Using whole genome predictions to leverage costly phenotypic data

June 2019

Koscielny, C.B., Gardner, S.W., Technow, F., Duncan, R.W.

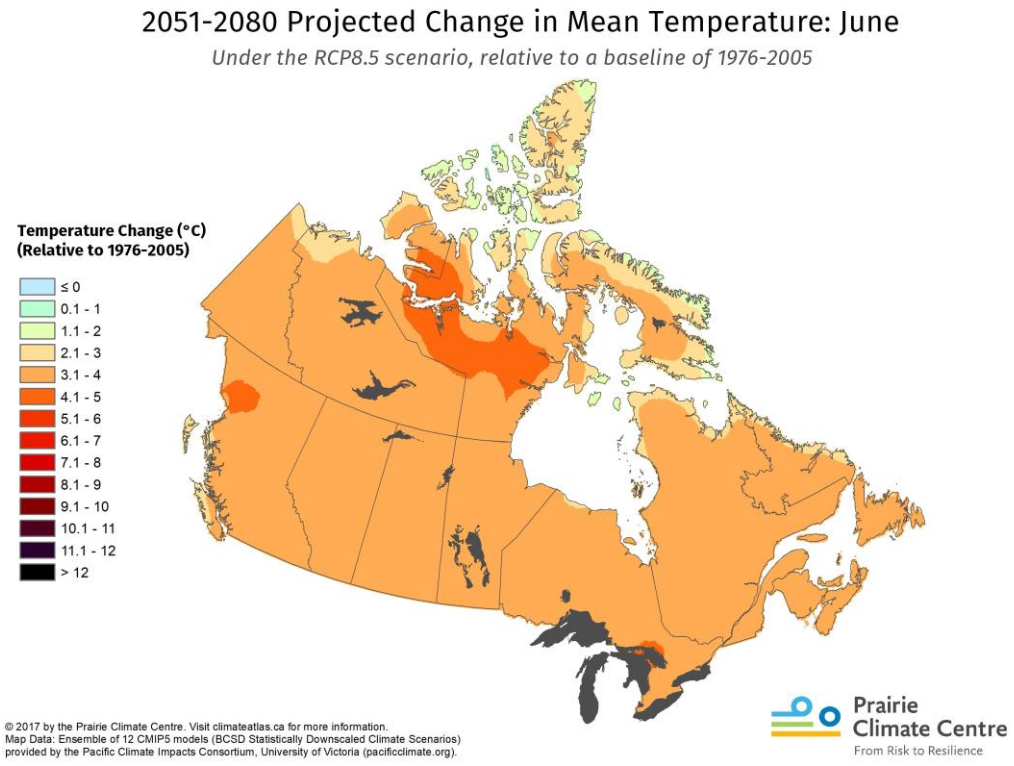
Outline

- ❑Impact of heat on spring canola
- ❑Objective
- ❑Experiment design and results
- ❑Interpretation and future work

Impact of heat on spring canola

- Nuttall *et al.*, 1992
  - 0.4 t ha^{-1} loss with a 3 °C rise in temperature
- Kutcher *et al.*, 2010
  - Mean temperature increase, -75.5 kg ha^{-1} $°C^{-1}$
  - Days > 30 °C, -18.4 kg ha^{-1} day^{-1}

https://www.canolacouncil.org/media/509593/canola_growing_regions_map.jpg



Impact of heat on spring canola

- Impact of a 3 °C rise
  - 3 °C * 75.5 kg ha^{-1} $°C^{-1}$ = 226.5 kg ha^{-1} loss
  - 0.2265 * 9.2 = 2M t of lost production
  - 2M * $500 = > 1B in lost revenue

- If no change in climate
  - Brandon, MB receives 14.2 days $\geq$ 29.5 °C
  - 14.2 days * 18.4 kg ha^{-1} day^{-1} = 261 kg ha^{-1} loss
  - Only occurs on 1/3 of the area
  - .261 * 3M ha = 783,000 t of lost production
  - 783k * $500 = $391.5M in lost revenue

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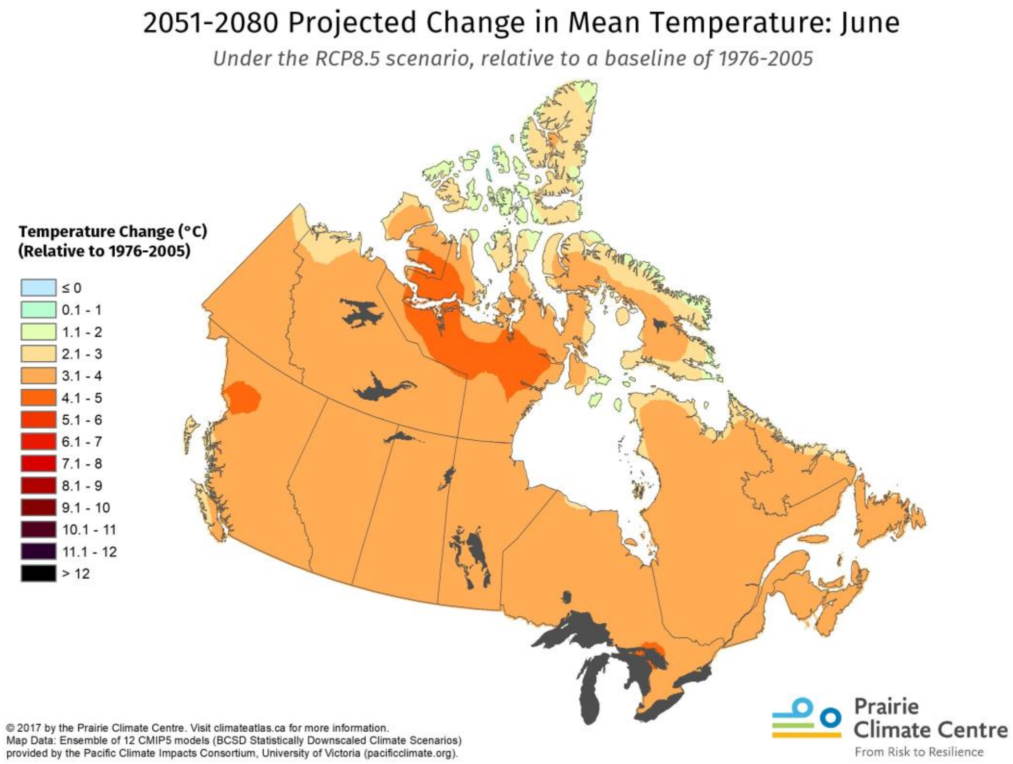


Objective

- Investigate the ability of whole genome predictions (WGP) to provide flexibility in the use of costly phenotypic data across environments with varying temperatures

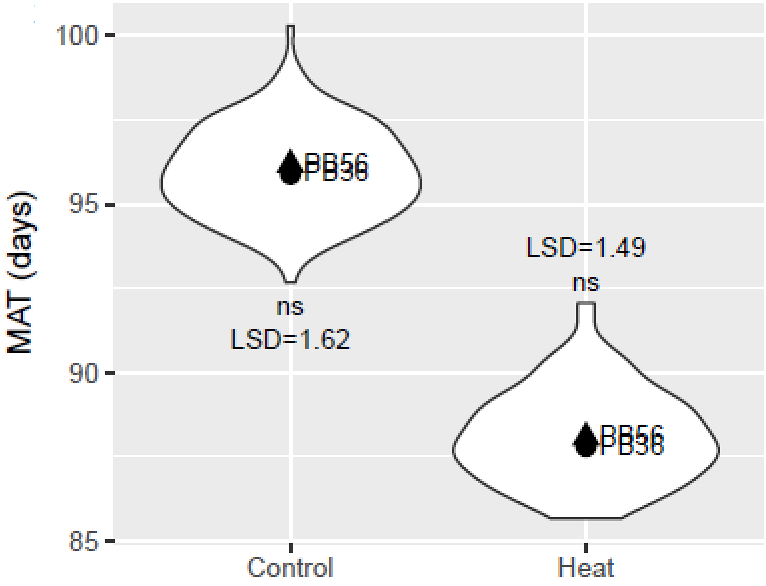
Experimental Design

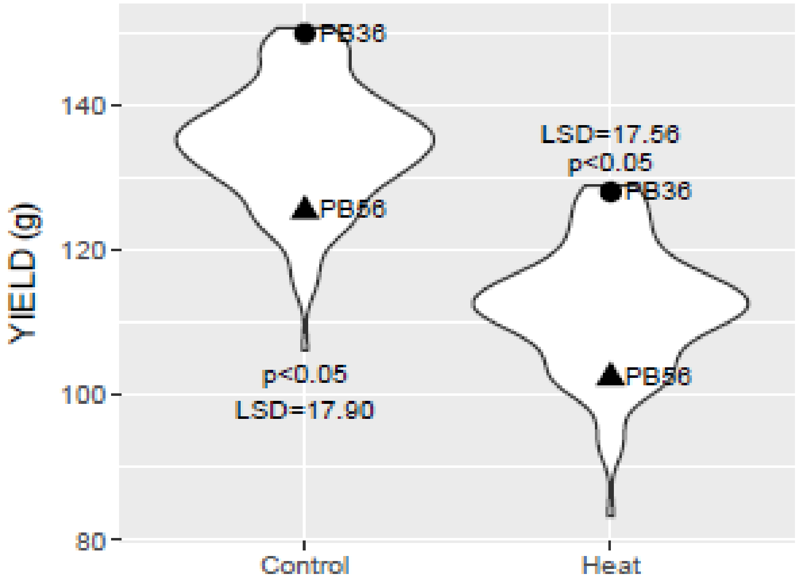
University of Manitoba

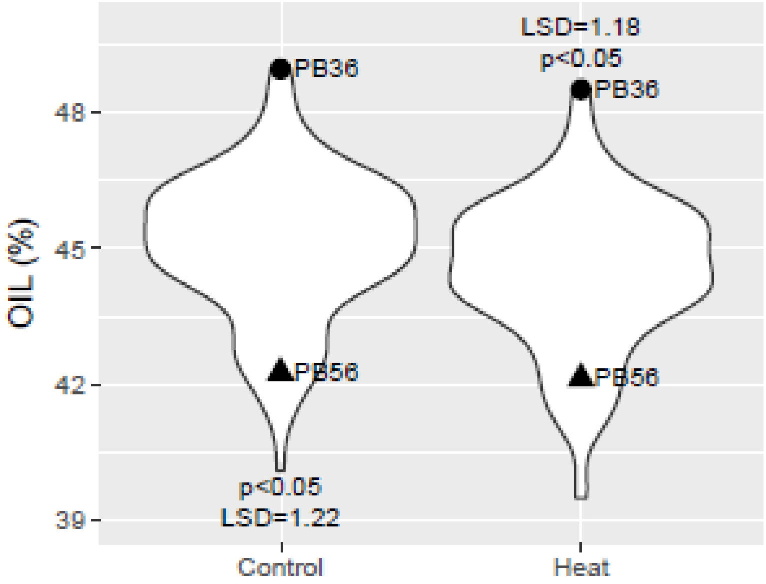
- Plant materials
  - F1 cross between a heat tolerant and heat susceptible inbreds
  - Doubled haploid population of 148 genotypes
- Environments
  - 3 environments
  - 2 treatments (planting dates)
  - 2 replicates
- Genotyping
  - 368 polymorphic SNPs
  - Total genetic distance of 1725cM (avg 4.7cM between SNPs)
- Analysis
  - ASReml to calculate BLUPs with the following mixed model *y* = X*b* + *Zu* + *e*
  - $H^2 = 1 - \frac{SED^2}{2 * \sigma_g^2}$ (Cullis *et al*., 2006)
  - rrBLUP used to calculate GBLUP
  - Prediction accuracies were calculated using random cross validation (104 training, 44 validation)
  - Validation replicated 500 times for each treatment trait combination

Results

Location	Planting Date	Tmean† (°C)	Tmax‡ (°C)	Tmin§ (°C)	Days > 29.5 °C	Soil Moisture (%)	Day Length (hrs)
Carman, 2015	12-May	17.8	24.4	10.8	10	35.6	16:14
	01-Jun	19.4	26.2	12.4	14	34.3	16:02
Viluco, 2015	29-Sep	17.5	25.6	9.3	28	Irrigated	14:06
	30-Oct	19.5	28.1	10.9	40	Irrigated	14:22
Carman, 2017	10-May	17.5	24.0	10.6	9	31.2	16:14
	05-Jun	18.7	25.5	11.6	12	37.0	15:59







Results

Trait	Treatment	H^2	Mean accuracy
MAT	CT	0.77	0.43
	HT	0.86	0.58
YIELD	CT	0.73	0.35
	HT	0.64	0.14
OIL	CT	0.92	0.38
	HT	0.92	0.42

Trait	Prediction set	Training set	Mean accuracy
MAT	CT	HT	0.51
	HT	CT	0.43
YIELD	CT	HT	0.21
	HT	CT	0.17
OIL	CT	HT	0.41
	HT	CT	0.41

Discussion

- Limitations
  - Single population of limited size
  - Plot size
- Implications
  - Enable the understanding of high temperature environments
  - Understand the impact of unique environments on each trait collected
  - Combine or separate data to maximize its impact
  - Utilize predictions to increase phenotyping capacity
- Future work
  - Expand beyond this single population
  - Explore modelling the impact of heat stress - CGM

Acknowledgements

- Co-authors
  - Dr. Robert Duncan
  - Dr. Stuart Gardner
  - Dr. Frank Technow
- Technical Support
  - Fred Thoonen
  - Rodrigo Bravo
  - Sarika Saini
  - Victoria Mungall
  - Erin Lemky