

Pea and soybean breeding

Tom Warkentin, Crop Development Centre, University of Saskatchewan

To: AgBio Advancements in Agricultural Research Seminar Series

Land acknowledgment



As we gather here today, we acknowledge we are on Treaty 6 Territory and the Homeland of the Métis. We pay our respect to the First Nations and Métis ancestors of this place and reaffirm our relationship with one another.



UNIVERSITY OF
SASKATCHEWAN

A black and white photograph capturing a dramatic moment in a hockey game. A player in a dark jersey is suspended in mid-air, arms outstretched in celebration, having just scored a goal. Another player in a light-colored jersey stands nearby, watching the play. The goal net is visible on the left, and a large, cheering crowd fills the background. The text "THE GOAL!" is overlaid in the top left, and "THE GOAL?" is overlaid in the bottom right.

THE GOAL!

THE GOAL?



GOALS ...

- 1) profitable component of diverse rotations that enhance farm sustainability ...
- 2) ... produce a safe supply of pulses to meet growing demand ...
- 3) desirable end-use quality

National Pulse Research Strategy

National Pulse Research Strategy Committee

November, 2021

AgriScience Program Clusters Component

Applicant Guide

- 1) Climate change and environment**
- 2) Economic growth
- 3) Sector resilience

CDC Strategic Research Program

Overview of Workplans for **2018-2023**

Field Pea

Principal Investigator: Tom Warkentin

Objectives:

- To develop early to medium maturity, high yielding yellow, green and specialty market class field pea cultivars with improved resistance to foliar and root diseases, improved lodging resistance, improved competitiveness with weeds, as well as enhanced quality for export and domestic markets.

CDC Strategic Research Program

Overview of Workplans for **2023-2028 (tentative)**

Field Pea

Principal Investigator: Tom Warkentin

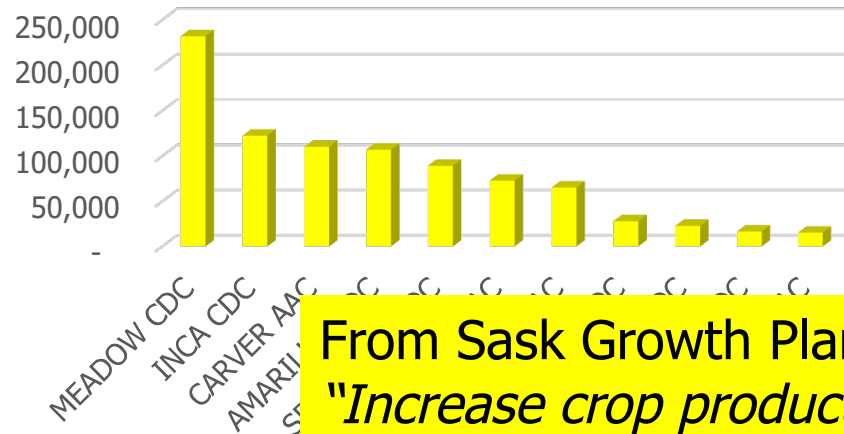
Objectives:

- Yield
- Market classes
- Root rot, ascochyta, powdery mildew resistance
- Lodging resistance
- Heat/drought tolerance
- Improved seed quality, protein, flavour ...
- Improved N fixation
- Improved phenotyping and genotyping
- Germplasm resources

High yielding varieties

CDC Amarillo – 2012
 CDC Inca – 2015
 CDC Spectrum – 2016
 CDC Canary – 2017
 CDC Lewochko – 2018
 CDC Hickie – 2021
 CDC Tollefson – 2021
 CDC Citrine - 2022

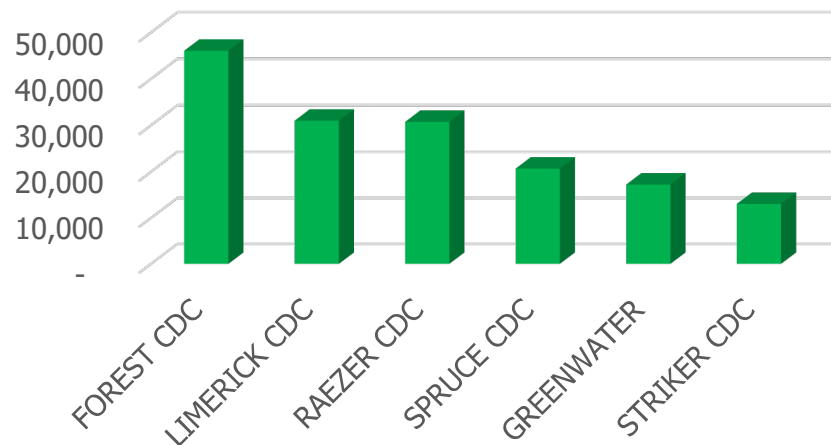
Top yellow pea varieties in SK in 2022



From Sask Growth Plan 2030:
"Increase crop production to 45 million metric tonnes ..."

CDC Raezer – 2011
 CDC Limerick – 2012
 CDC Greenwater – 2014
 CDC Spruce – 2016
 CDC Forest – 2017
 CDC Rider – 2022
 CDC Huskie - 2023

Top green pea varieties in SK in 2022



CDC pea breeding program...

- ~40 cultivars released in the last two decades
- >65% of acreage in western Canada

From Sask Growth Plan 2030:
"Delivering on Saskatchewan's climate change plan to reduce carbon emissions".

Pea root rot **complex**

➤ *Aphanomyces euteiches*

➤ *Fusarium avenaceum*



➤ *Fusarium solani*

➤ other *Fusariums*

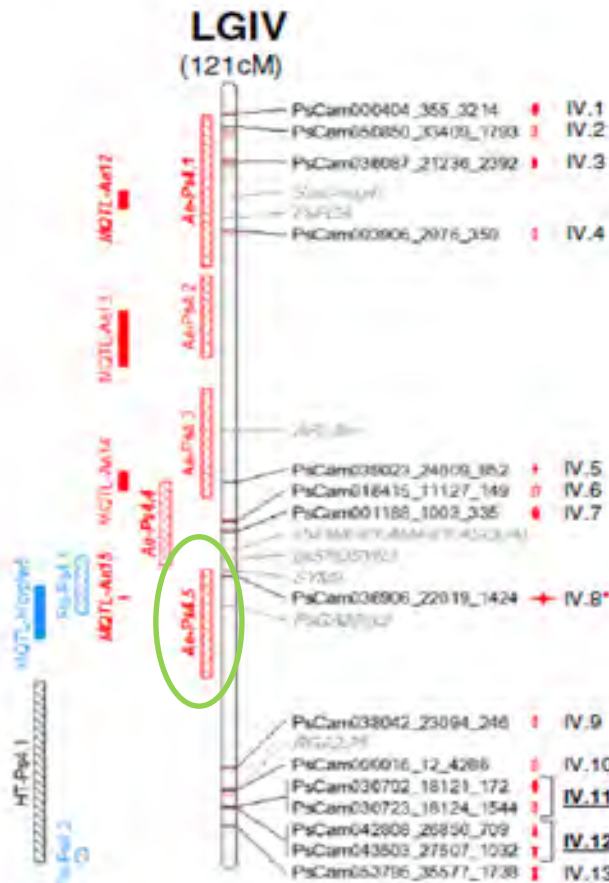
Genomic regions associated with resistance to *Aphanomyces*

Pathogen	Plant material	Genomic region / marker	Major QTL	Reference
<i>Aphanomyces euteiches</i>	Puget X 90-2079	7 QTLs	LG IVb (Aph1)	Pilet-Nayel et al. 2002
<i>Aphanomyces euteiches</i>	Puget X 90-2079	10 QTLs	LG IVb (Aph1)	Pilet-Nayel et al. 2005
<i>Aphanomyces euteiches</i>	Baccara X PI180693	75 additive-effect QTLs	LG III (Ae-Ps3.1)	Hamon et al. 2011
	Baccara X 552	60 additive-effect QTLs	LG VII (Ae-Ps7.6b)	
<i>Aphanomyces euteiches</i>	Puget X 90-2079	27 meta-QTLs, 318 candidate genes	LG VII (MQTL-Ae25)	Hamon et al. 2013
	Baccara X PI180693		LG VII (MQTL-Ae26)	
	Baccara X 552			
	Dark Skin Perfection X 90-2131			
<i>Aphanomyces euteiches</i>	175 Pisum sativum lines (referred as the "pea-Aphanomyces collection")	52 QTLs	LG IV (Ae-Ps4.4-4.5)	Desgroux et al. 2016
<i>Aphanomyces euteiches</i>	266 pea collection	11 genomic intervals	LG VII (Ae-Ps7.6)	Desgroux et al. 2018
			LG VII (Ae-Ps7.6)	

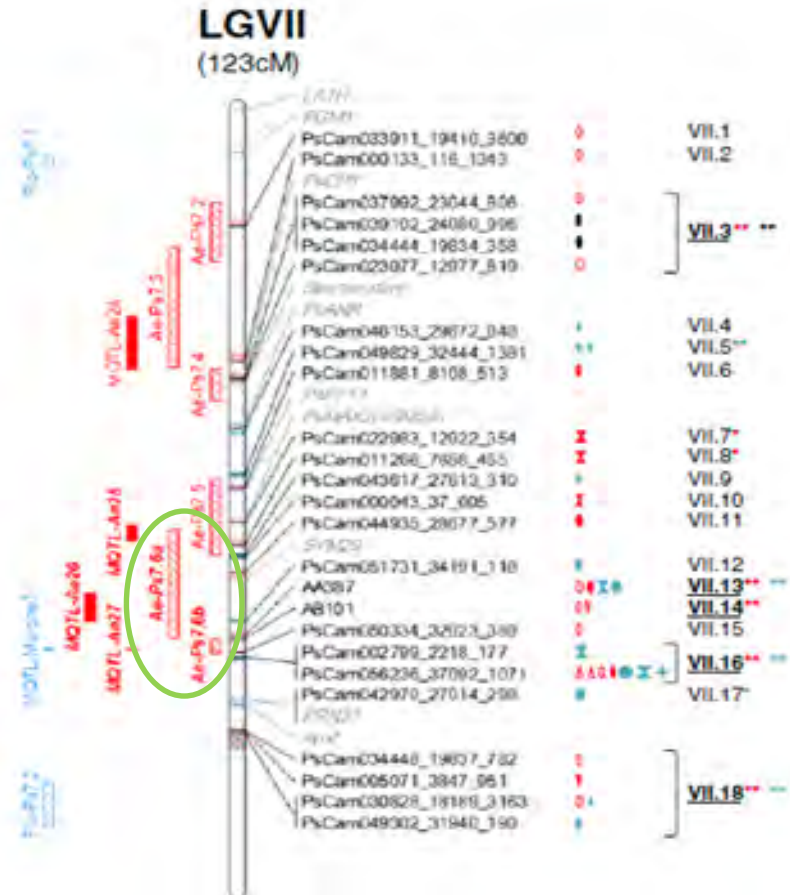


Jha AB, Gali KK, Alam Z, Lachagari VBR, and Warkentin TD (2021) Potential application of genomic technologies in breeding for fungal and oomycete disease resistance in pea. *Agronomy* 11, 1260.
<https://doi.org/10.3390/agronomy11061260>.

“Major” QTLs for *Aphanomyces* root rot resistance in pea



LG IV (Ae-Ps4.5)



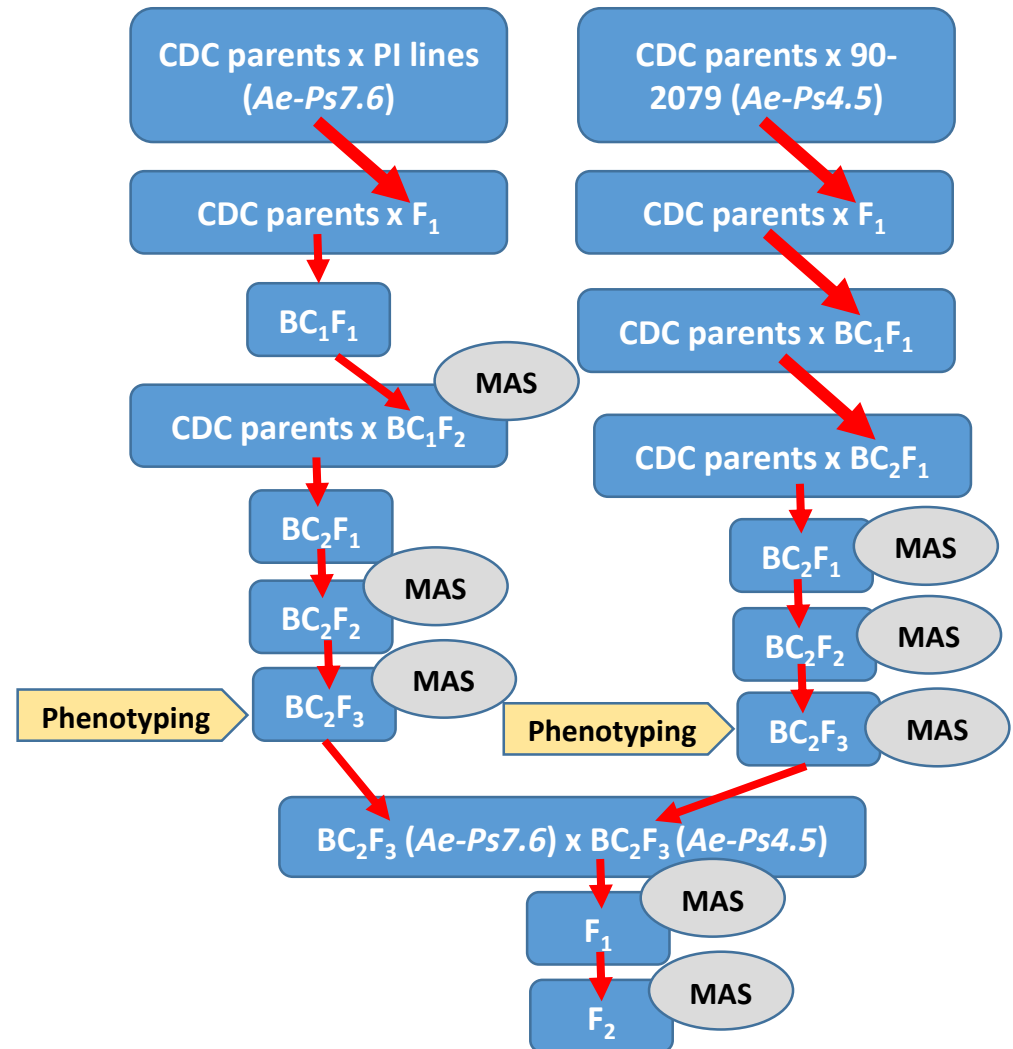
LG VII (Ae-Ps7.6)

Backcrossing breeding for improved *Aphanomyces* resistance

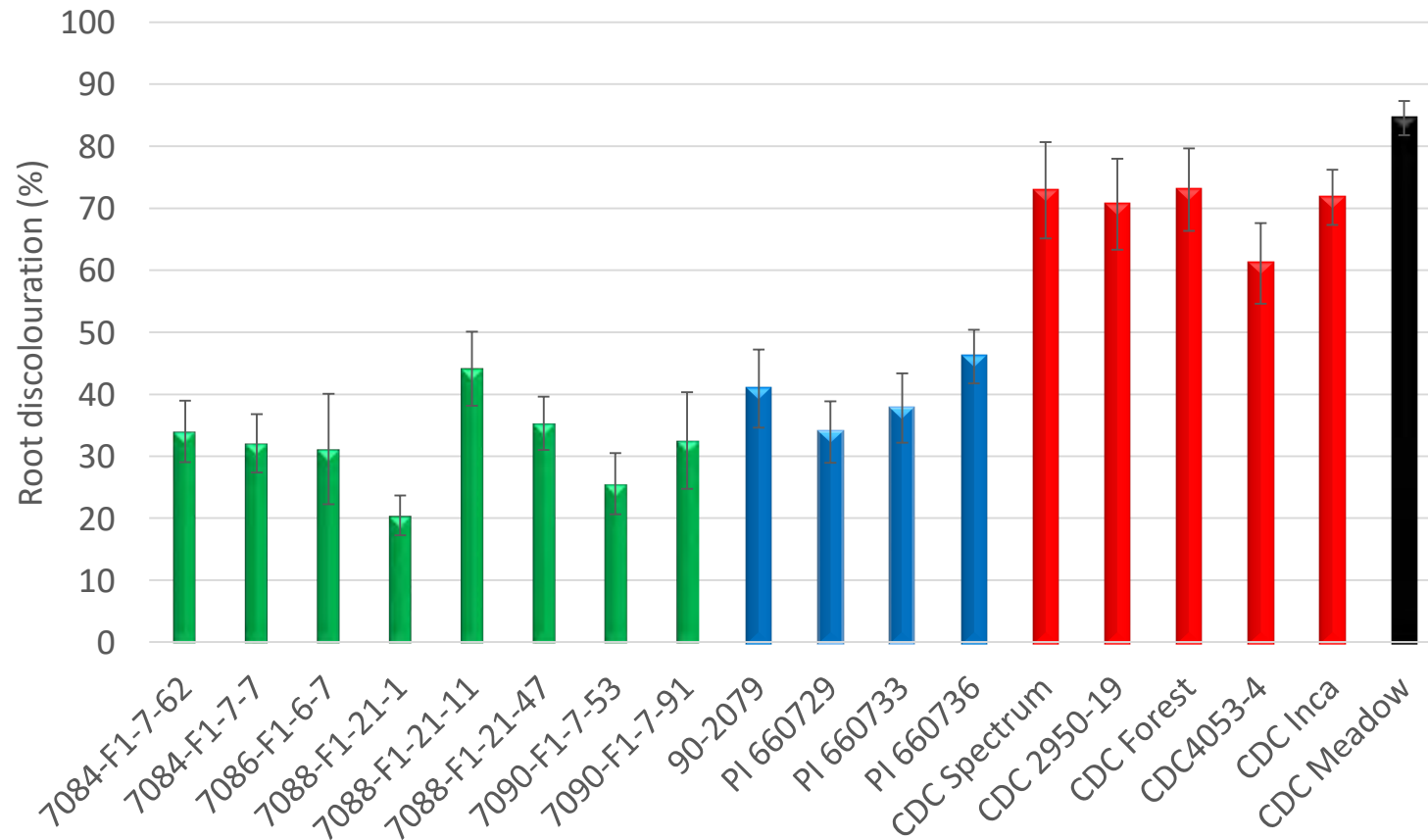
- Multiple CDC pea varieties
- 'Major' and 'minor' QTLs introgressed

QTL	LG	R ² min-max
<i>Ae-Ps1.2</i>	I	4-15%
<i>Ae-Ps2.2</i>	II	6-27%
<i>Ae-Ps3.1</i>	III	6-27%
<i>Ae-Ps4.1</i>	IV	5-21%
<i>Ae-Ps4.5</i>	V	6-44%
<i>Ae-Ps5.1</i>	VI	7-38%
<i>Ae-Ps7.6a</i>	VII	6-60%

Hamon et al. 2013. BMC Plant Biol 13, 45 (2013)



Some CDC lines carrying QTLs *Ae-Ps4.5* and *Ae-Ps7.6*

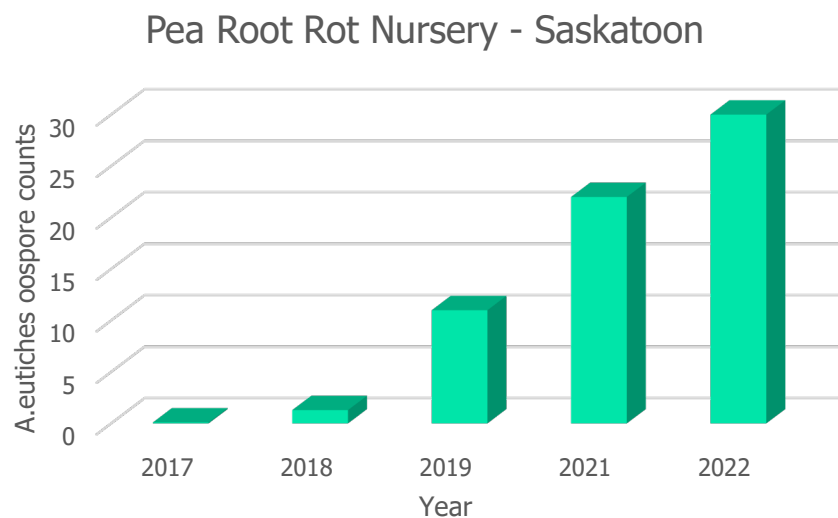


- Most promising lines arising were tested in 2021 yield trials, 2022 pre-breeder seed development, and will enter 2023 pea Co-op Test

Pea root rot nursery - USask



Photo: Steve Shirtliffe team



Graph: Nimllash Sivachandra

Root rot organisms identified (as per Cheryl Cho):

Aphanomyces euteiches

Fusarium avenaceum

Fusarium solani

Fusarium redolens

Fusarium clavum

Moving along ...

Line	Type	Leaf	Flower	Yield	Aph	# QTLs	2023 test
7088-F1-21-1-Y	Y	SL	W	good	MR	2	Co-op
7088-F1-21-1-G	G	SL	W	good	MR	2	Co-op
7084-F1-7-62	G	SL	W	good	MR	2	Co-op
7090-F1-7-91	G	SL	W	good	MR	2	Co-op



GWAS-2 – a multi-use germplasm panel

Mapping Population - 01

GWAS-2

Targets:

-Identify trait-associated markers for agronomic and seed quality traits

-Training set to develop genomic selection models

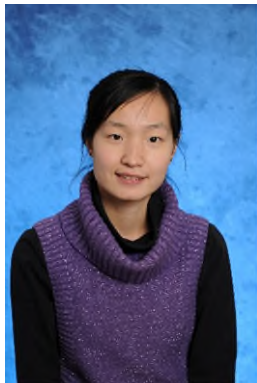
Composition (255 accessions):

1. Breeding lines from 21 global pea breeding programs (84)
2. Germplasm accessions selected based on genome-wide diversity (80)
3. Core germplasm accessions selected based on high seed protein (20)
4. Commercial pea varieties from CDC and AAFC (48)
5. Non-nodulating mutant (1)
6. Wild accessions (22)



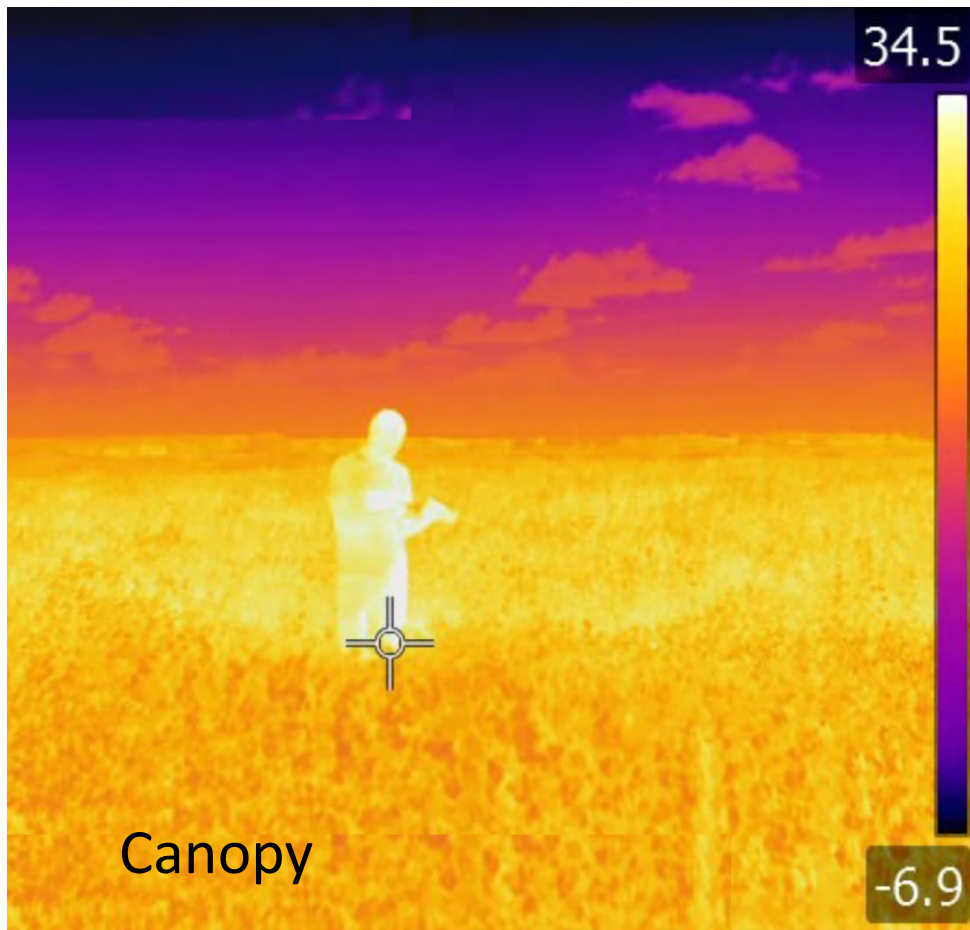
Improved heat tolerance in pea

- Bueckert, R.A., Wagenhoffer, S., Hnatowich, G., and Warkentin, T.D. (2015) Effect of heat and precipitation on **pea yield and reproductive performance** in the field. Can. J. Plant Sci. 95: 629-639.
- Huang, S., Gali, K.K., Tar'an, B., Warkentin, T.D., and Bueckert, R.A. (2017) **Pea phenology**: crop potential in a warming environment. Crop Sci. 57:1540-1551.
- Huang S, Gali KK, Lachagari RVB, Chakravartty N, Bueckert RA, Tar'an B, and Warkentin TD (2021) Identification of **heat responsive genes in pea stipules and anthers** through transcriptional profiling. PLoS One. <https://doi.org/10.1101/2021.04.22.440885>
- Jiang, Y., Diapari, M., Bueckert, R.A., Tar'an, B., and Warkentin, T.D. (2017) Population structure and **association mapping of traits related to reproductive development** in field pea. Euphytica doi.org/10.1007/s10681-017-2006-1.
- Jiang Y, Lahlali R, Karunakaran C, Warkentin TD, Davis AR, and Bueckert RA (2019) **Pollen, ovules and pollination in pea**: success, failure and resilience in heat. Plant Cell Environment. 42:354-372.
- Tafesse, E, Warkentin, TD, and Bueckert, RA (2019) **Canopy architecture** and leaf type as traits of heat resistance in pea. Field Crops Research doi.org/10.1016/j.fcr.2019.107561.
- Tafesse, EG, Gali, KK, Lachagari, VBR, Bueckert, RA, and Warkentin, TD (2020) **Genome-wide association mapping for heat stress** responsive traits in field pea. International Journal of Molecular Sciences, Int. J. Mol. Sci. 21:2043.
- Tafesse EG, Gali KK, Lachagari VRB, Bueckert, R, and Warkentin, TD (2021) **Genome-wide association mapping for heat and drought** adaptive traits in pea. Genes 2021, 12(12), 1897; <https://doi.org/10.3390/genes12121897>
- Osorio E, Davis AR, Warkentin TD, and Bueckert RA (2023) **Ovule abortion and seed set** of field pea (*Pisum sativum* L.) grown under high temperature. Can. J Plant Sci. DOI: 10.1139/CJPS-2022-0156.



Photos:
Gloria Gingera

Canopy temperature; the brightest is the hottest and the most heat stressed



Photos: Brandon Louie using infra-red thermal camera; Rosthern, SK, summer 2015

Improved N fixation in pea

Performance of pea lines over 10 site-years in Saskatchewan

Variety	Yield (kg ha ⁻¹)	Protein (%)	Protein- (kg ha ⁻¹)	Nodulation
CDC Meadow	2759	24.0	658	
CDC Dakota	2771	24.9	691	
CDC Amarillo	2932	24.1	707	
Frisson P56 (non-nod)	656	23.4	131	0
(Meadow*Sym29) *Meadow-3	2857	24.7	706	67.8
(Dakota*Sym29) *Dakota-4	2783	26.4	730	65.1
(Dakota*nod3) *Dakota-9	3015	24.8	743	62.6
(Dakota*nod3) *Dakota-25	2887	25.2	724	60.9
(Dakota*Sym29) *Dakota-27	2885	25.0	718	61.9

From Sask Growth Plan 2030:
"Promoting the quality and sustainability of Saskatchewan's agricultural and natural resource exports"



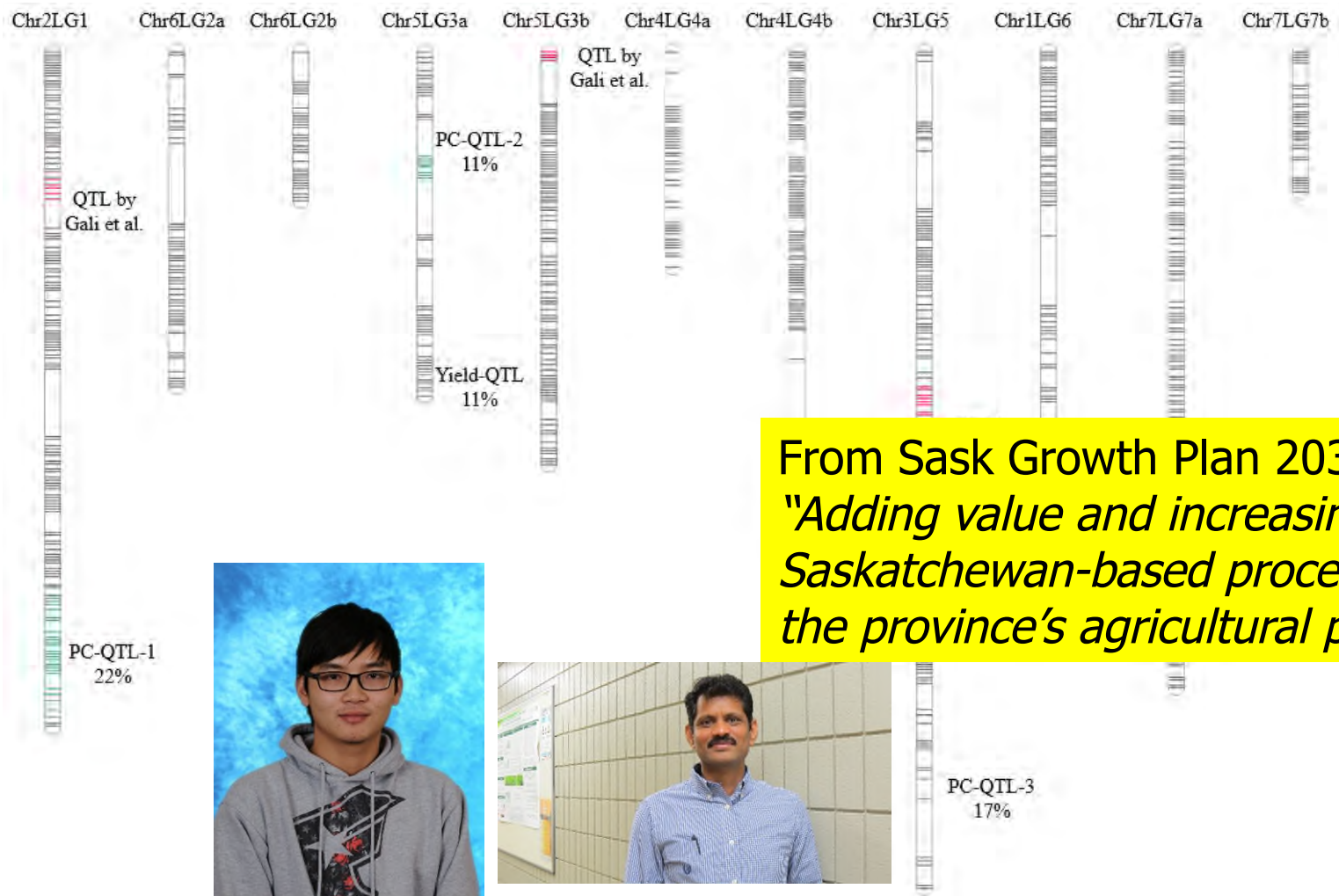
STEPS 2 and 3 (nearly completed)

- Markers for N fixation traits from GWAS-2
- Examining pea root system architecture for clues to N fixation and drought resistance



Dhillon LK, Lindsay D, Yang, C, Zakeri, H, Tar'an B, Knight JD, and Warkentin TD (2022) Evaluation of biological nitrogen fixation potential of pea lines derived from crosses with nodulation mutants. Field Crops Research, <https://doi.org/10.1016/j.fcr.2022.108731>

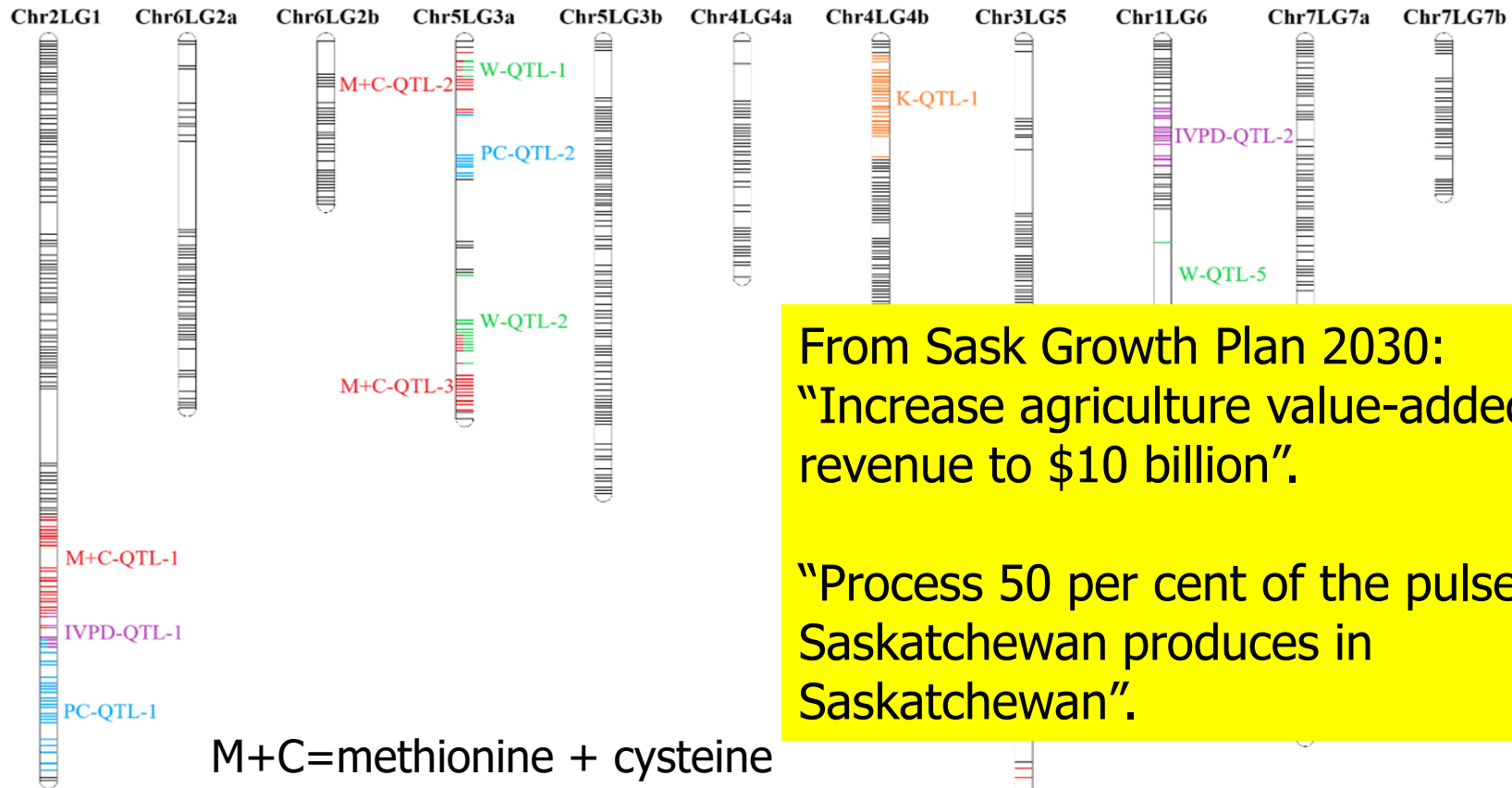
Improved protein conc. in pea



From Sask Growth Plan 2030:
*"Adding value and increasing
Saskatchewan-based processing of
the province's agricultural products".*

Zhou J, Gali KK, Jha AB, Tar'an B, and Warkentin TD (2022) Identification of quantitative trait loci associated with seed protein concentration in a pea recombinant inbred line population. *Genes* 13(9), 1531; <https://doi.org/10.3390/genes13091531>.

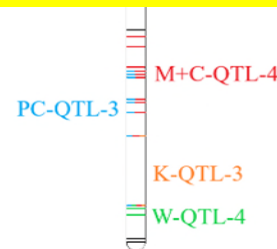
Improved protein quality in pea



M+C=methionine + cysteine
W=tryptophan
K=lysine
IVPD=in vitro protein digestibility

From Sask Growth Plan 2030:
 “Increase agriculture value-added revenue to \$10 billion”.

“Process 50 per cent of the pulse crops Saskatchewan produces in Saskatchewan”.



Overall goal: high yielding, high BNF, disease resistant (root and foliar), heat/drought tolerant, GHG reducing, C-sequestering, high protein ...



Soybean breeding at the University of Saskatchewan

Tom Warkentin, Ketema Daba, and Kishore Gali
Crop Development Centre, University of Saskatchewan

Breeding objectives

- Yield, yield, yield! (Dr. A.E. Slinkard)
 - Appropriate maturity
 - Abiotic stress resistance
 - High protein
 - Light hilum colour
- (so far, disease and insect stresses are minimal)



Photo: TW

Soybean breeding/genomics at USask

BREEDING

AAFC Cluster 2013-2018 – collaboration with AAFC, Ottawa

AAFC Cluster 2018-2023 – collaboration with AAFC, Ottawa and CEROM, Montreal

PROPOSED-AAFC Cluster 2023-2028 - collaboration with AAFC, Ottawa and CEROM, Montreal

NEW! ADF-SPG 2023-2028

GENOMICS

Genome Canada/Genome Quebec, Soyagen project (2015-2021)

Genome Canada/Genome Quebec, GAPP project: (2021-2024)



F2-derived family method [2023-2028]

Crosses: SX, TX, DX – growth chambers [~60]

F1 growouts – greenhouse or polyhouse

F2 space planted – Saskatoon-irrigated [~5000 plants pulled]

F_{2:3} micro-plots – Saskatoon – 1 rep [~4000]

F_{2:4} yield trials – Saskatoon, Floral – 1 rep X 2 locations [864]

F_{2:5} yield trials – Saskatoon, Floral, Rosthern, Outlook – 2 reps X 4 locations [108]

F_{2:6} yield trials – Saskatoon, Floral, Rosthern, Outlook, Morden, Portage la Prairie – 2 reps X 6 locations [24]

F7 provincial trials (SK) – 3 reps X 6-8 locations [3-5]

F8 provincial trials (SK) – 3 reps X 6-8 locations [2-3]

F9 Variety release [1-2]

Breeder seed development

F6 single plant selections – 100-200 per line

F_{6:7} micro-plots

F_{7:8} long plots

F9 bulk



Photo: Ketema Daba

Crossing in the phytotron Agriculture Building, University of Saskatchewan



Photos: Ketema
Daba

F2 Nursery

- Campus Field, Saskatoon - irrigated



From Sask Growth Plan 2030:
*"Expand irrigation in
Saskatchewan".*



Variation for maturity in soybean yield trials, Campus Field, Saskatoon, 2019

Photo: Ketema Daba



2018 yield trials at Rosthern (note pea/soybean)



2021 provincial trials at Melfort (latitude 52.86)

Photo: TW



Sept 5, 2018 Investigation nursery, Saskatoon
frost injury on a late maturing variety

Photo: TW

Seed yield (kg/ha) of Soybean lines in SB RVT 2022

Entries	Avonlea	Rosthern	Saskatoon IRR	Outlook IRR	Creelman	Redvers	% of Prudence	DMT (+/- Prudence)
OAC Prudence	2135	1403	1983	2642	2522	3551	100	0
AAC Halli	2257	1496	2127	2647	2273	3714	102	-2
X6029- 6- S1- S1- 1	2049	1453	2029	2747	2489	3217	99	-5
X6110-10	2847	1396	2149	2423	2575	3847	107	-2
TH 33003R2Y	2325	1395	2258	2230	2664	3493	102	2
NSC Watson RR2Y	1894	1606	2247	2953	2710	3764	107	-3
CHECK MEAN	2135	1403	1983	2642	2522	3551		
CV	10.9	8.4	6.9	5.5	8.0	5.9		
GRAND MEAN	2251	1458	2132	2607	2539	3598		

Average DTM of OAC Prudence was 113 in 2022

Data compiled by Laurie Friesen, Seed Program Manager, SPG

Two-year (2021 -2022) data summary for lines in SB RVT

Entry	Mean seed yield (Kg/ha) 11 sites	% of Prudence	DTM (11 sites)	% Protein (4 sites)	Hilum color
OAC Prudence	2297	100	0	36.5	Yellow
AAC Halli	2324	101	-2	35.4	Yellow
X6029- 6- S1- S1- 1	2159	94	-7	36.4	Imperfect Yellow
TH 33003R2Y	2257	98	2	34.9	Brown
NSC Watson RR2Y	2288	100	-4	33.5	Imperfect Yellow

DTM = +/- OAC Prudence

Acknowledgments

- CDC pulse crop breeding staff
- CDC pulse pathology staff
- CDC Grains Innovation Lab
- CDC breeder seed staff
- USask administrative staff
- Research colleagues in Saskatoon, Canada, International



Saskatchewan
Ministry of
Agriculture



Thank You