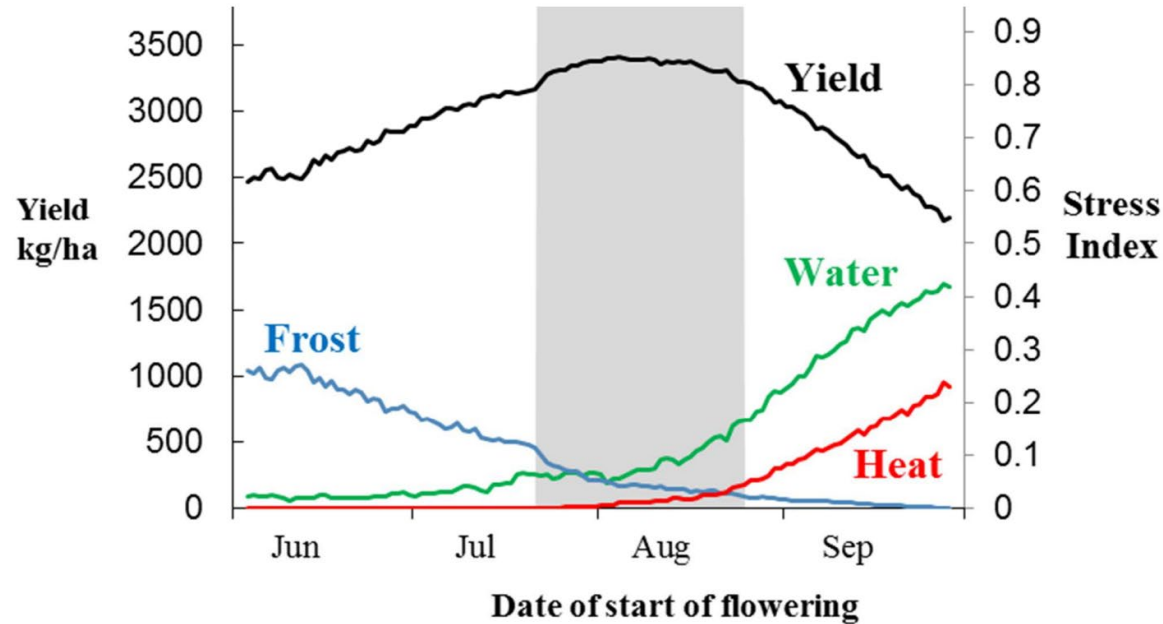


Predicting canola phenology through integration of genomic prediction (GP) and crop growth models (CGM)

Bangyou Zheng, Jeremy Wish, Julianne Lilley, Alexandre Boyer, Alec Zwart, Matthew Nelson, Chris Helliwell, Shannon Dillon

CSIRO Agriculture and Food,
27 September 2023

Optimum sowing and flowering time as limited by abiotic stresses

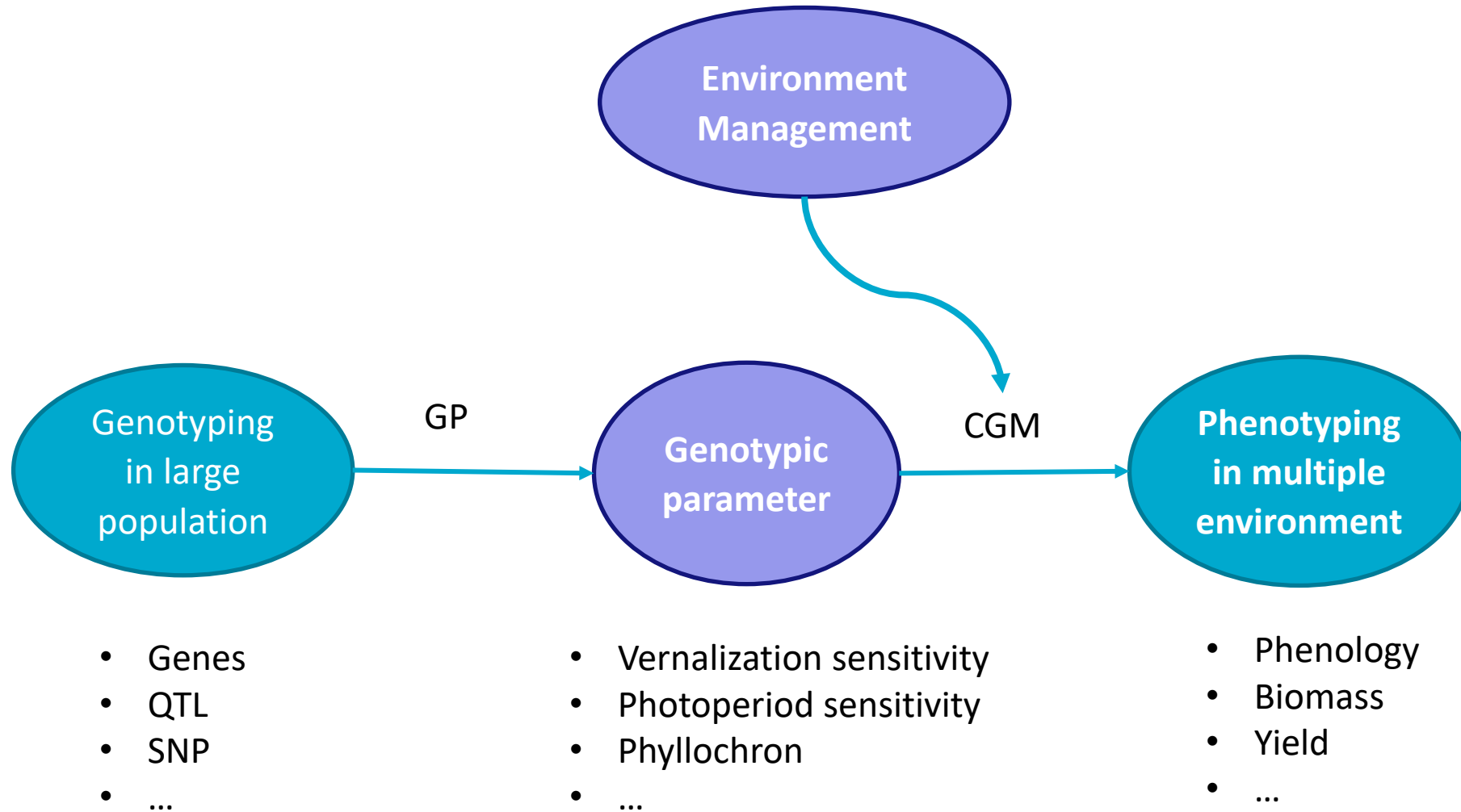


Canola, Lilley et al. 2017

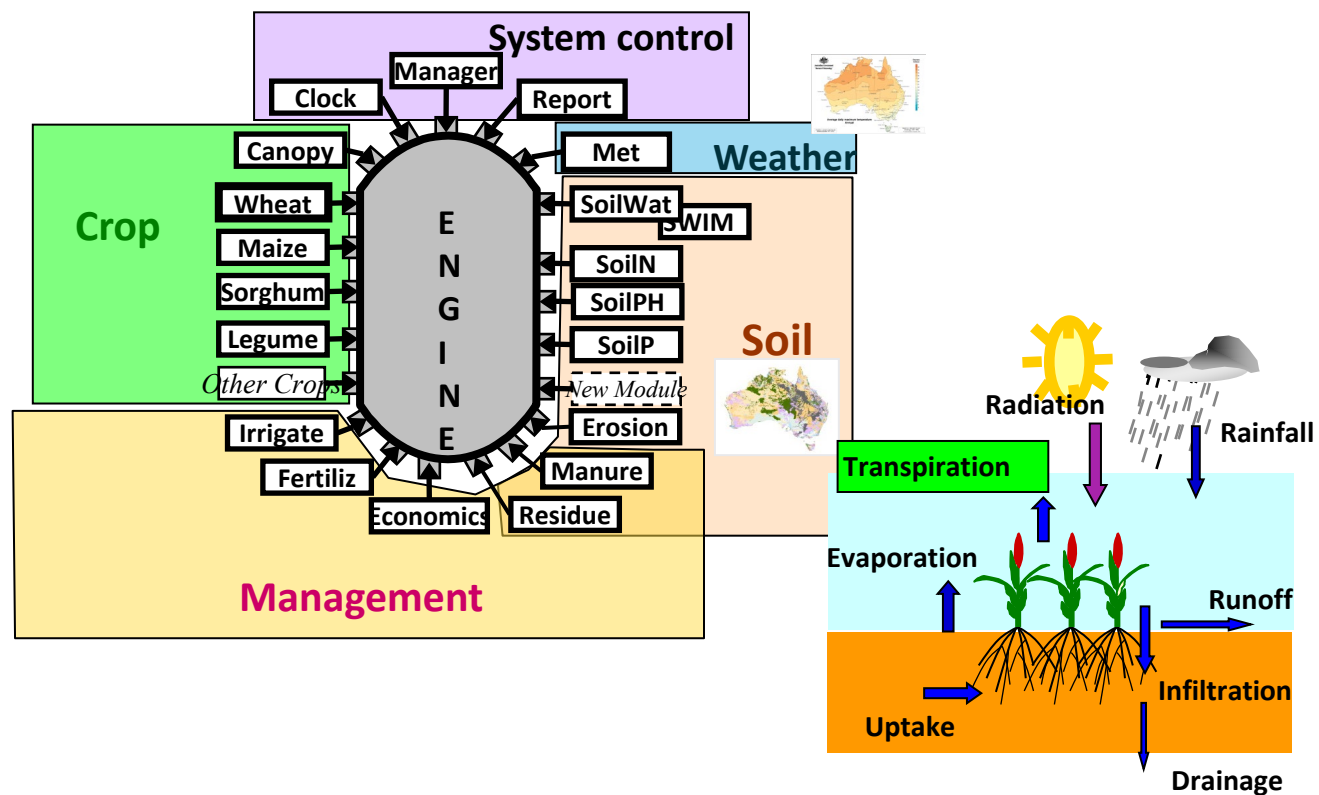
Characterisation for new cultivars through multiple environmental trials (MET)

- Several years and locations
- Expensive

From genotyping to phenotyping in GP and CGM



APSIM Cropping Systems model

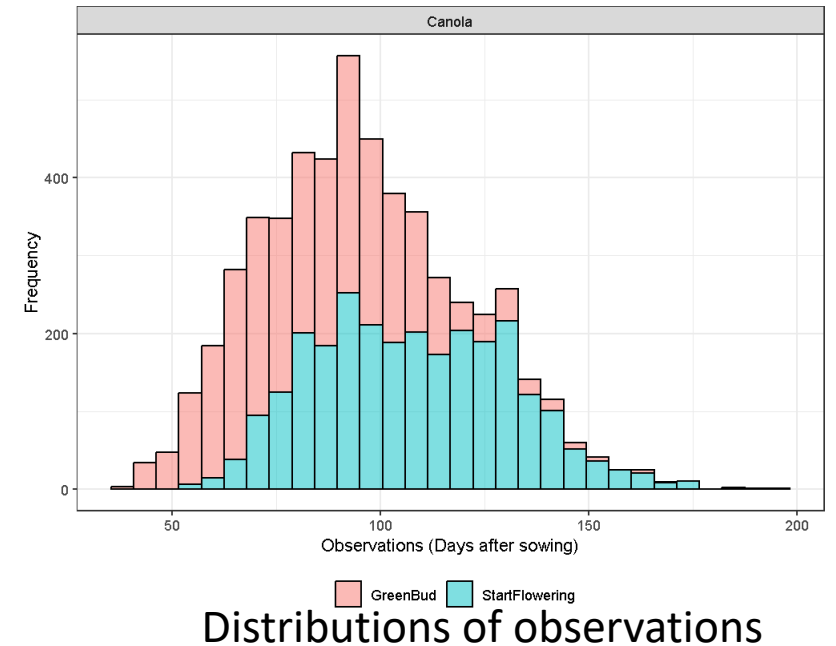
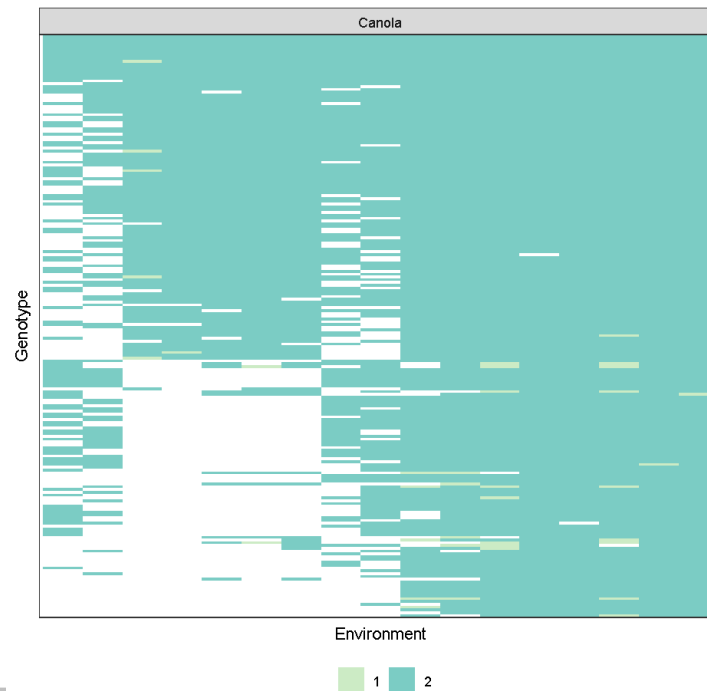


Field experiment

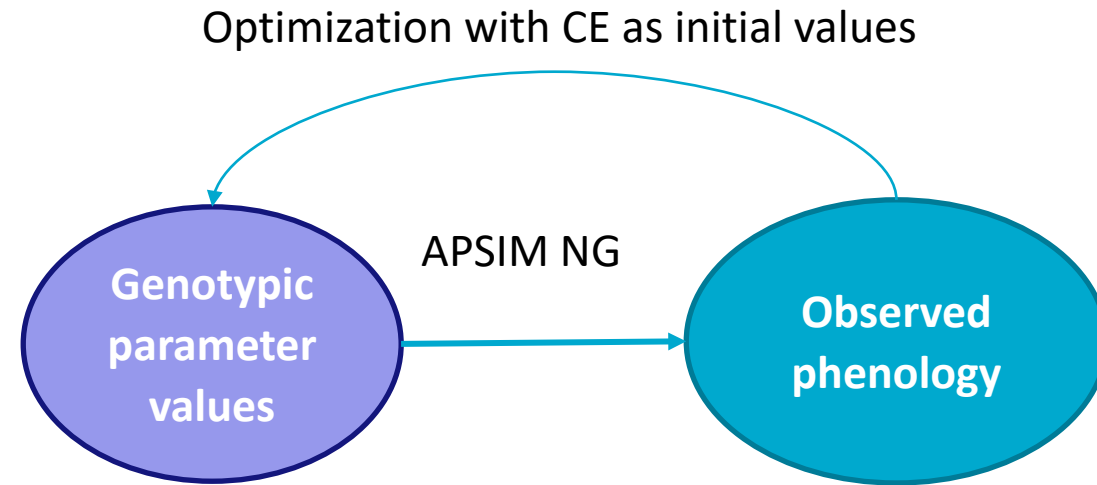
- 4 sites across Australia
- 2/3 Time of Sowing in each site
- 2019 and 2021
- 17 trials in total
- 208 varieties
- 4452 observations



G x E for observations



Prediction of crop phenology using Crop Growth Model



- Canola
 - 3 parameters for vernalisation time vs thermal time
- Green Bud
- Start of Flowering

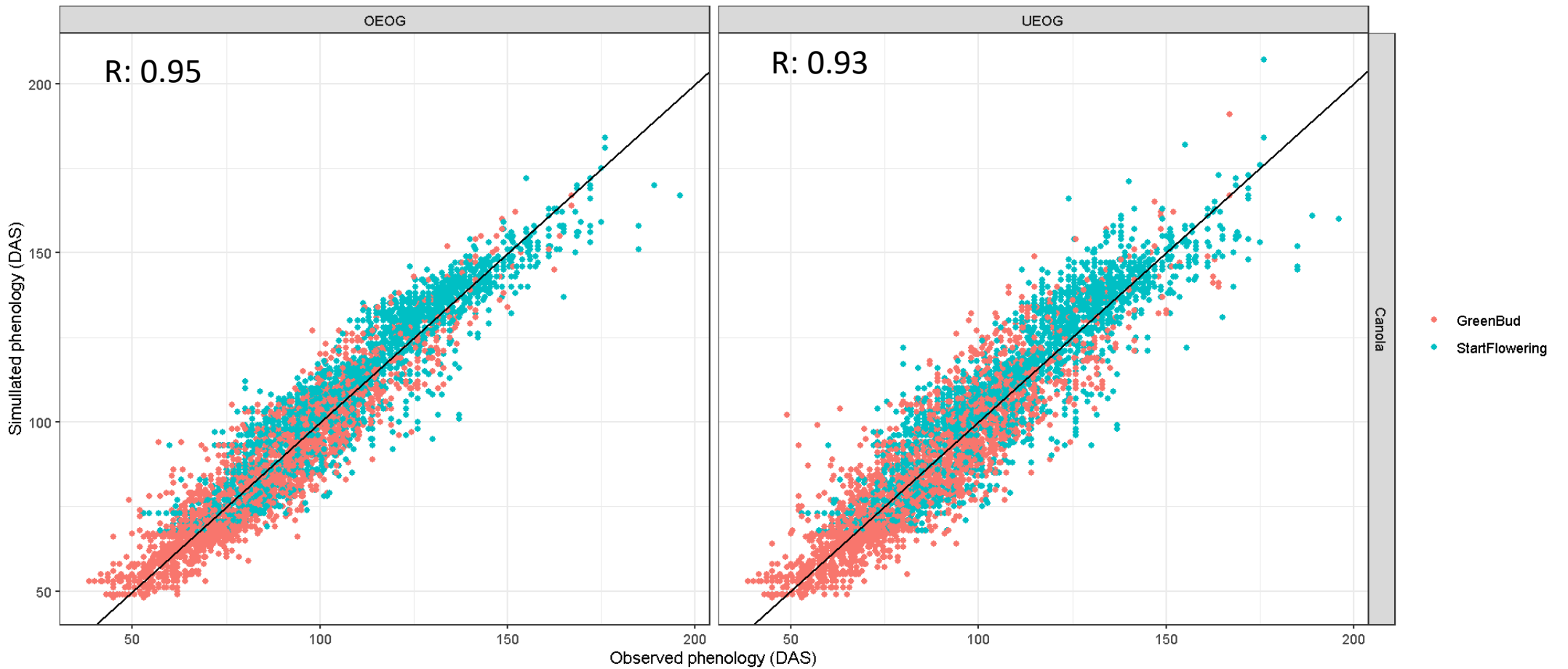
Independent optimization for each cultivar

Evaluation of Crop Growth Model (APSIM NG) under two scenarios

	Observed Genotype (OG)
Observed Environment (OE)	E: All experiments G: Each variety
Unobserved Environment (UE)	E: Split experiments into validation G: Each variety

ONE calibration and ONE validation for each variety

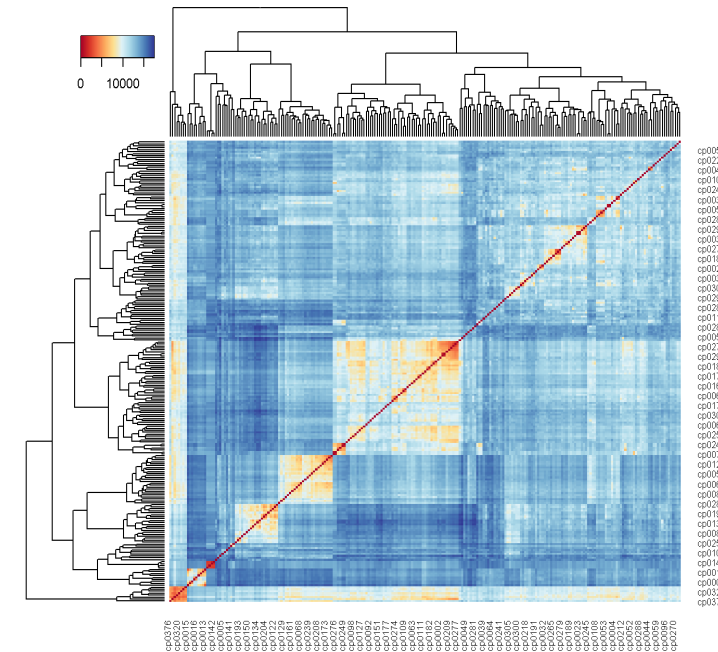
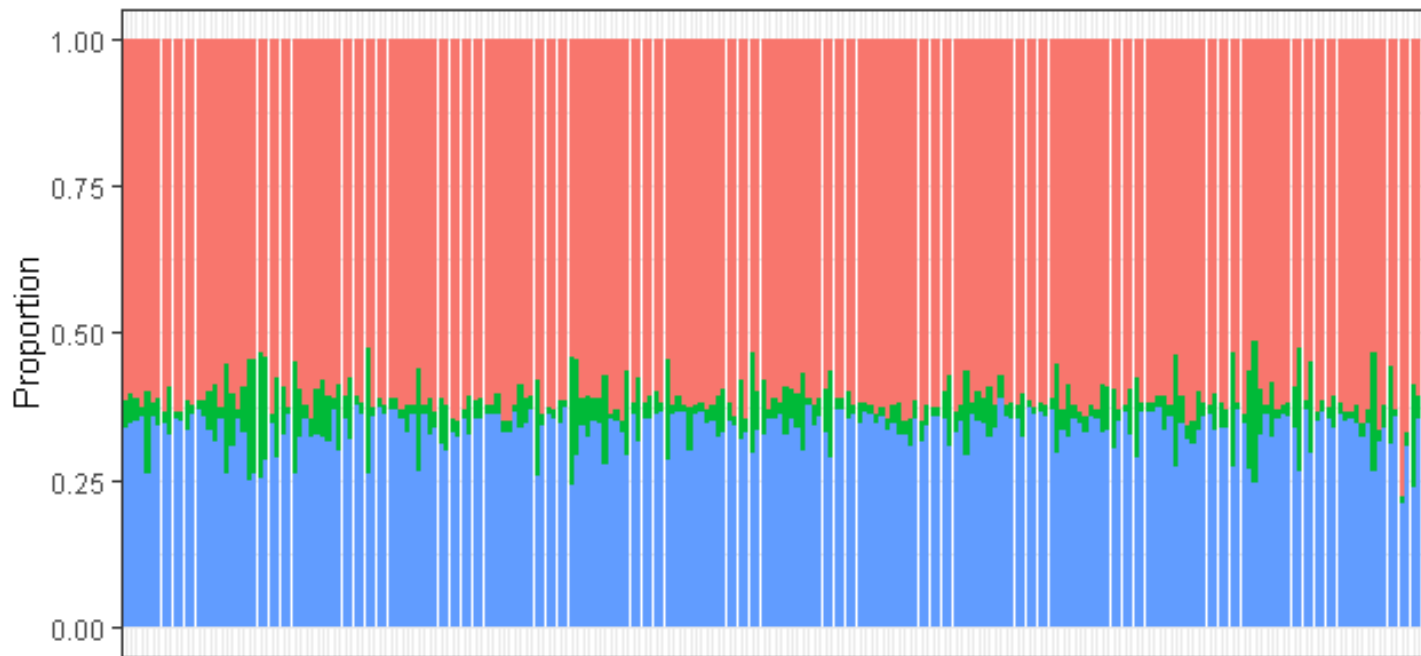
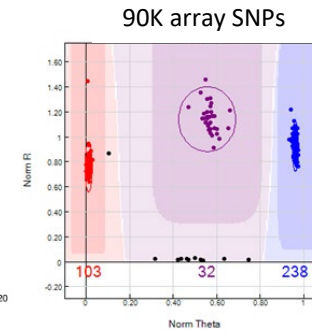
Prediction accuracy for Crop Growth Model



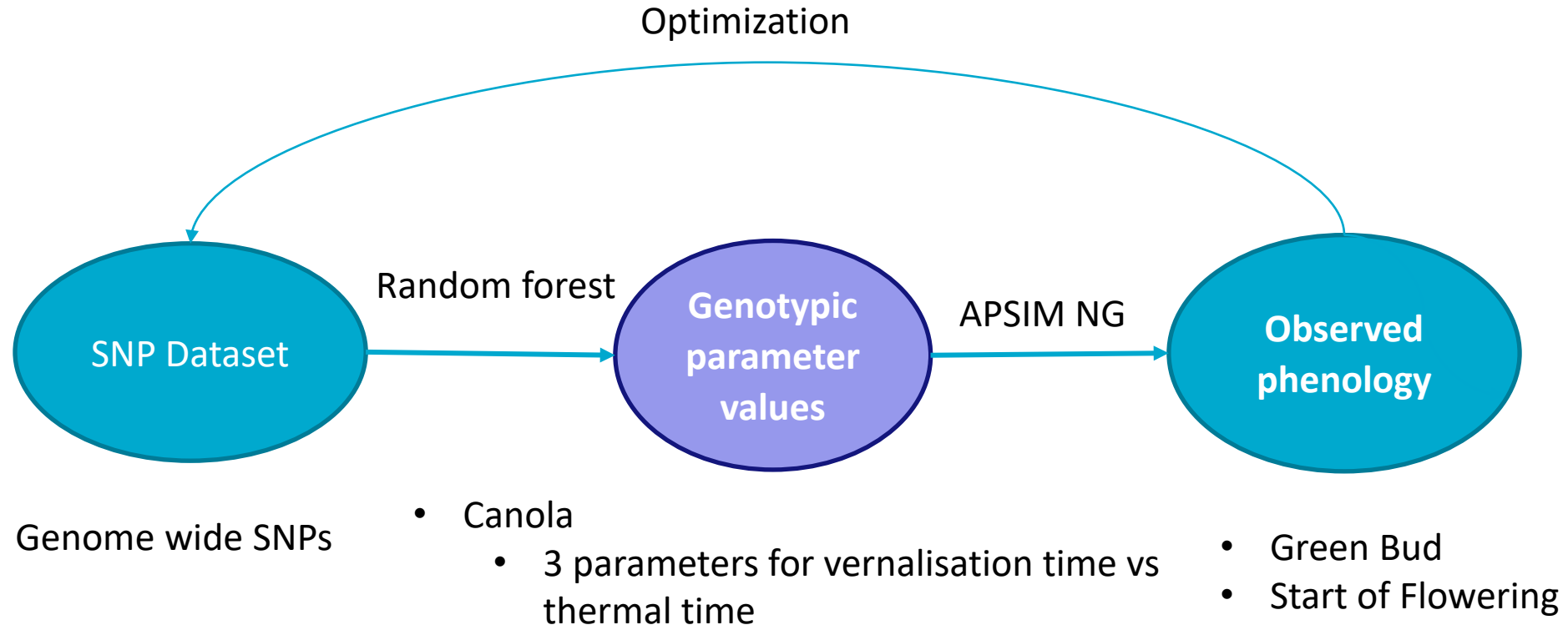
R: Prediction accuracy, Pearson correlation between observation and prediction

SNP Dataset

- Genome wide SNPs
 - 90K brassica array (~30K)
 - Transcript SNPs (~120K)
- Selected 20711 SNPs from 150 K datasets
- 208 varieties



GP-APSIMNG: Using SNP Dataset to predict wheat phenology



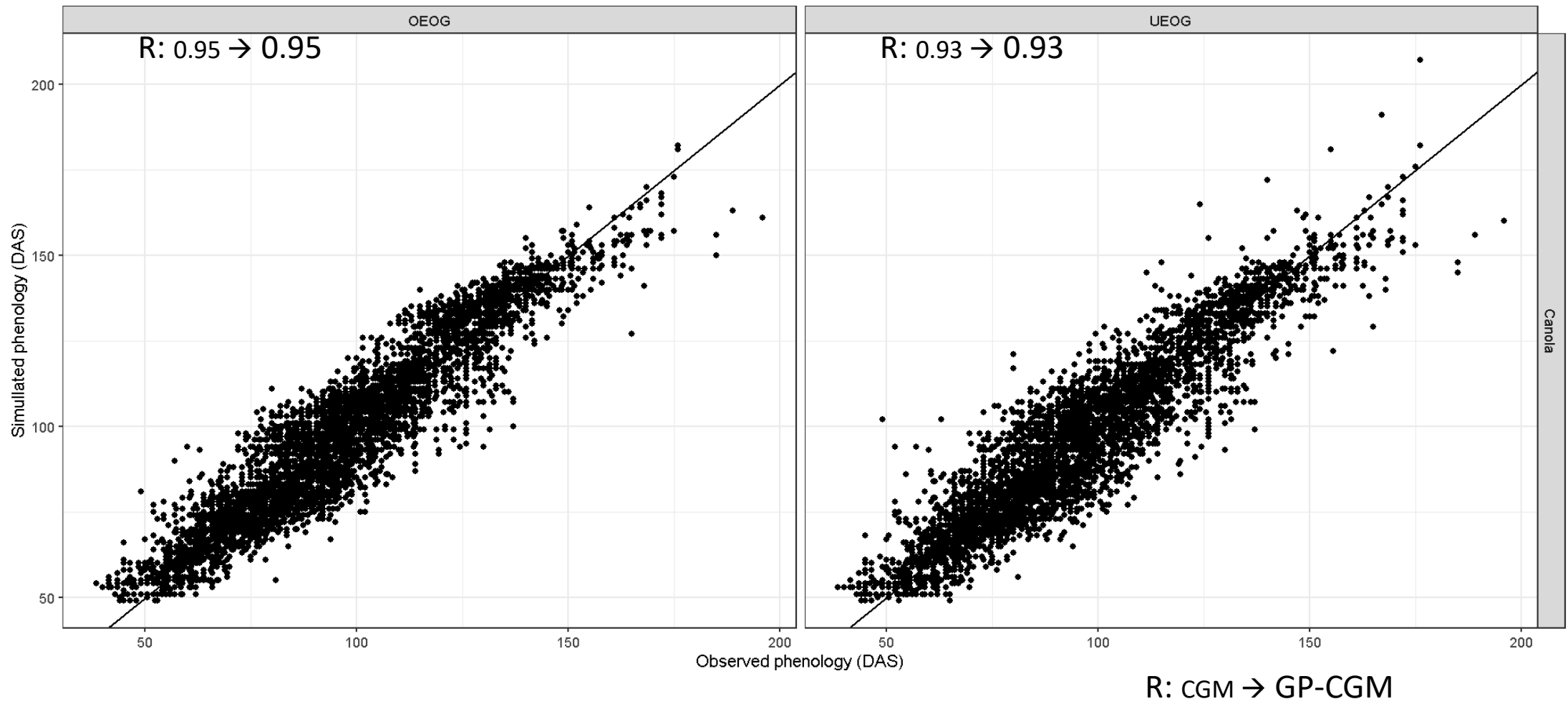
One step optimization for all cultivars

Evaluation of GP-APSIMNG model under four scenarios

	Observed Genotype (OG)	Unobserved Genotype (UG)
Observed Environment (OE)	E: All experiments G: All varieties	E: All experiments G: drop one out cross validation
Unobserved Environment (UE)	E: Split experiments into validation G: All varieties	E: Split experiments into validation G: drop one out cross validation

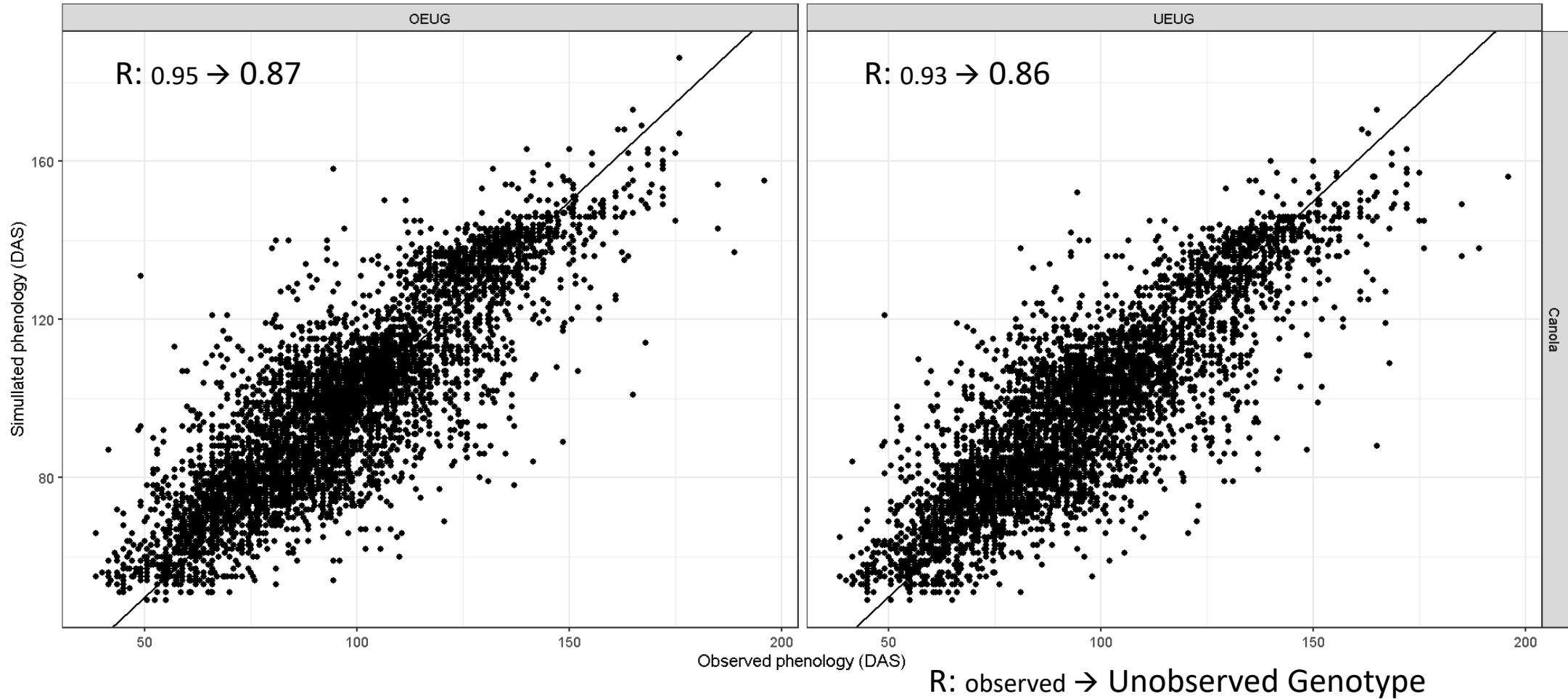
ONE calibration and THREE validations for all varieties

Prediction accuracy from CGM to GP-CGM for observed genotypes



R: Prediction accuracy, Pearson correlation between observation and prediction

Prediction accuracy from observed to unobserved genotypes in GP-CGM



R: Prediction accuracy, Pearson correlation between observation and prediction

Conclusion

- Crop Growth Model APSIM NG can be used to link genotyping (SNPs) and phenotyping to predict the canola phenology
- The new GP-CGM combines two components, i.e. genomic prediction (e.g. random forest) and crop growth model (e.g. APSIM NG)
- The GP-CGM can be used to predict crop phenology in new environments and for new genotypes and capture about 0.7 prediction accuracy

Acknowledgements

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Thank you

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