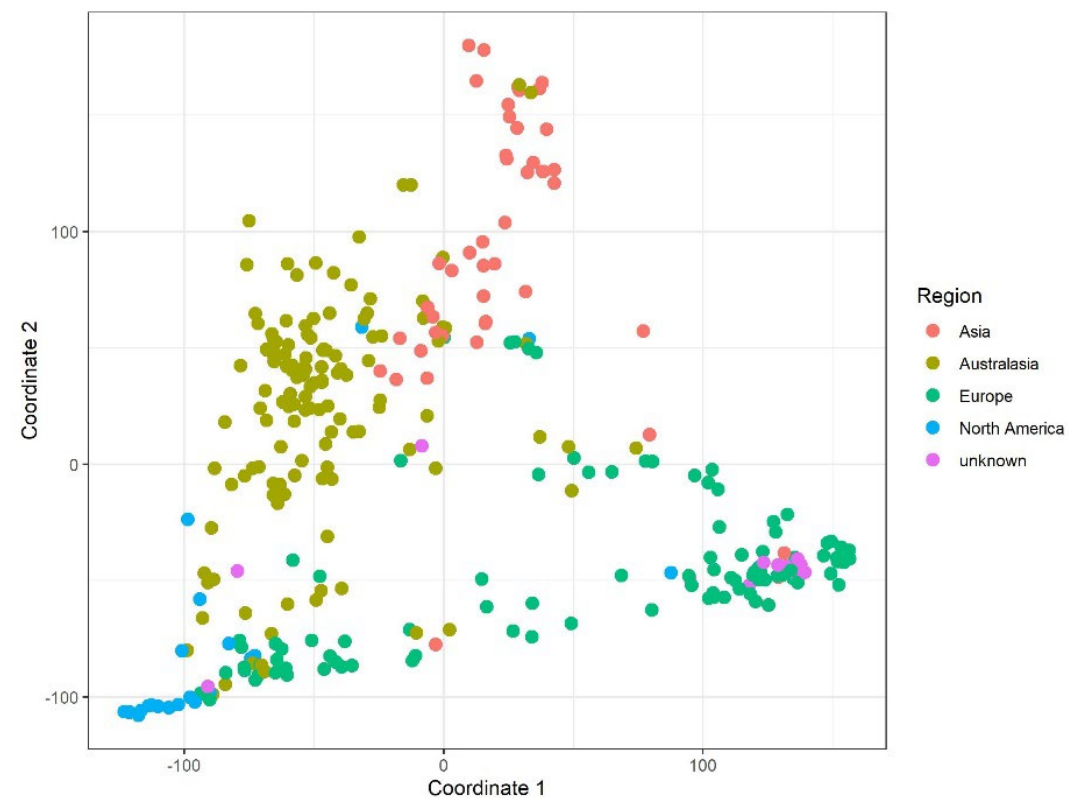
300K SNPs Trans-SNPs



50K expression Transcript

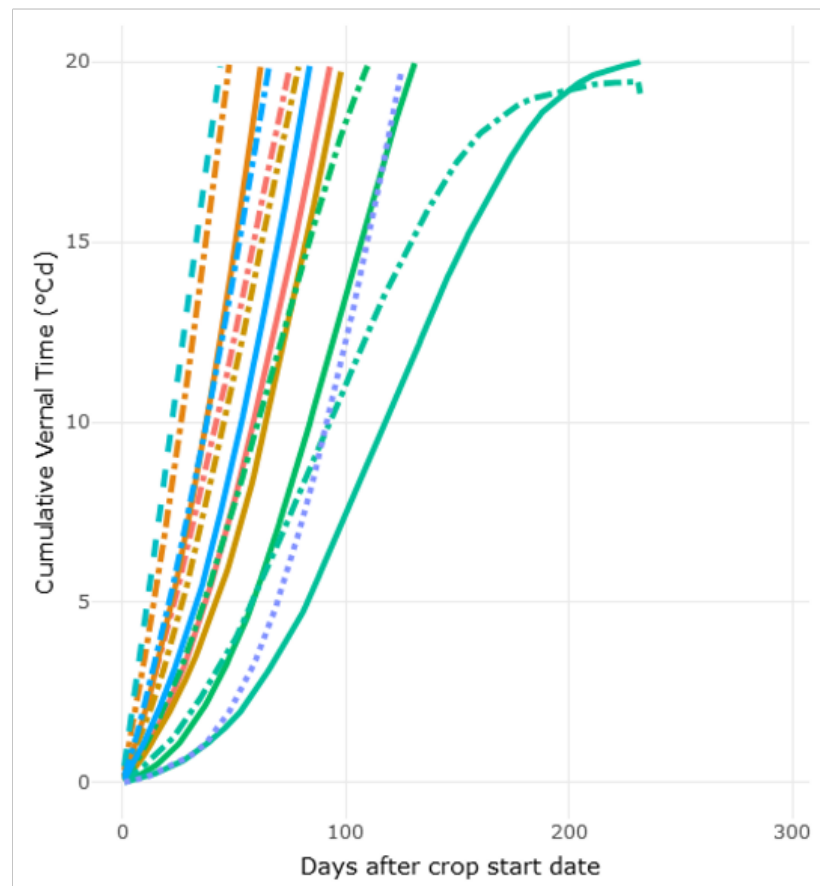
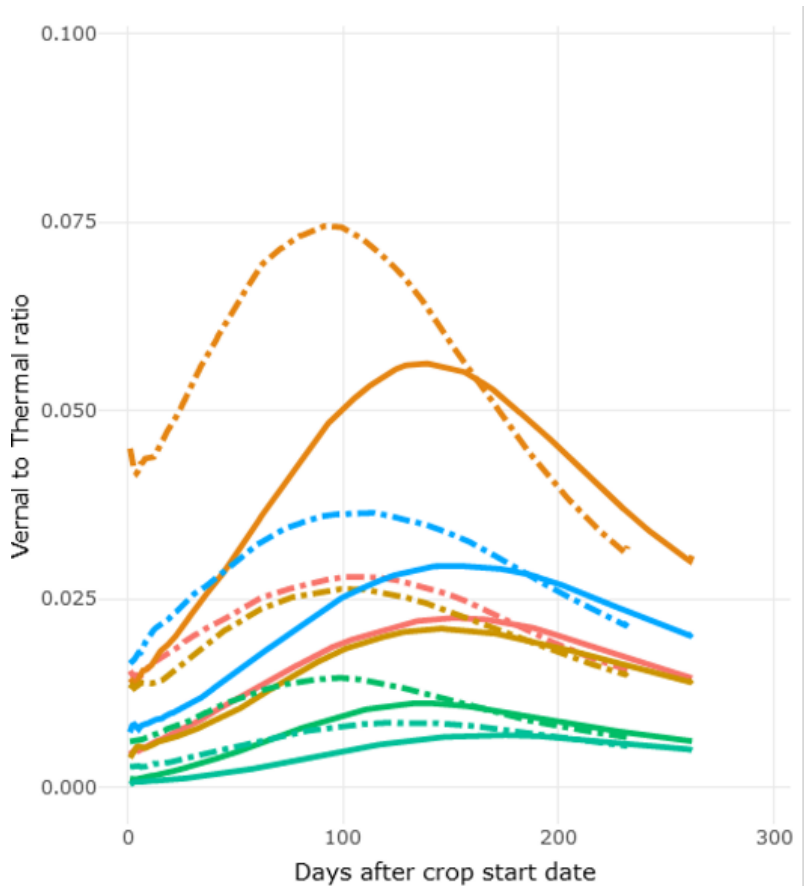


Genomic diversity





Selecting representative environments



- (Beverley, April 15)
- (Beverley, May 15)
- (Boorowa, April 15)
- (Boorowa, May 15)
- (Cummins, April 15)
- (Cummins, May 15)
- (Gatton, April 15)
- (Gatton, May 15)
- (GrealtonAero, April 15)
- (GrealtonAero, May 15)
- (Kojonup, April 15)
- (Kojonup, May 15)

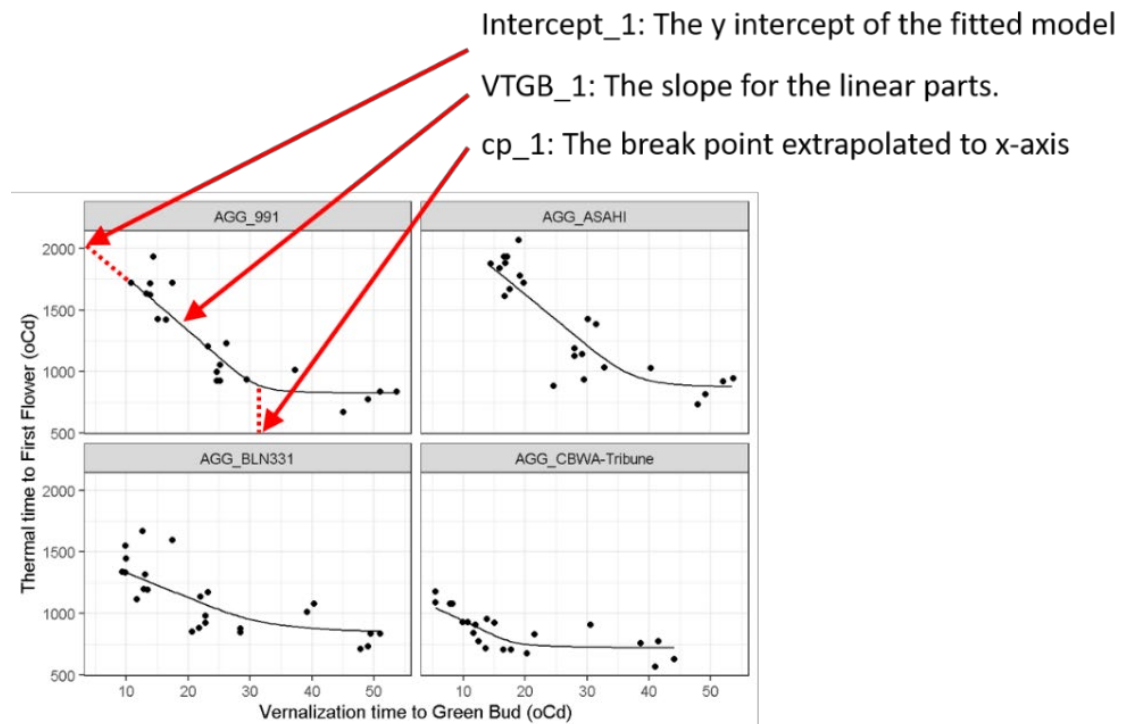
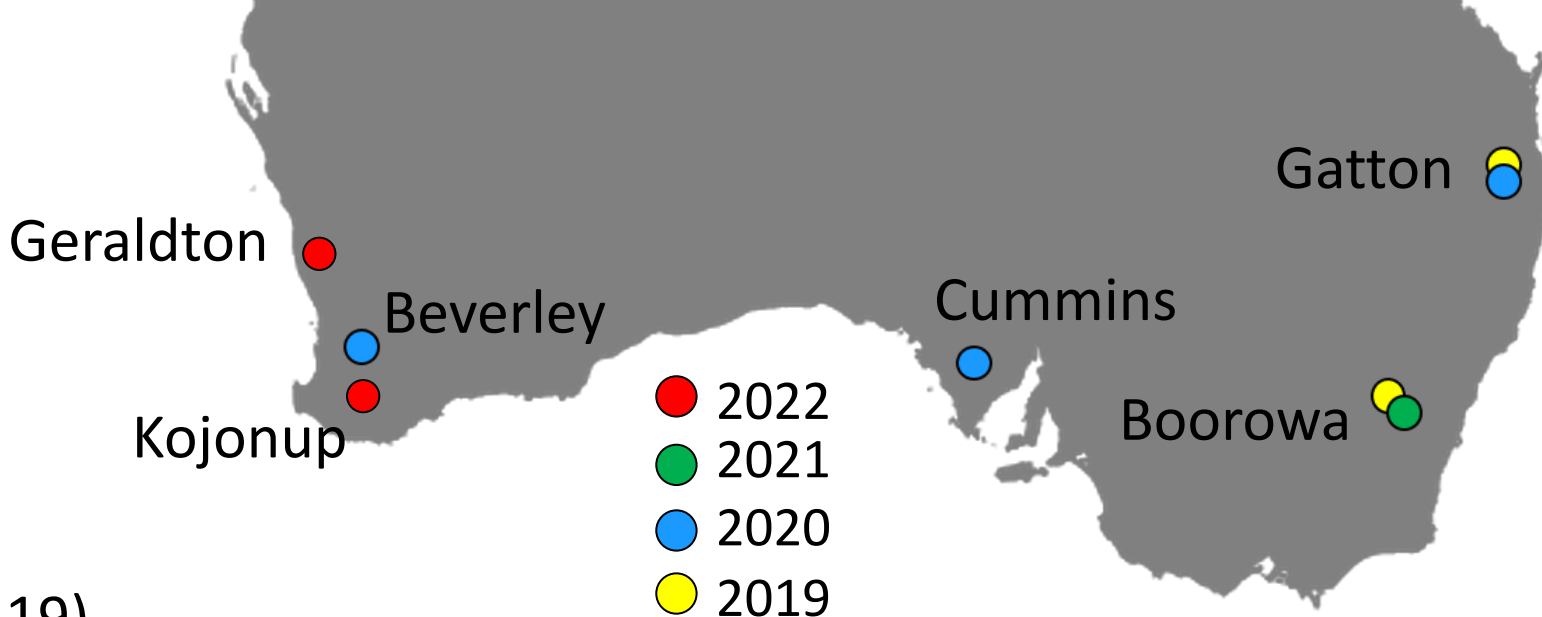


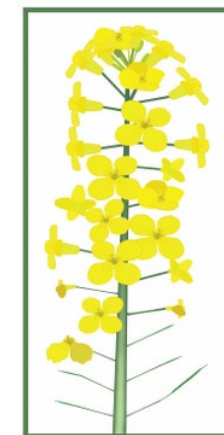
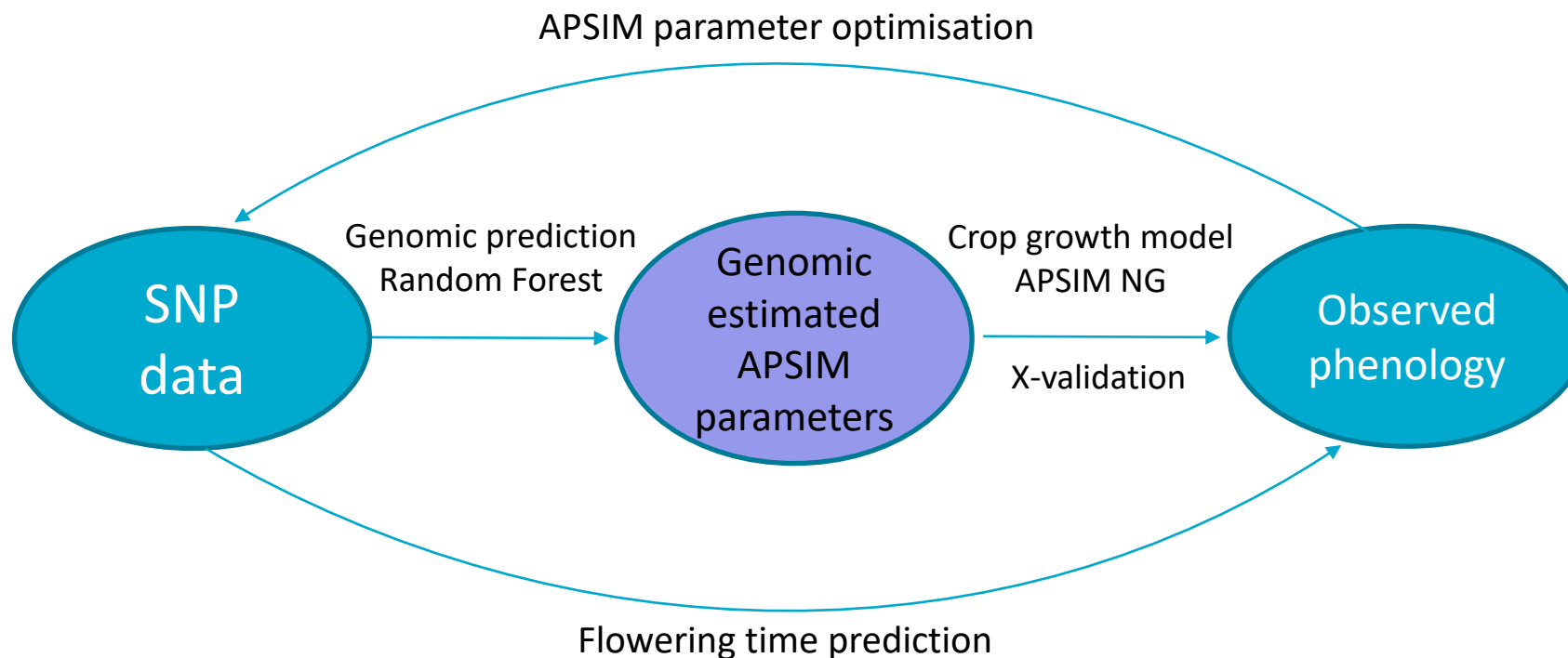
Field trials

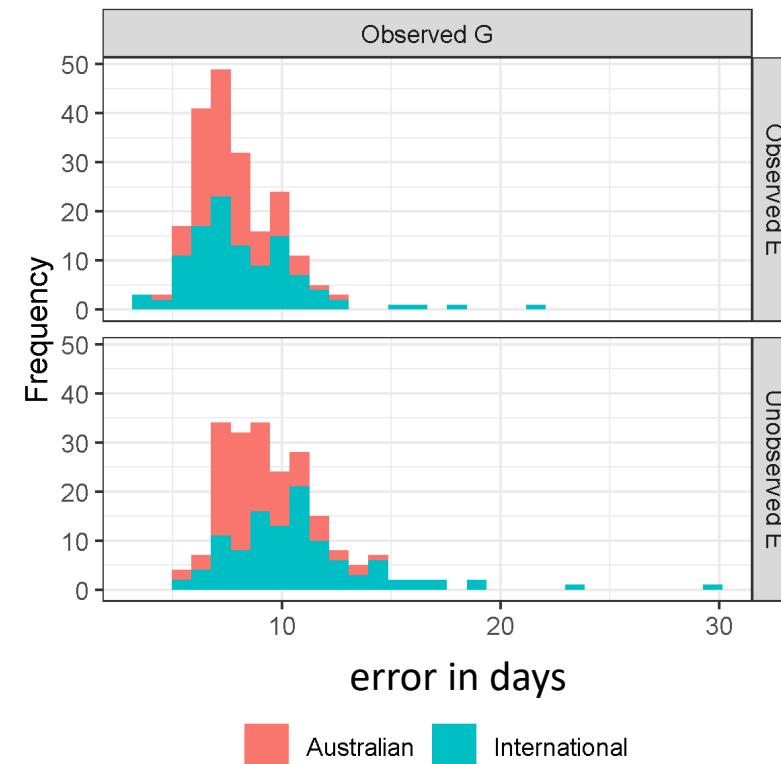
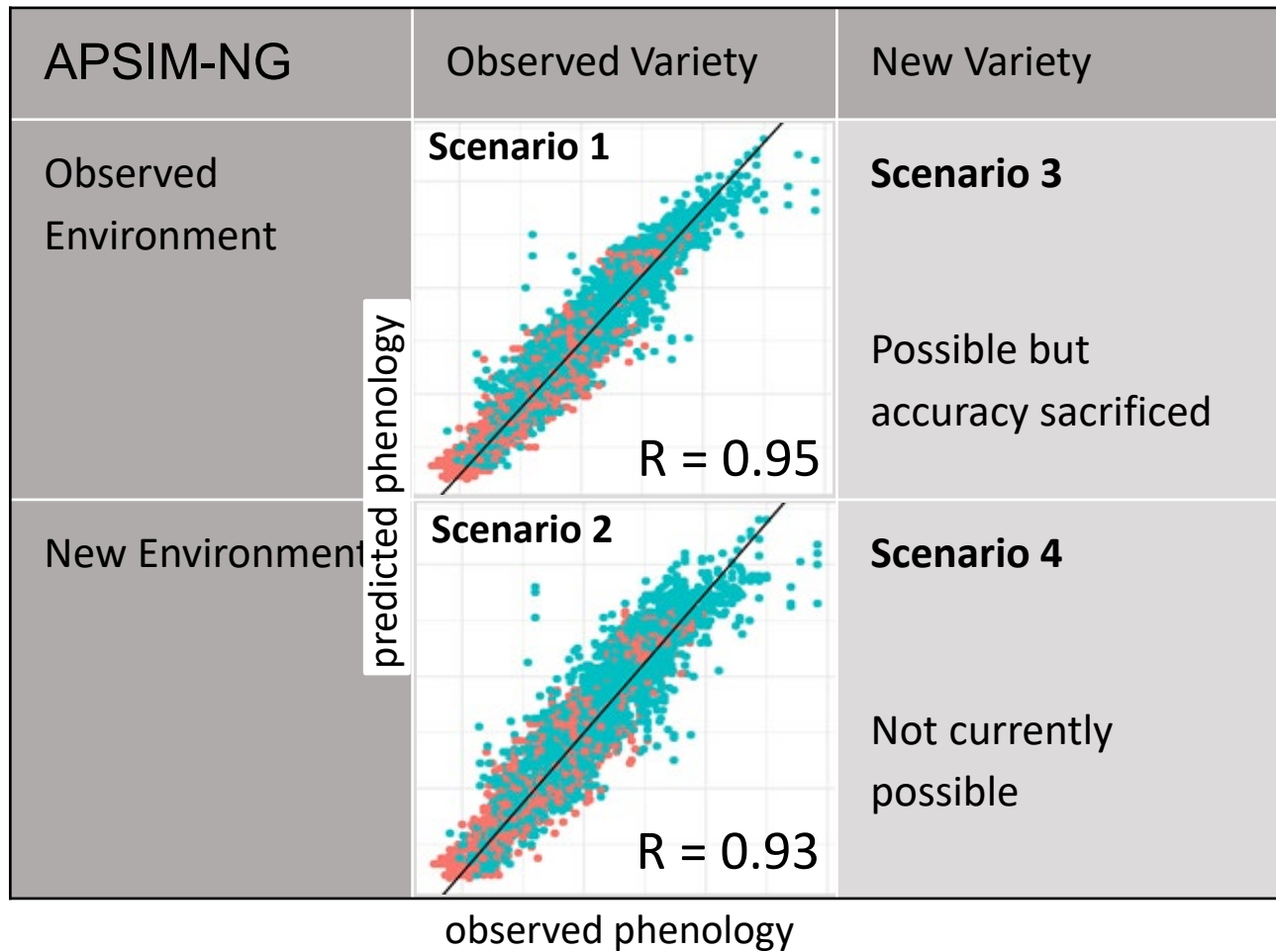
18 site/year/TOS combinations

Phenology scored

- Emergence (stage 9)
- leaf appearance (stages 10 – 19)
- bud visible (stage 51)
- first flower (stage 60)

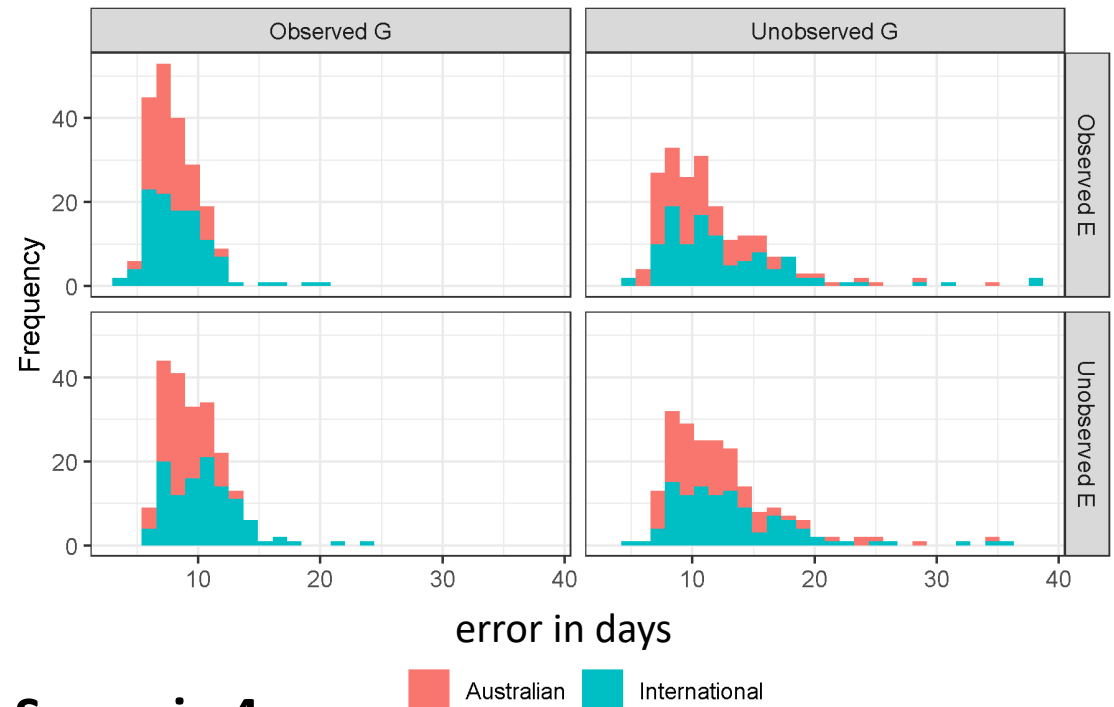
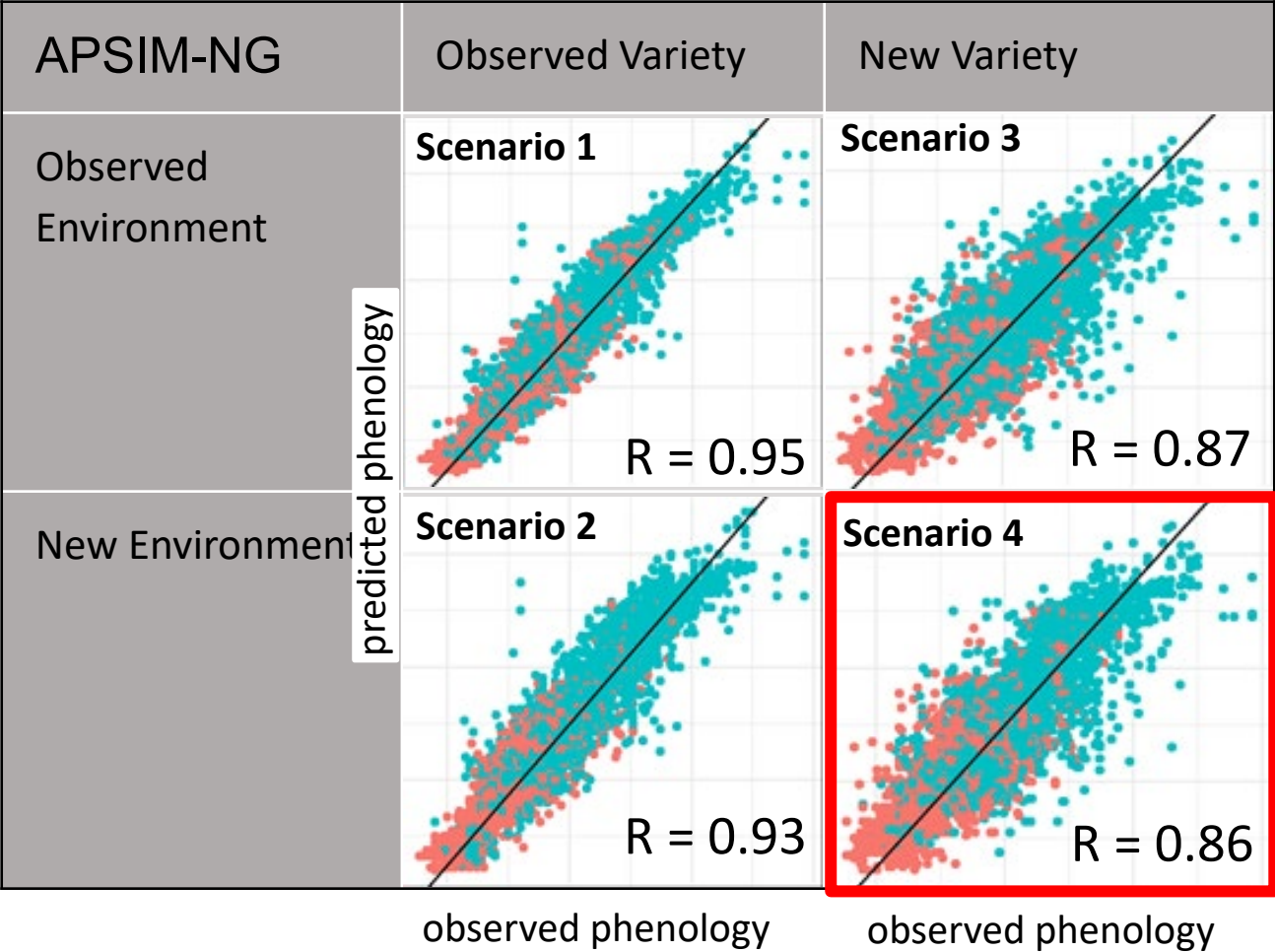








The hybrid genomic-CGM model



Scenario 4
 $R = 0.87$ AUS and international varieties
 Error within < 10 days on for AUS lines



How to access the tool



New “Phenology APP”

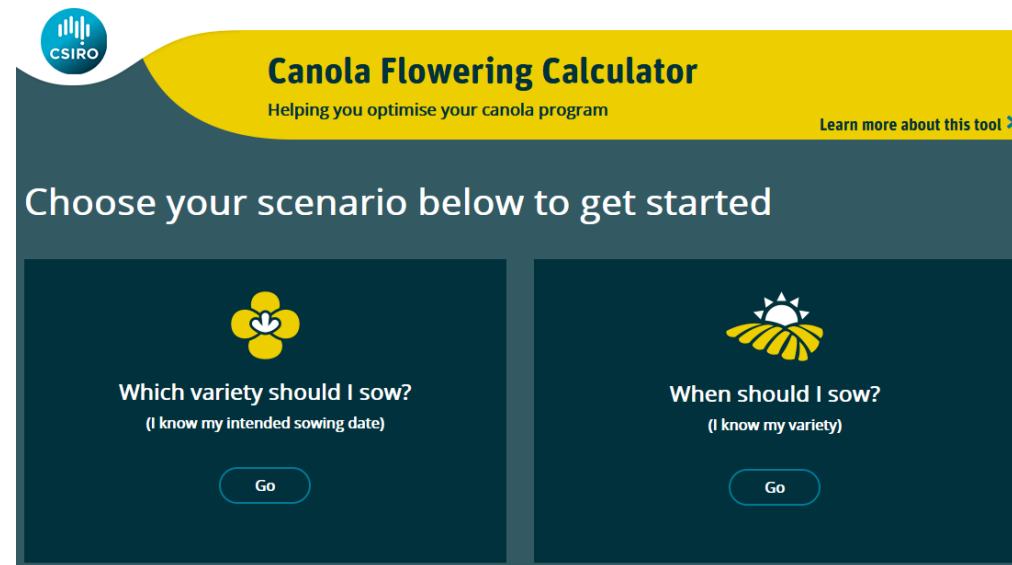
- GRDC investment (started 2022)
- incorporating genomic model
- update model and app annually via NVT

Help Growers

- choose variety or sowing time best suited to their site

Help breeders

- characterise phenology for new and existing varieties in wider range of locations
- incorporate into hybrid and OP breeding programs



<https://www.canolaflowering.com.au>





Genome wide association

Phenology scored:

Controlled environments

Long days (12hrs)

Short days (8hrs)

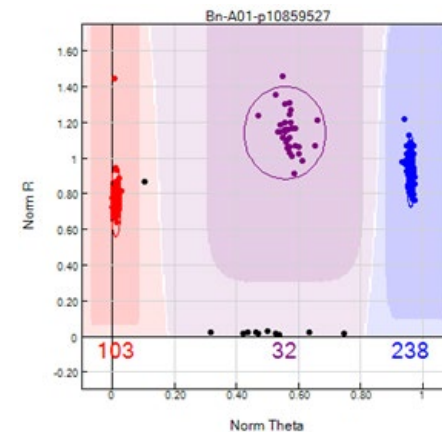
Short days with vernalisation

Field experiments

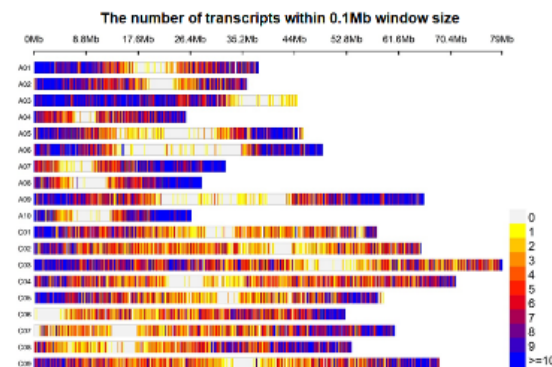
18 site/TOS/years



SNPs

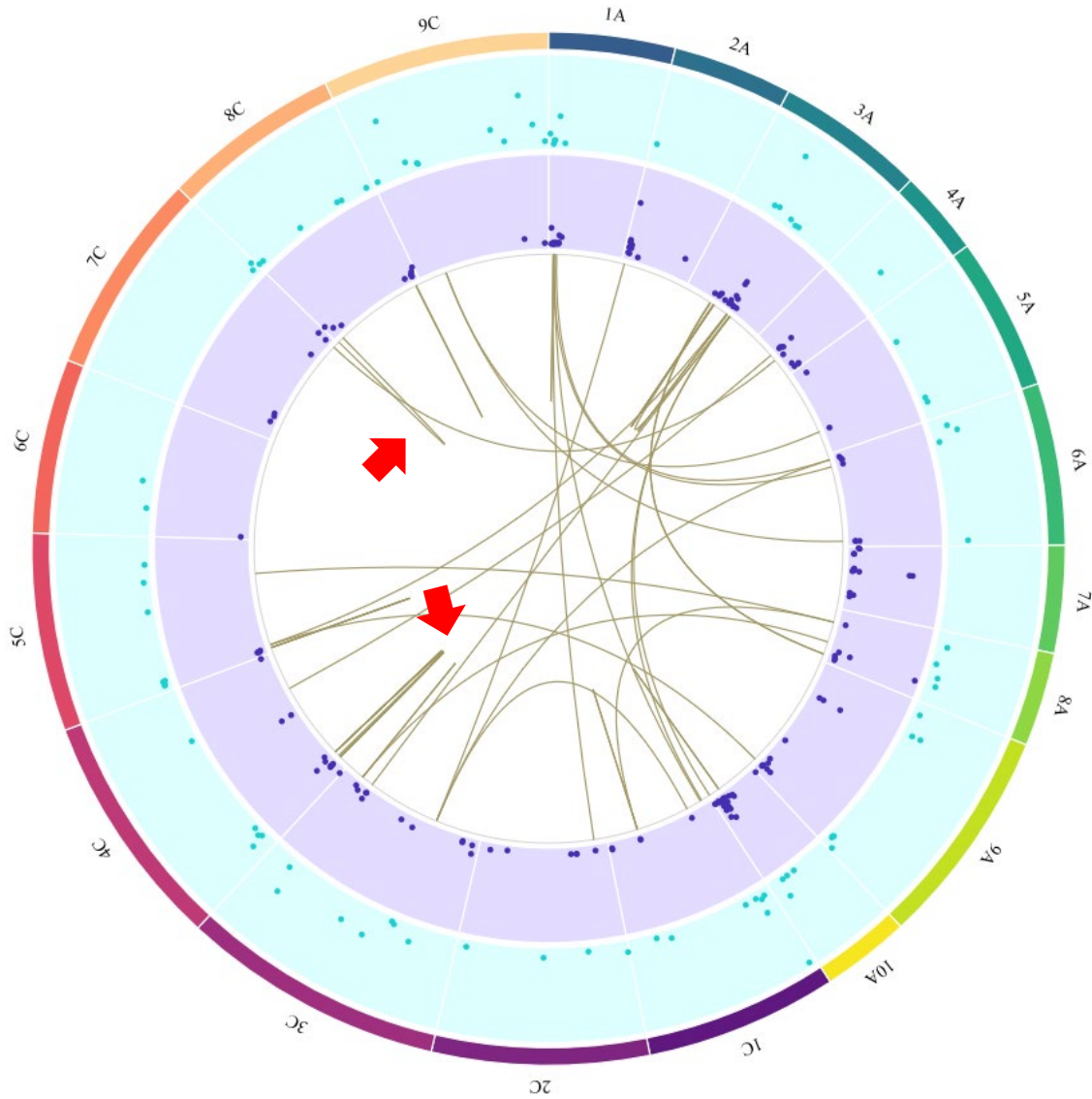


Gene transcripts





Glass house : GWAS & TWAS



SNP loci

transcripts

Top 50 features

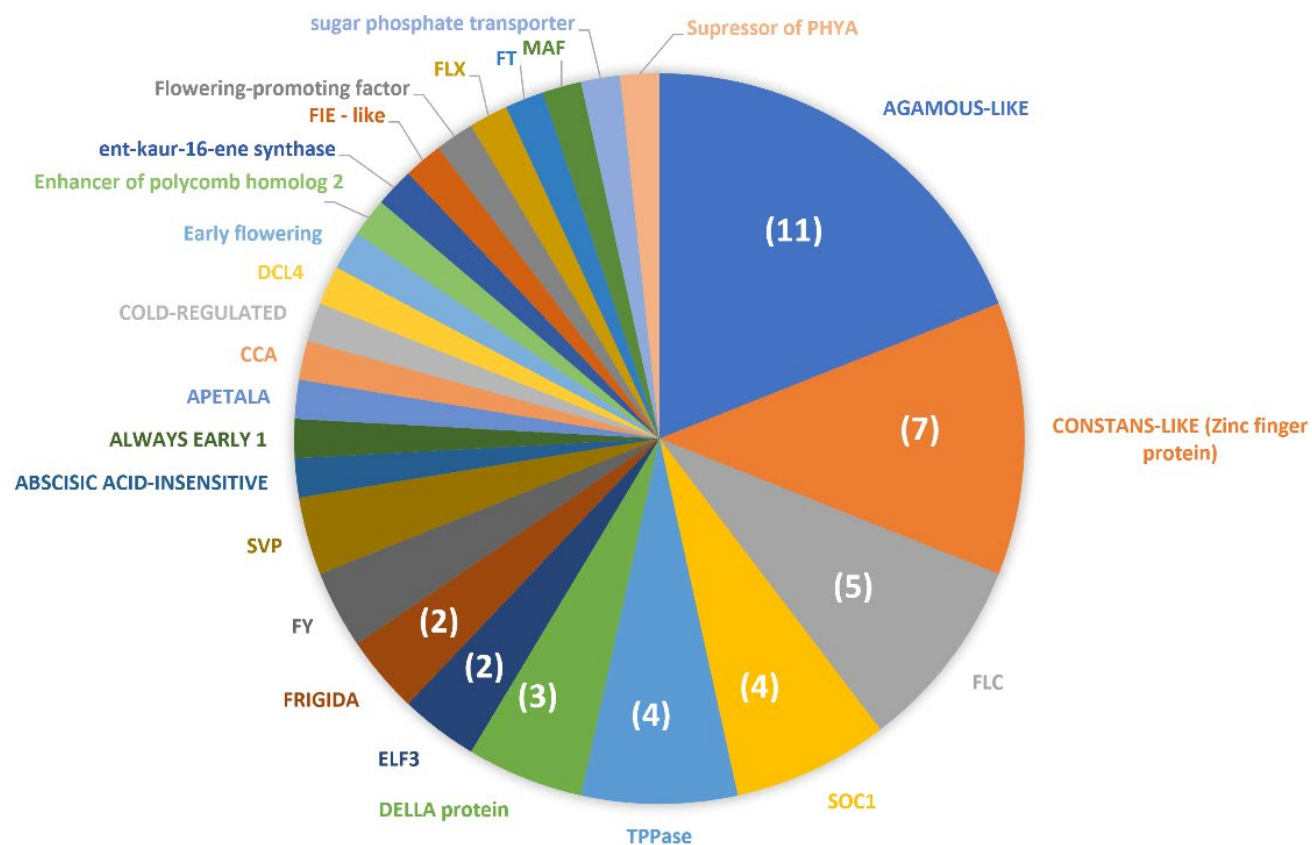
SNPs			long_rank_Assoc	short_rank_Assoc	shortV_rank_Assoc
Chr	rank				
A1	4		red	orange	green
A1	22		red	orange	green
A2	12		red	orange	green
A2	48		yellow	orange	green
A2	21		red	orange	green
A3	7		red	orange	green
A3	50		yellow	orange	green
A3	3		red	orange	green
A3	1		red	orange	green
A4	49		green	orange	yellow
A4	32		yellow	orange	green
A4	5		yellow	orange	green
A4	44		yellow	orange	green
A7	11		yellow	orange	green
A7	9		red	orange	green
A7	19		yellow	orange	green
A7	33		yellow	orange	green
A8	35		yellow	orange	green
A8	23		yellow	orange	green
A9	18		red	orange	green
A9	36		yellow	orange	green
A9	27		red	orange	green
A10	30		yellow	orange	green
A10	45		yellow	orange	green
A10	25		yellow	orange	green
A10	2		red	orange	green
A10	42		yellow	orange	green
A10	34		yellow	orange	green
A10	29		yellow	orange	green
C2	13		yellow	orange	green
C2	31		yellow	orange	green
C3	15		red	orange	green
C3	10		red	orange	green
C3	40		yellow	orange	green
C3	8		yellow	orange	green
C3	41		yellow	orange	green
C4	17		orange	orange	green
C5	46		yellow	orange	green
C6	6		yellow	orange	green
C6	16		yellow	orange	green
C8	38		green	orange	yellow
C8	37		orange	orange	green
C9	28		yellow	orange	green

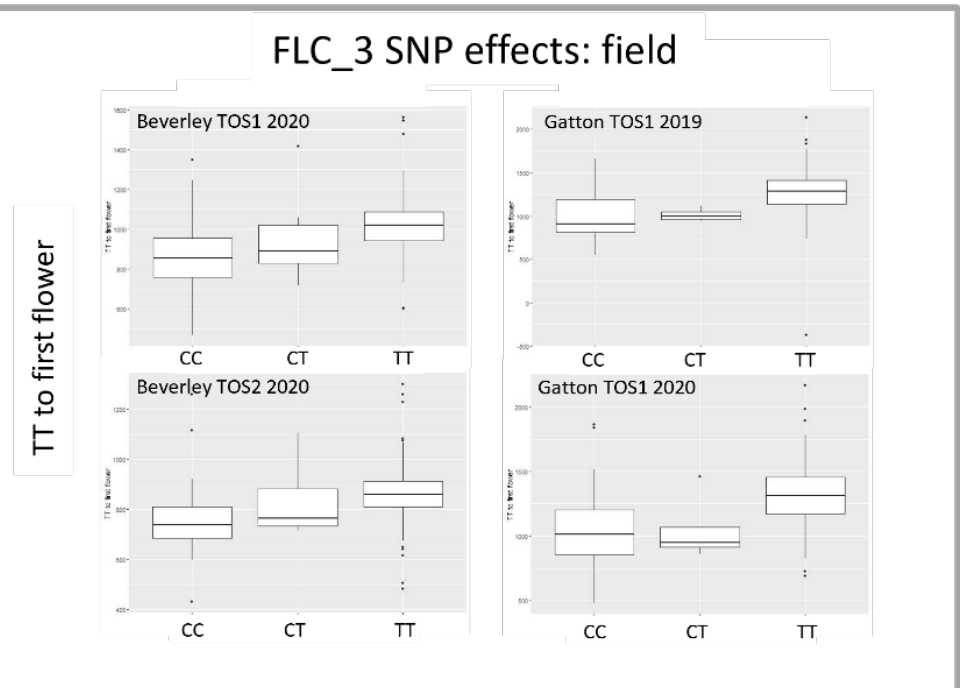
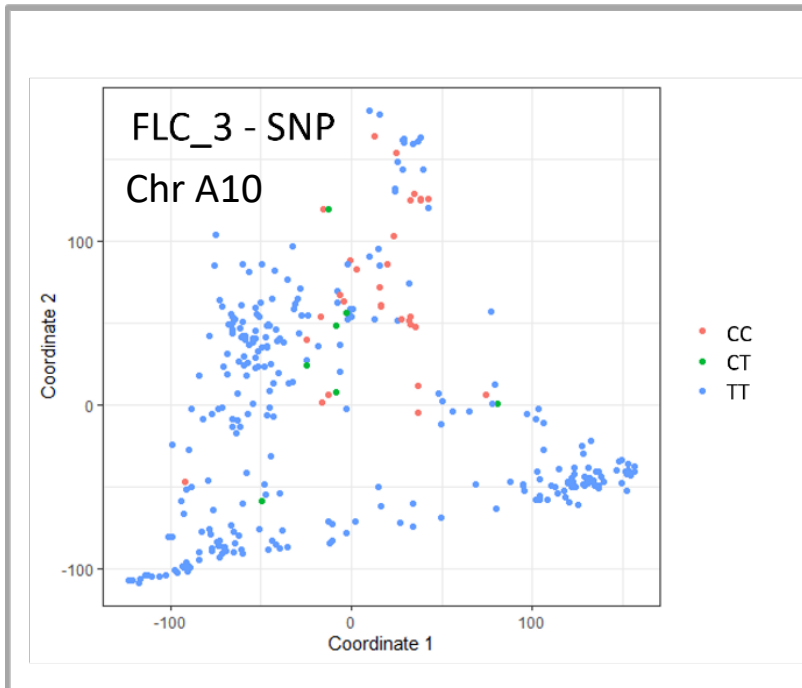
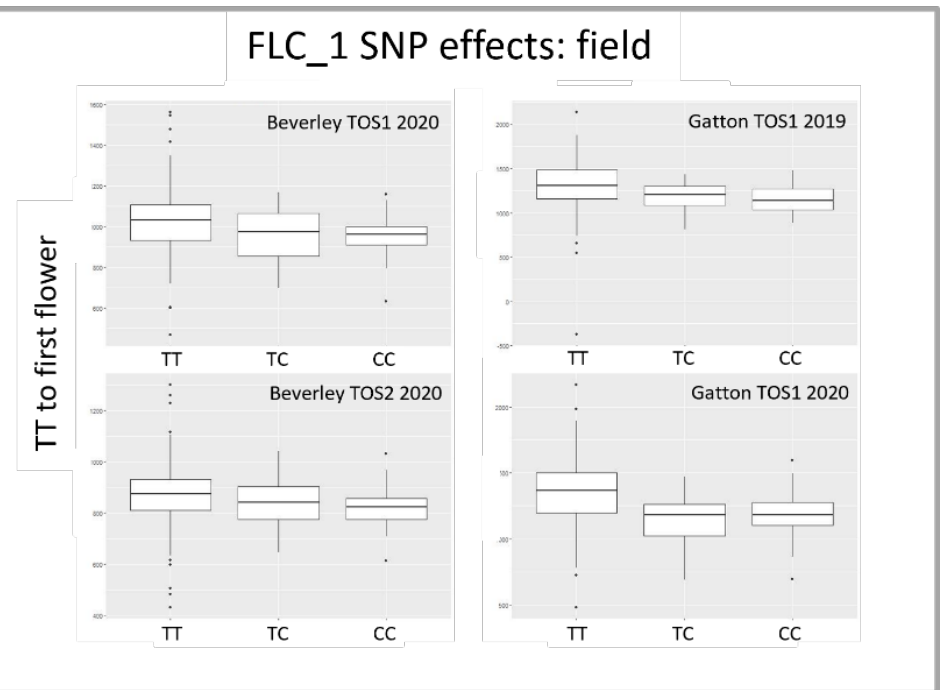
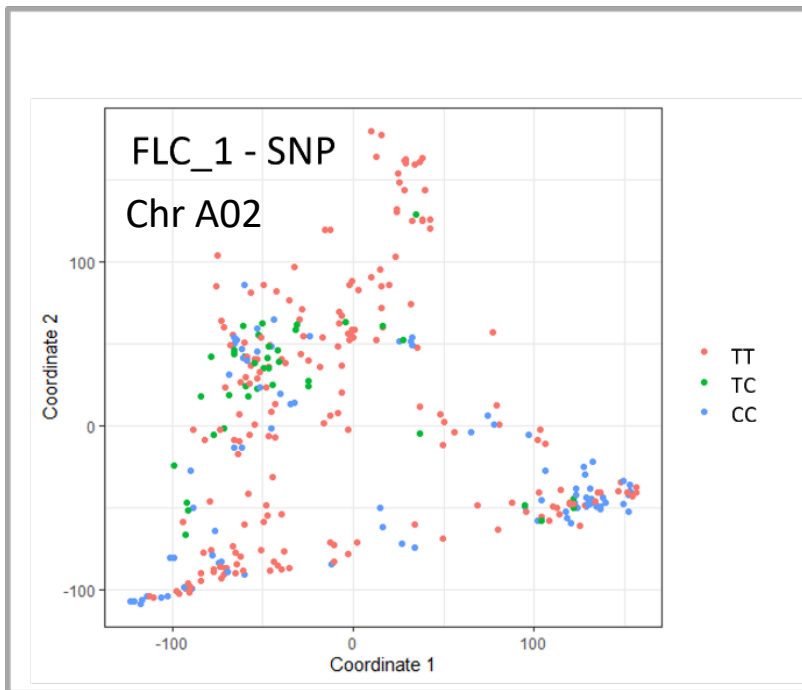
transcripts			long_rank_Assoc	short_rank_Assoc	shortV_rank_Assoc
Chr	rank				
A1	28		red	orange	green
A2	27		yellow	orange	green
A2	15		yellow	orange	green
A2	3		green	orange	yellow
A3	6		orange	orange	green
A3	5		orange	orange	green
A3	23		red	orange	green
A3	8		red	orange	green
A3	48		green	orange	yellow
A3	32		yellow	orange	green
A4	11		yellow	orange	green
A4	50		yellow	orange	green
A4	36		yellow	orange	green
A4	44		yellow	orange	green
A5	40		yellow	orange	green
A7	9		yellow	orange	green
A8	47		green	orange	yellow
A8	34		yellow	orange	green
A9	39		yellow	orange	green
A10	31		yellow	orange	green
C1	20		yellow	orange	green
C1	46		yellow	orange	green
C1	49		yellow	orange	green
C1	22		orange	orange	green
C2	38		green	orange	yellow
C2	16		orange	orange	green
C2	21		yellow	orange	green
C3	13		red	orange	green
C3	17		yellow	orange	green
C3	7		red	orange	green
C3	19		red	orange	green
C3	12		red	orange	green
C3	29		red	orange	green
C3	43		yellow	orange	green
C3	4		yellow	orange	green
C4	10		orange	orange	green
C4	45		green	orange	yellow
C5	30		green	orange	yellow
C5	35		yellow	orange	green
C5	42		yellow	orange	green
C6	37		yellow	orange	green
C6	14		yellow	orange	green
C6	24		green	orange	yellow
C6	33		yellow	orange	green
C7	18		yellow	orange	green
C7	25		yellow	orange	green
C8	2		red	orange	green
C9	26		yellow	orange	green
Un	41		yellow	orange	green



Combined results

- 142 associations with flowering time
- Tagging 112 unique QTL
- Significance detected in both GH and field experiments
- Many small to moderate effect loci
 - $R^2 \sim 0.05$ to 0.2
 - complex regulation?
- Over half resided within or near genes annotated as having function in FT control – some extensively reported in canola – e.g. FLC family



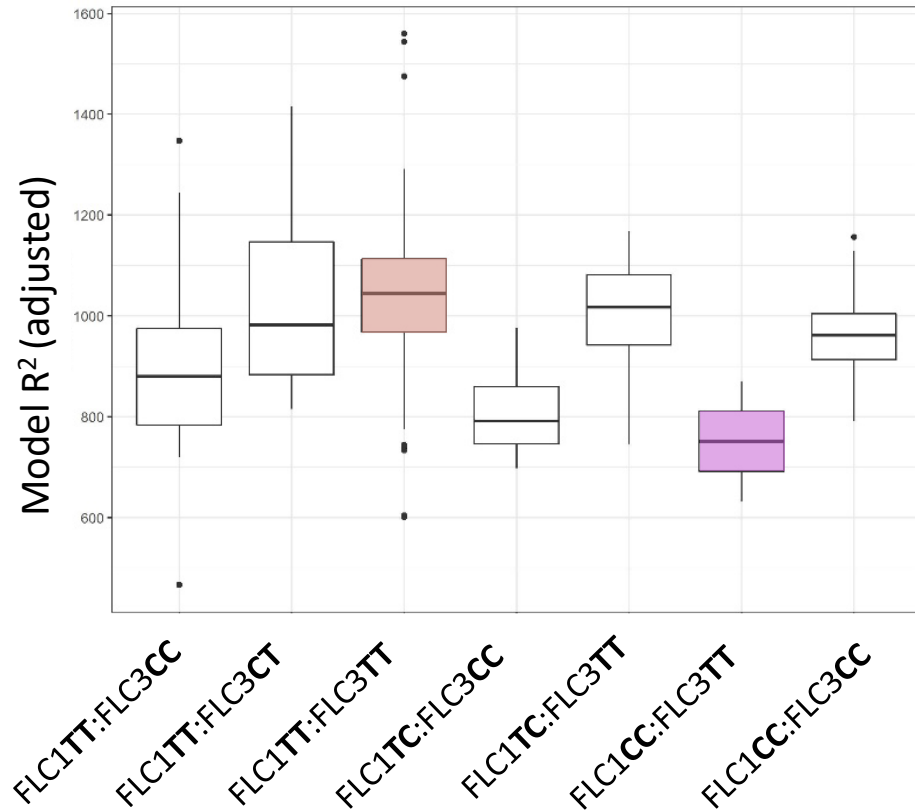
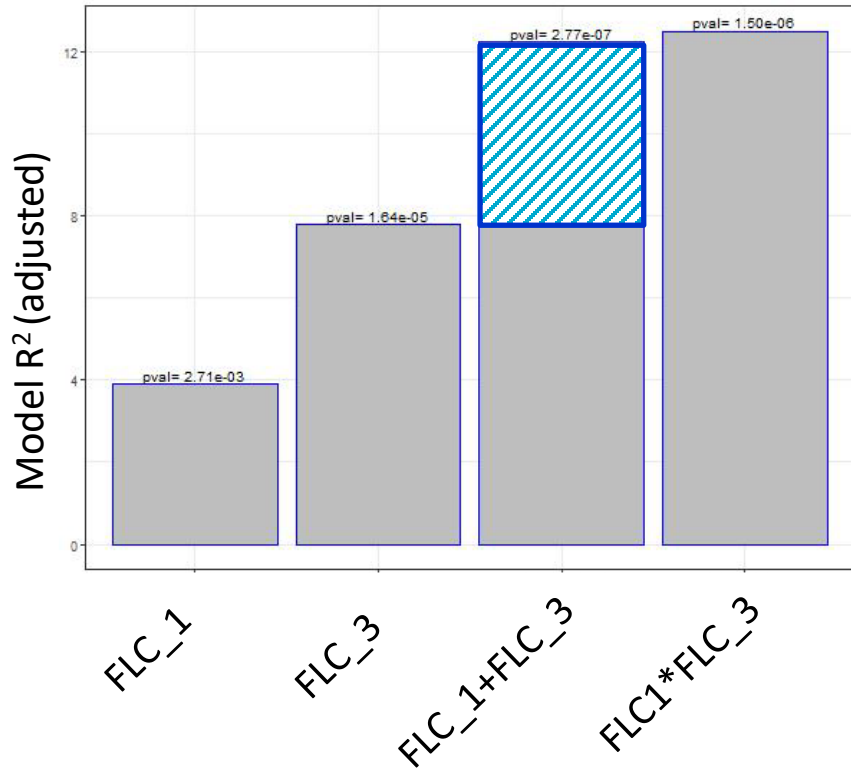




FLC family genes

Variance explained:

$$Y_i = \beta_0 + \sum_{j=1}^p \beta_j X_{i,j} + \varepsilon_i$$





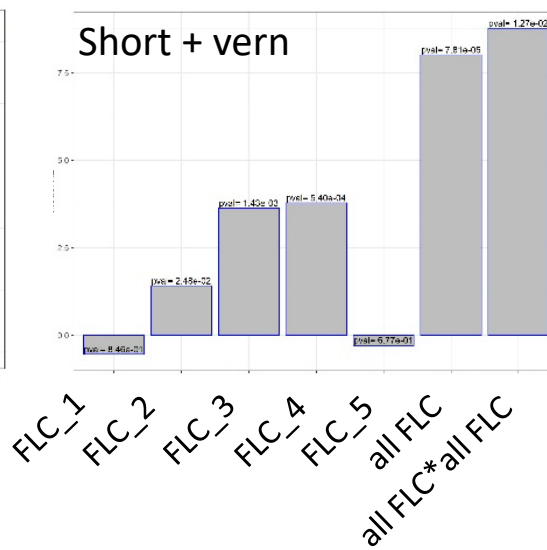
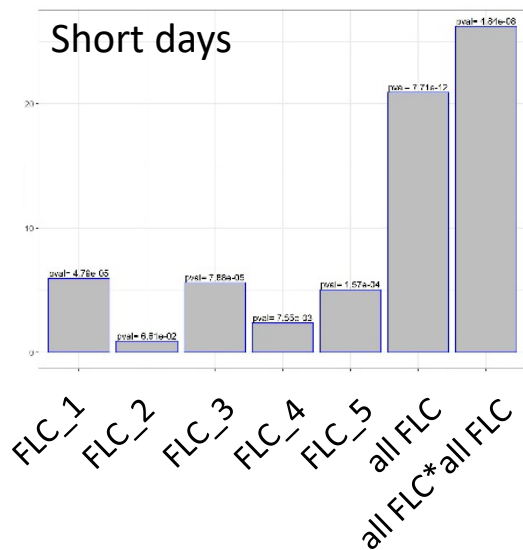
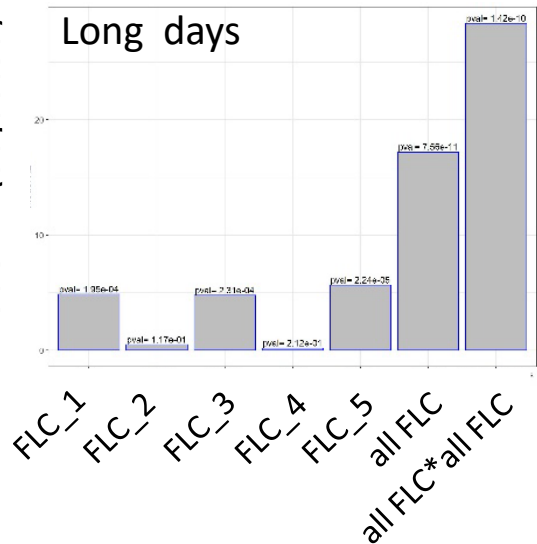
FLC family genes – controlled env.



Variance explained:

$$Y_i = \beta_0 + \sum_{j=1}^p \beta_j X_{i,j} + \varepsilon_i$$

Model R² (adjusted)



Epistatic interactions

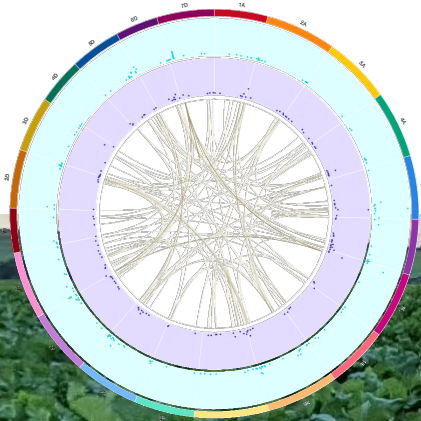
FLC_2:FLC_5

FLC_2:FLC_3

FLC_3:FLC_5

FLC_2:FLC_3:FLC_5

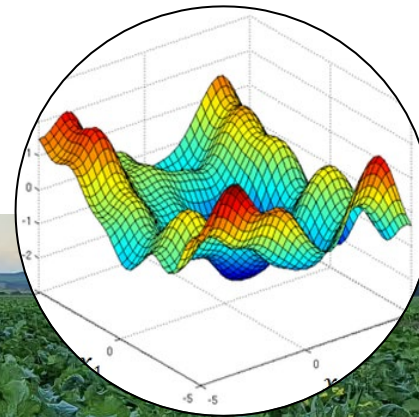
Strategies for integrating phenology genetics into variety design



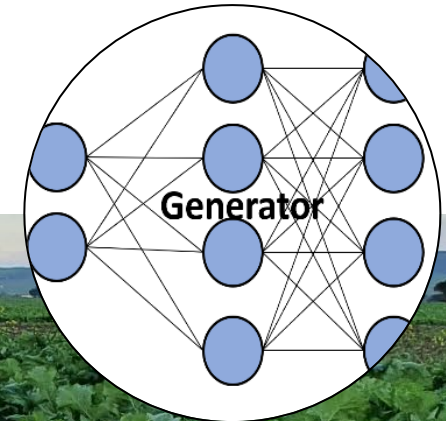
Marker assisted breeding



Phenology app



Genomic selection



Generative AI variety design



Thank you

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Emmett Leyne
Alec Zwart
Bjorg Sherman

Bangyou Zheng
Jeremy Whish
Julianne Lilley
Matt Nelson
Brett Cocks
Ian Greaves

Jing Wang
Geoff Bull
Bill Bovill
Susie Sprague



Alternative models

Direct modelling of phenology

Model trained on empirical data

- genomic markers
- flowering time

Higher accuracy: R 0.94 - 0.97

Limitation – data availability or accessibility (not in public domain at sufficient scale)

Secure multi-party data sharing approaches – developed at CSIRO – in future could provide a way to access existing privately owned data data sets across the canola growing regions.

Predicted TT to first flower

