Chickpea and Flax Breeding and Genetics at CDC: a journey of two superfood

Bunyamin Tar'an

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28 March 2023

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(share responsibility with pea, lentil, bean & faba bean programs)

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Kevin Mikituk
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Dayna Raymond
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Kiah Bryce
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Flax research project:
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Yune Qiu
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Students
Xinjie Yu (PhD student)

Grain Innovation Lab: Gene Arganosa

Breeder Seed Facility: Dave Benallack and Craig Ells

CDC Pulse Pathology Program

CDC Cereal and Flax Pathology Program

All collaborators at CDC and U of S

All former students, technicians and postdocs

National and International collaborators

Superfood claims!

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HEALTH

In the Future, Everything Will Be Made of Chickpeas

America is finally embracing an ingredient that much of the world has relied on for millennia.

By Amanda Mull

MARCH 14, 2019 SHARE

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SPEAKING OF HEALTH

Superfood of the Month: Chickpeas

Chickpeas are incredibly easy to include in your diet because they are affordable and available in most grocery stores.

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Superfood spotlight: cooking with chickpeas

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Superfood claims!

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SPEAKING OF HEALTH | TUESDAY, MARCH 31, 2015

Flaxseed is nutritionally powerful

TOPICS IN THIS POST

Nutrition | Get Healthy Recipes And Tips

Flaxseed may be small, but its health benefits are big. It contains numerous salubrious components, with highlighted nutrients being omega-3 fatty acid ALA (alpha-linolenic acid), fiber and lignans.

Omega-3 fatty acids are good fats that may help lower total cholesterol and low-density lipoprotein (LDL or bad) cholesterol levels, reduce inflammation and reduce the risk of certain cancers. Fiber can help relieve constipation, control cholesterol levels and keep you feeling full longer. Flaxseed also contains lignans, which provide antioxidant protection.

The Guardian

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Superfoods

Linseeds

Golden linseeds (also known as flaxseeds) are powerhouses of nutrition. They have a subtle nutty, slightly earthy flavour and are a cheap superfood that everyone can include in their diet. They are available whole or - for easier absorbtion - split, ground or as linseed or flaxseed oil.

INGREDIENT INTELLIGENCE

The Original Superfood: Flax Seeds

By Emma Christensen
Updated May 2, 2019

(Image credit: Apartment Therapy)

Protein and Oil contents of chickpea germplasm collection and elite lines/released cultivars across 3 locations in SK (2017-2019)

Trait	Population	*N*	Range	Mean	SD
Protein (% DWB)	Germplasm	184	13.6 - 27.5	19.5	2.5
	Varieties	100	13.5 - 27.3	19.0	2.1
Oil (% DWB)	Germplasm	184	2.5 - 9.4	6.4	1.0
	Varieties	100	3.5-10.2	6.7	0.8

Source: Orsak, 2022

Total Carotenoids

Kabuli type *Desi type*

CDC-Frontier (12 µg g-1)

CDC-Cory (24 µg g-1)

CDC-Jade (31 µg g-1)

Golden Rice 2
37 µg g-1

Mineral Micronutrient Content of Cultivars of Field Pea, Chickpea, Common Bean, and Lentil Grown in Saskatchewan, Canada

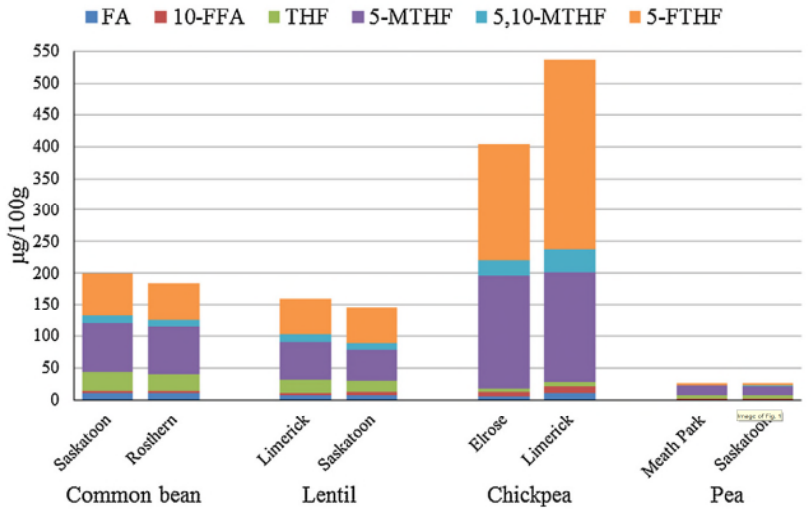
Heather Ray, Kirstin Bett, Bunyamin Tar'an, Albert Vandenberg, Dil Thavarajah, and Thomas Warkentin*

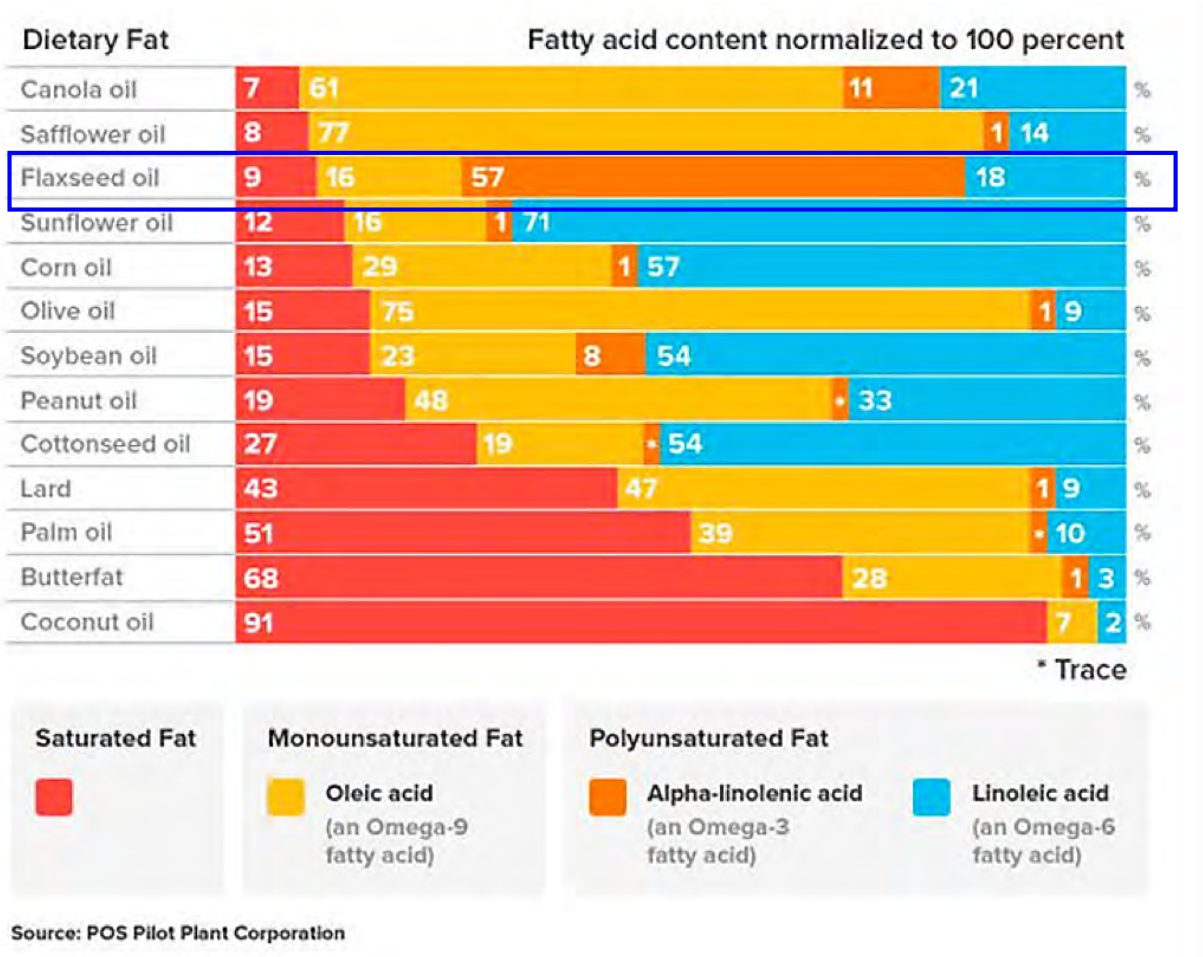
Table 8. Chickpea (*Cicer arietinum*) cultivars and mineral contents. Cultivars found not to be significantly different by Tukey's test (0.05 level) are indicated by same letter, within each column. For Mg, Fe, Zn, Mn, Cu, and Se there were no pairwise significant differences.

	Mg	Ca	Fe	Zn	Mn	Cu	Se
	µg/g						ng/g
Amit	1648	441 abc	51.7	27.1 bcd	22.9	6.6	731
CDC Cabri	1634	448 abc	55.0	26.4 abcd	22.3	6.7	636
CDC Corinne	1525	393 ab	48.6	24.4 abcd	25.5	7.1	712
CDC Frontier	1678	430 ab	54.1	21.1 ab	24.4	6.6	868
CDC Luna	1893	467 abc	52.2	21.2 abc	26.0	6.9	629
CDC Vanguard	1634	540 bcd	50.8	25.2 abcd	21.9	7.3	736
CDC Xena	1676	409 ab	49.1	27.7 cd	23.0	8.1	864
Myles	1902	644 cd	55.6	28.3 cd	25.4	8.7	677
Mean	1699	472	52.1	25.2	23.9	7.3	732

Genetic diversity of folate profiles in seeds of common bean, lentil, chickpea and pea

Ambuj B. Jha [a,1], Kaliyaperumal Ashokkumar [a,1], Marwan Diapari [a], Stephen J. Ambrose [b], Haixia Zhang [b], Bunyamin Tar'an [a], Kirstin E. Bett [a], Albert Vandenberg [a], Thomas D. Warkentin [a,*], Randall W. Purves [a,b]




Dietary Fat
Fatty acid content normalized to 100 percent
Canola oil 7 61 11 21 %
Safflower oil 8 77 1 14 %
Flaxseed oil 9 16 57 18 %
Sunflower oil 12 16 1 71 %
Corn oil 13 29 1 57 %
Olive oil 15 75 1 9 %
Soybean oil 15 23 8 54 %
Peanut oil 19 48 * 33 %
Cottonseed oil 27 19 * 54 %
Lard 43 47 1 9 %
Palm oil 51 39 * 10 %
Butterfat 68 28 1 3 %
Coconut oil 91 7 2 %
* Trace
Saturated Fat
Monounsaturated Fat
Oleic acid (an Omega-9 fatty acid)
Polyunsaturated Fat
Alpha-linolenic acid (an Omega-3 fatty acid)
Linoleic acid (an Omega-6 fatty acid)
Source: POS Pilot Plant Corporation

If chickpeas and flax are so super….

Why not everyone eat it?

Why do we not produce them in million tons?

What are the challenges?

If chickpeas and flax are so super….

Why not everyone eat it?

Why do we not produce them in million tons?

What are the challenges?

If chickpeas and flax are so super….

Why not everyone eat it?

Why do we not produce them in million tons?

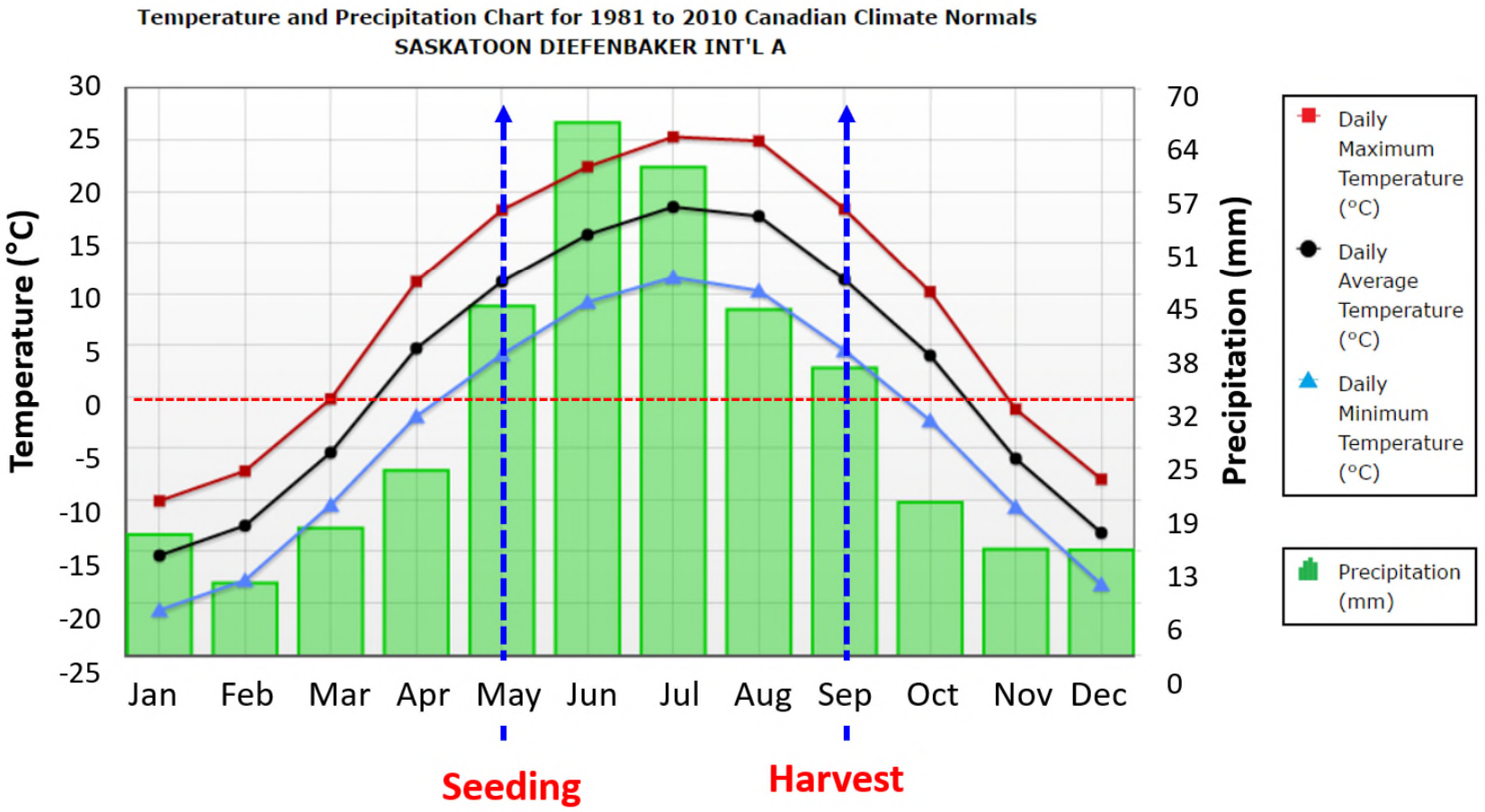
What are the challenges?

Challenge #1: Short growing season in Saskatchewan

Average frost-free period: 110 days → chickpea matures in ~120 days

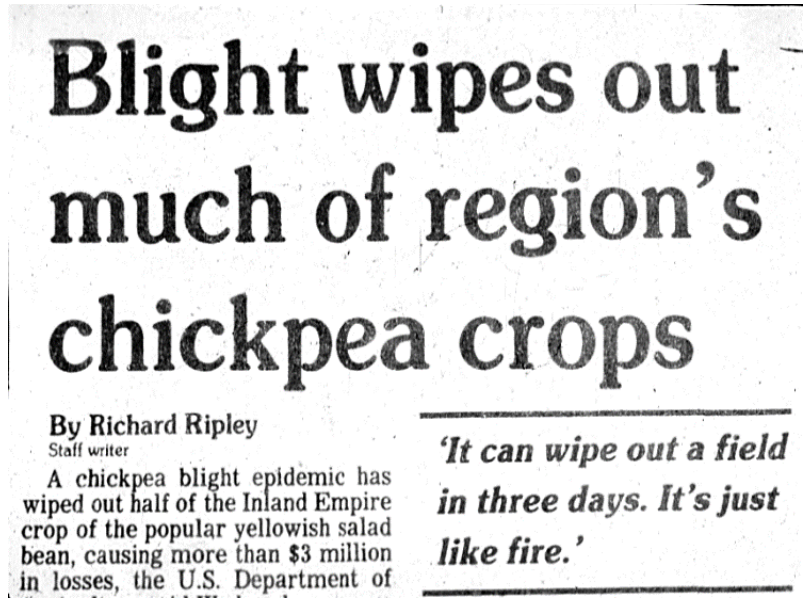
Seasonal cumulative DD_5: 1274 (May – August) → Chickpeas= 1150-1350;

Mean annual precipitation: 368 mm



Challenge #2: High pressure of Ascochyta blight disease

- The most devastating disease globally caused by fungus *Ascochyta rabiei*
- Cool summer with some moisture in Saskatchewan → very conducive for the disease development.



Blight wipes out much of region's chickpea crops

By Richard Ripley
Staff writer

A chickpea blight epidemic has wiped out half of the Inland Empire crop of the popular yellowish salad bean, causing more than $3 million in losses, the U.S. Department of

'It can wipe out a field in three days. It's just like fire.'

Challenge #3: Emerging Issue

PULSE ADVISOR
November 2020

SASKATCHEWAN pulse Growers

Saskatchewan Chickpea Health Issue Report

Overview

A plant health issue was brought to the attention of Saskatchewan Pulse Growers (SPG) in late July of 2019 and occurred again in 2020. Samples from 2019 were evaluated by researchers Dr. Sabine Banniza from the Crop Development Centre (CDC) at the University of Saskatchewan and Dr. Michelle Hubbard from Agriculture and Agri-Food Canada (AAFC) Swift Current. Due to the late sampling in 2019 the samples all had a high level of *Ascochyta rabiei* that was insensitive to strobilurin fungicides, while no other foliar pathogens were identified. Some root samples did show signs of root rot with high prevalence of *Fusarium solani* and *Fusarium redolens* identified. In 2020, local growers and agronomists conducted extensive sampling on behalf of SPG for analysis of herbicide residues, nutrient levels, and foliar and root pathogens, performed at a commercial lab. Results from these tests have not identified any one cause of the chickpea health issue and it is likely that a combination of factors are involved. Further evaluations are currently underway.

Field Symptoms

Figure 2. Leaf chlorosis, tip die back, and whitening within the chickpea canopy (left). Wilting and chlorosis of leaflets of main and secondary

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The mystery of the chickpea health issue

February 26, 2021

By Bruce Barker

Root rot? Herbicide carry-over? Insect damage? Nutrient deficiency?

Leaf tip chlorosis later in the season. Photos courtesy of Sherrilyn Phelps.

Challenge #3: ‘New’ Diseases!

frontiers | Frontiers in Plant Science

TYPE Original Research
PUBLISHED 06 February 2023
DOI 10.3389/fpls.2023.1117788

Check for updates

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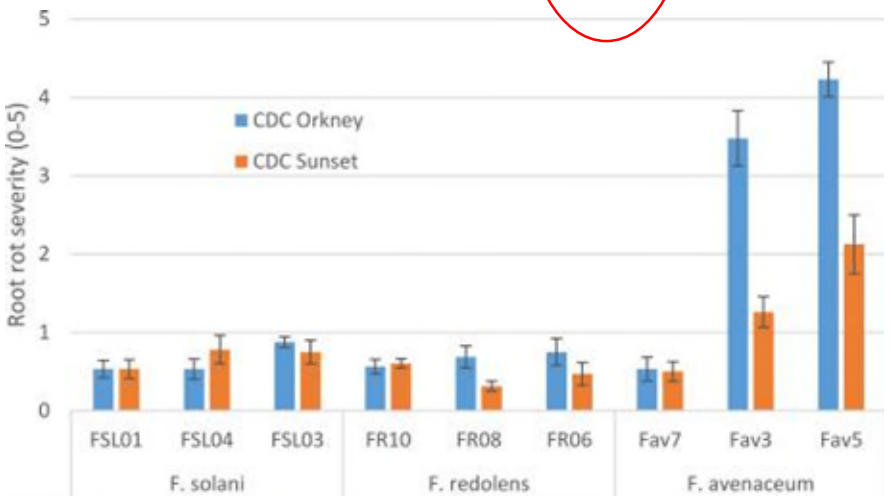
The chickpea root rot complex in Saskatchewan, Canada- detection of emerging pathogens and their relative pathogenicity

Cheryl Armstrong-Cho*†, Nimllash Thangam Sivachandra Kumar†, Ramanpreet Kaur and Sabine Banniza

Crop Development Centre, University of Saskatchewan, Saskatoon, SK, Canada

Root rot symptoms of CDC Leader kabuli chickpea under controlled conditions. From left to right: non-inoculated control, *Macrophomina phaseolina*, *Berkeleyomyces basicola*, *Verticillium dahliae*, ***Fusarium avenaceum***.



Root rot severity (0-5 scale) caused by three isolates each of three *Fusarium* species on 3-week-old plants

(Source: Armstrong-Cho et al. 2023)

Wheat

Canola

Flax

Chickpea

Challenge #4: acreage competition with other commodities, especially in a non-subsidized production and open market system

- Competitive advantage → increasing net return for farmers

Main goals of chickpea breeding program

1. **Competitive advantage for farmers**:

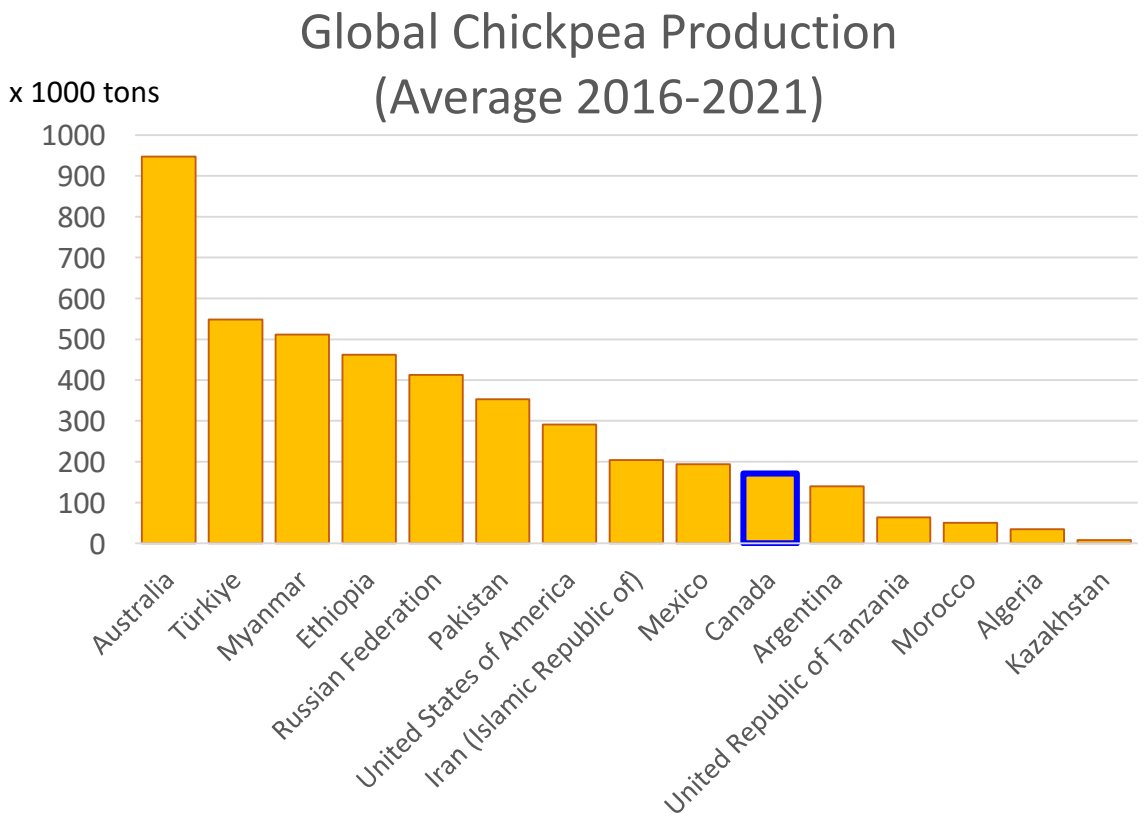
   Yield x seed size (*x nutritional quality*) x price

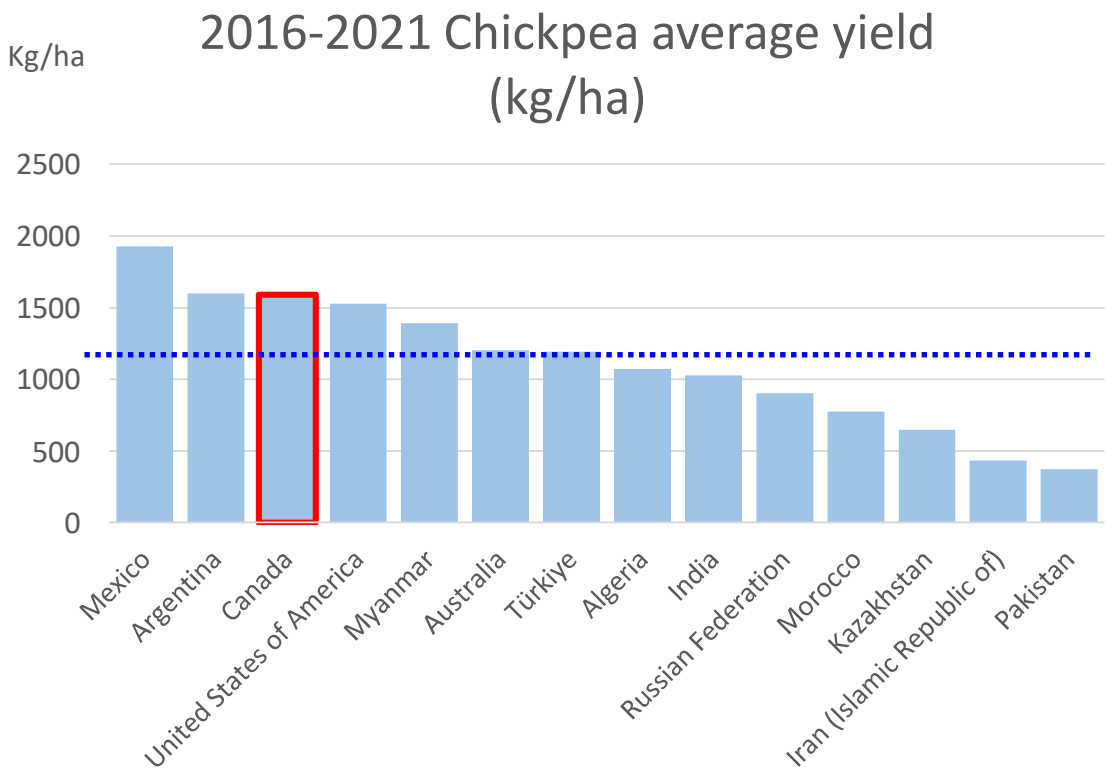
2. **Reduce risks and production cost**: ascochyta blight resistance; fusarium root rot; early maturity; frost and heat tolerance

3. **Ease of management**: herbicide tolerance; upright plant stature

4. **Consumer preference**:

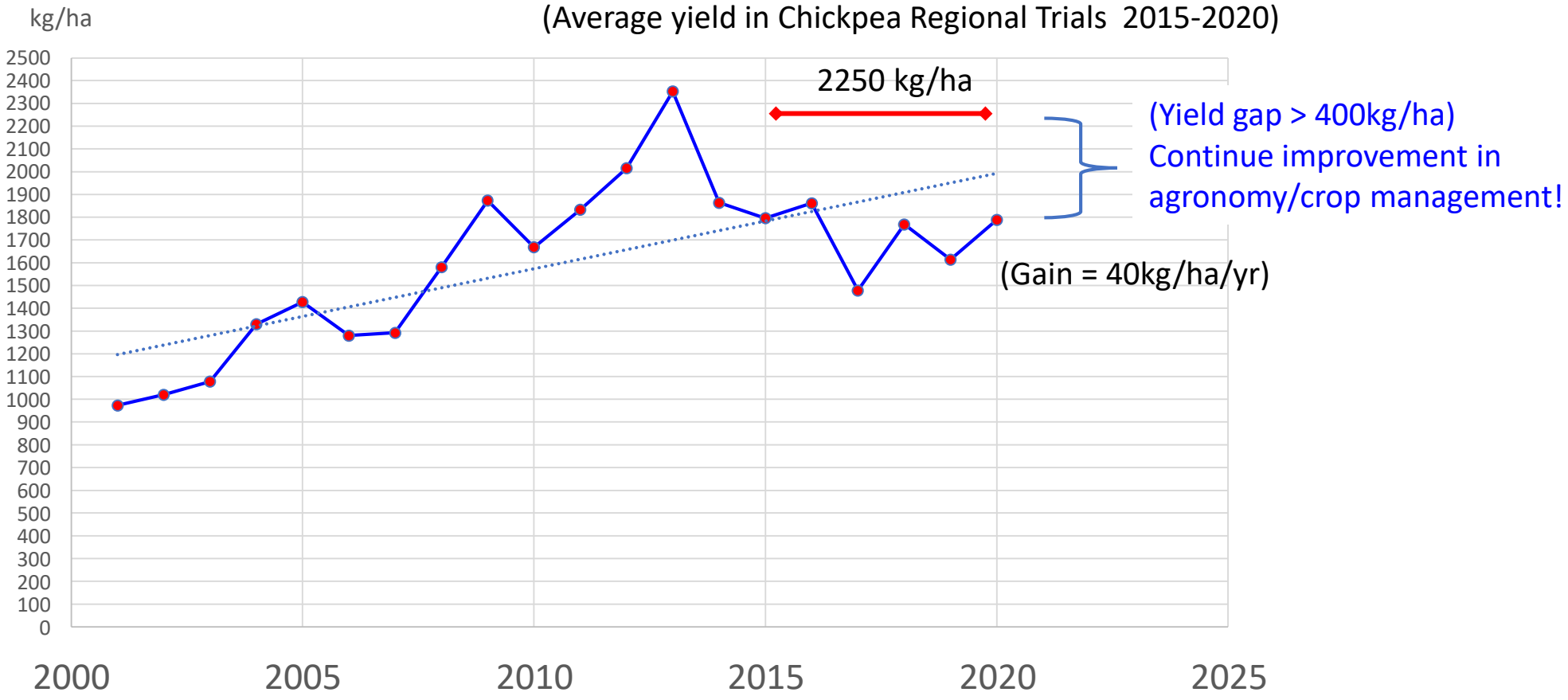
- Seed appearance (size, shape, colour);
- Grain processors: canning, milling efficiency;
- Nutritional characteristics (protein, oil, micronutrients, carotenoids);
- Alternative and new products: hummus, frozen green chickpea





(at the same period India produced: 10.1 M tons)

Source FAOSTAT 2023



Canada average chickpea yield (kg/ha) from 2001 to 2020

FAOSTAT 2023

Early Maturity

Plant Physiology®

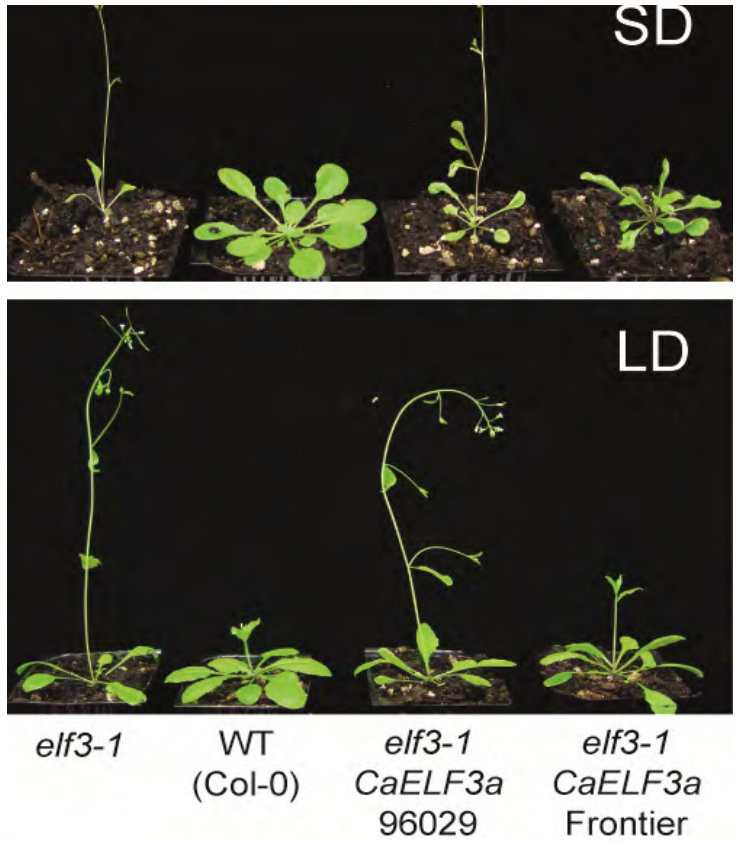
The chickpea Early Flowering 1 (Efl1) locus is an ortholog of Arabidopsis ELF3

Stephen Ridge, Amit Deokar, Robyn Lee, Ketema Daba, Richard C. Macknight, James L. Weller, Bunyamin Tar'an

Published August 2017. DOI: https://doi.org/10.1104/pp.17.00082 Altmetric 7

Characterization of Ca*ELF3* - *key gene for early flowering*

- Sequencing of ELF3 in ICCV 96029 and CDC Frontier: 11-bp deletion in highly conserved domain of ICCV 96029 resulting in a premature stop codon
- *elf3* mutation strongly associated with reduced photoperiod sensitivity



- Transformation of *Arabidopsis elf3-1* mutant with CDC Frontier and ICCV 96029 forms
- Complementation of flowering phenotype of the *Arabidopsis elf3-1* mutant by the Frontier form, but not the 96029 form of *35S::CaELF3a*

Early maturity strategy: *Early flowering; Less sensitive to photoperiod*
→ *3-5 days earlier maturity than the recurrent parent*

Introgression of early flowering *elf3 gene*

ICCV96029 x CDC Frontier

↓

F1 x CDC Frontier

↓

BC1F1 x CDC Frontier — Foreground selection for *elf3* & two flanking SNP markers

↓

BC2F1 x CDC Frontier — Foreground selection for *elf3* & background selection with 40 markers (5 markers per chr)

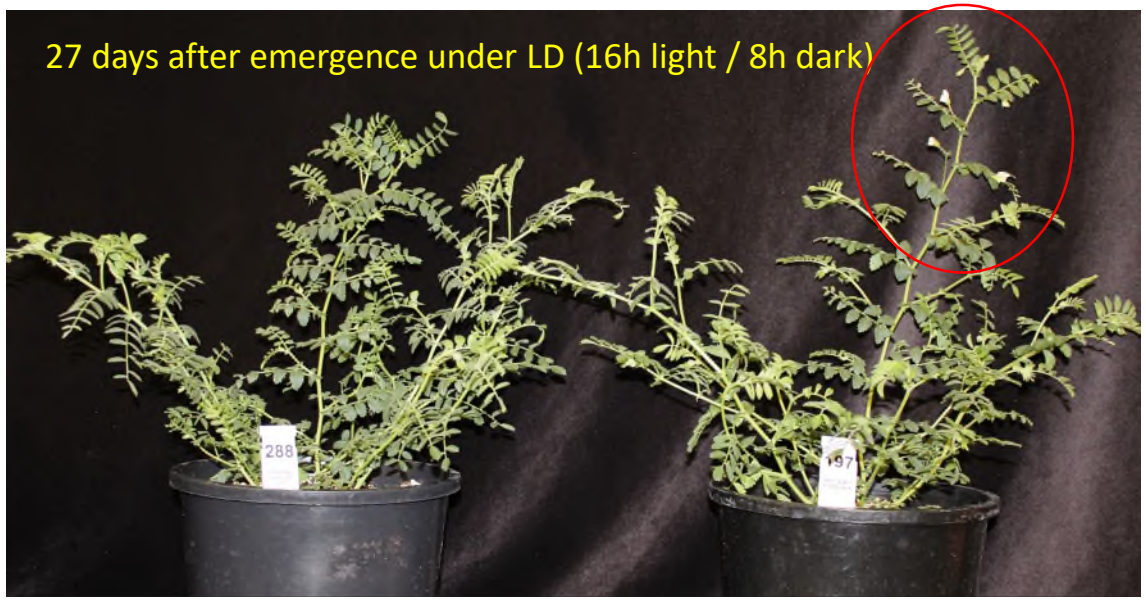
↓

BC3F1

⊗ ⇣

BC3F6 — Lines homozygous for *elf3* were selected

Phenotyping



DC Frontier (wild type/ELF3)

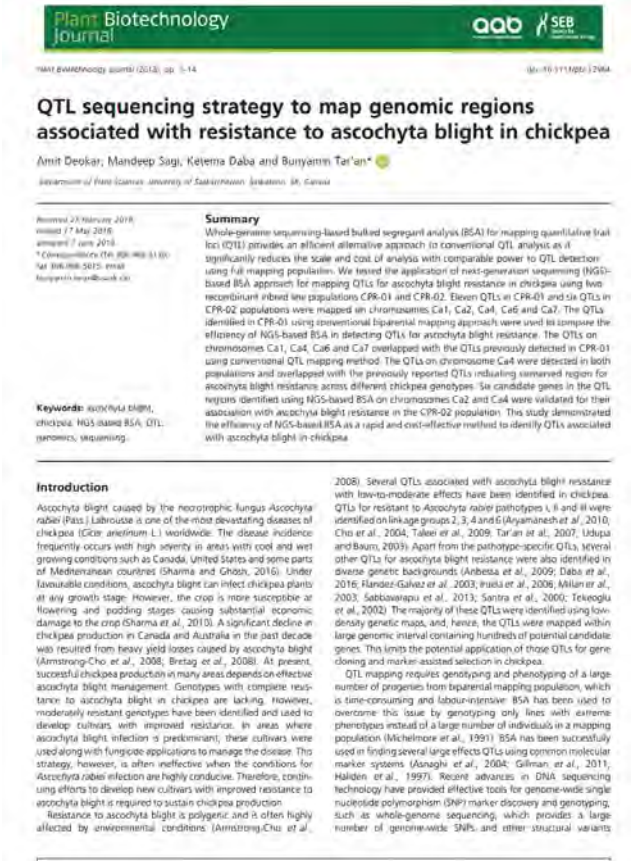
CDC Frontier with elf3 introgression

Resistance to fungal diseases:

- Description
  - Resistance to ascochyta blight & potential new disease (s)

- Value Proposition
  - Increased harvestable yield
  - Stabilized yield
  - Improved grain quality

- Approach
  - Native resistances
  - QTL, GWAS, Candidate genes
  - Accelerated breeding strategy
  - Gene editing and transgenic solutions (?)



Plant Biotechnology Journal

QTL sequencing strategy to map genomic regions associated with resistance to ascochyta blight in chickpea

Amit Deokar, Mandeep Sagi, Ketema Daba and Bunyamin Tar'an*

Summary

Whole-genome sequencing-based bulked segregant analysis (BSA) for mapping quantitative trait loci (QTL) provides an efficient alternative approach to conventional QTL analysis as it significantly reduces the scale and cost of analysis with comparable power to QTL detection using full mapping population. We tested the application of next-generation sequencing (NGS)-based BSA approach for mapping QTLs for ascochyta blight resistance in chickpea using two recombinant inbred line populations CPR-01 and CPR-02. Eleven QTLs in CPR-01 and six QTLs in CPR-02 populations were mapped on chromosomes Ca1, Ca2, Ca4, Ca6 and Ca7. The QTLs identified in CPR-01 using conventional biparental mapping approach were used to compare the efficiency of NGS-based BSA in detecting QTLs for ascochyta blight resistance. The QTLs on chromosomes Ca1, Ca4, Ca6 and Ca7 overlapped with the QTLs previously detected in CPR-01 using conventional QTL mapping method. The QTLs on chromosome Ca4 were detected in both populations and overlapped with the previously reported QTLs indicating conserved region for ascochyta blight resistance across different chickpea genotypes. Six candidate genes in the QTL regions identified using NGS-based BSA on chromosomes Ca2 and Ca4 were validated for their association with ascochyta blight resistance in the CPR-02 population. This study demonstrated the efficiency of NGS-based BSA as a rapid and cost-effective method to identify QTLs associated with ascochyta blight in chickpea.

Keywords: ascochyta blight, chickpea, NGS-based BSA, QTL, genomics, sequencing.

Introduction

Ascochyta blight caused by the necrotrophic fungus *Ascochyta rabiei* (Pass.) Labrousse is one of the most devastating diseases of chickpea (*Cicer arietinum* L.) worldwide. The disease incidence frequently occurs with high severity in areas with cool and wet growing conditions such as Canada, United States and some parts of Mediterranean countries (Sharma and Ghosh, 2016). Under favourable conditions, ascochyta blight can infect chickpea plants at any growth stage. However, the crop is more susceptible at flowering and podding stages causing substantial economic damage to the crop (Sharma *et al.*, 2010). A significant decline in chickpea production in Canada and Australia in the past decade was resulted from heavy yield losses caused by ascochyta blight (Armstrong-Cho *et al.*, 2008; Bretag *et al.*, 2008). At present, successful chickpea production in many areas depends on effective ascochyta blight management. Genotypes with complete resistance to ascochyta blight in chickpea are lacking. However, moderately resistant genotypes have been identified and used to develop cultivars with improved resistance. In areas where ascochyta blight infection is predominant, these cultivars were used along with fungicide applications to manage the disease. This strategy, however, is often ineffective when the conditions for *Ascochyta rabiei* infection are highly conducive. Therefore, continuing efforts to develop new cultivars with improved resistance to ascochyta blight is required to sustain chickpea production.

Resistance to ascochyta blight is polygenic and is often highly affected by environmental conditions (Armstrong-Cho *et al.*, 2008). Several QTLs associated with ascochyta blight resistance with low-to-moderate effects have been identified in chickpea. QTLs for resistant to *Ascochyta rabiei* pathotypes I, II and III were identified on linkage groups 2, 3, 4 and 6 (Anyamanesh *et al.*, 2010; Cho *et al.*, 2004; Taleei *et al.*, 2009; Tar'an *et al.*, 2007; Udupa and Baum, 2003). Apart from the pathotype-specific QTLs, several other QTLs for ascochyta blight resistance were also identified in diverse genetic backgrounds (Anbessa *et al.*, 2009; Daba *et al.*, 2016; Rakshit-Gallvez *et al.* 2003; Iruela *et al.*, 2006; Millan *et al.*, 2003; Sabbavarapu *et al.*, 2013; Santra *et al.*, 2000; Tekeoglu *et al.*, 2002). The majority of these QTLs were identified using low-density genetic maps, and, hence, the QTLs were mapped within large genomic interval containing hundreds of potential candidate genes. This limits the potential application of those QTLs for gene cloning and marker-assisted selection in chickpea.

QTL mapping requires genotyping and phenotyping of a large number of progenies from biparental mapping population, which is time-consuming and labour-intensive. BSA has been used to overcome this issue by genotyping only lines with extreme phenotypes instead of a large number of individuals in a mapping population (Michelmore *et al.*, 1991). BSA has been successfully used in finding several large effects QTLs using common molecular marker systems (Asnaghi *et al.*, 2004; Gilliman *et al.*, 2011; Halilden *et al.*, 1997). Recent advances in DNA sequencing technology have provided effective tools for genome-wide single nucleotide polymorphism (SNP) marker discovery and genotyping, such as whole-genome sequencing, which provides a large number of genome-wide SNPs and other structural variants

NRC Research Press

ARTICLE

QTL mapping of early flowering and resistance to ascochyta blight in chickpea

Ketema Daba, Amit Deokar, Sabine Banniza, Thomas D. Warkentin, and Bunyamin Tar'an

Abstract: In western Canada, chickpea (*Cicer arietinum* L.) production is challenged by short growing seasons and infestations with ascochyta blight. Research was conducted to determine the genetic basis of the association between flowering time and reaction to ascochyta blight in chickpea. Ninety-two chickpea recombinant inbred lines (RILs) developed from a cross between ICCV 96029 and CDC Frontier were evaluated for flowering responses and ascochyta blight reactions in growth chambers and fields at multiple locations and during several years. A wide range of variation was exhibited by the RILs for days to flower, days to maturity, node of first flowering, plant height, and ascochyta blight resistance. Moderate to high broad sense heritability was estimated for ascochyta blight reaction (H^2 = 0.14–0.34) and for days to flowering (H^2 = 0.45–0.87) depending on the environments. Negative correlations were observed among the RILs for days to flowering and ascochyta blight resistance, ranging from r = –0.21 ($P \leq 0.05$) to –0.58 ($P < 0.0001$). A genetic linkage map consisting of eight linkage groups was developed using 349 SNP markers. Seven QTLs for days to flowering were identified that individually explained 9%–44% of the phenotypic variation. Eight QTLs were identified for ascochyta blight resistance that explained phenotypic variation ranging from 10% to 19%. Clusters of QTLs for days to flowering and ascochyta blight resistances were found on chromosome 3 at the interval of 8.6–23.1 cM and on chromosome 8 at the interval of 53.88–62.35 cM.

Key words: Cicer arietinum, *Ascochyta rabiei*, early flowering, QTLs.

Résumé : Au Canada, la production de pois chiches (*Cicer arietinum* L.) est confrontée à une saison de croissance courte et à l'anthracnose. Des travaux de recherche ont été réalisés pour établir l'assise génétique de l'association entre la date de floraison et la réaction à l'anthracnose du pois chiche. Quatre-vingt-douze RIL développées à partir d'un croisement entre ICCV 96029 et CDC Frontier ont été évaluées pour la date de floraison et la réaction à l'anthracnose en cabinets de croissance et en champs. Une grande variation a été observée pour les caractères suivants : la date de floraison, la date de maturité, le premier nœud porteur de fleurs, la taille des plantes et la résistance à l'anthracnose. Une héritabilité au sens large de modérée à élevée a été obtenue pour la résistance à l'anthracnose (H^2 = 0,14 à 0,34) et pour la date de floraison (H^2 = 0,45 – 0,87), selon l'environnement. Des corrélations négatives ont été observées entre la date de floraison et la résistance à l'anthracnose chez les RIL. Une carte génétique comptant huit groupes de liaison a été produite à l'aide de 349 marqueurs SNP. Sept QTL pour la date de floraison ont été identifiés ; ceux-ci expliquaient individuellement entre 9 % et 44 % de la variation phénotypique. Huit QTL ont été identifiés pour la résistance à l'anthracnose et ceux-ci expliquaient entre 10 % et 19 % de la variation phénotypique. Des groupements de QTL pour la date de floraison et la résistance à l'anthracnose ont été notés sur les chromosomes 3 et 8. [Traduit par la Rédaction]

Mots-clés : Cicer arietinum, *Ascochyta rabiei*, floraison hâtive, QTL.

Introduction

Chickpea (*Cicer arietinum* L., 2n = 2x = 16) is one of the most important food legumes in the world next to dry bean (FAOSTAT 2013). The crop was recently introduced to Canada, and since then, the area under chickpea production in Canada has been fluctuating. Flowering time and maturity are among the important characteristics of chickpea that are critical for the adaptation of chickpea cultivars world wide (Anbessa et al. 2006; Upadhyaya et al. 2015; Sharma and Ghosh 2016). Ascochyta blight caused by the fungus *Ascochyta rabiei* Pass. Lab. has emerged as one of the most destructive diseases of the crop globally (Stephens et al.

Received 8 February 2016. Accepted 13 April 2016.
Corresponding Editor: M. Francki.

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Theoretical and Applied Genetics

ORIGINAL ARTICLE

Genome-wide SNP discovery for development of high-density genetic map and QTL mapping of ascochyta blight resistance in chickpea (*Cicer arietinum* L.)

Amit Deokar[1] · Mandeep Sagi[1] · Bunyamin Tar'an[1]

Received: 5 December 2018 / Accepted: 11 March 2019

Abstract

Key message **A high-density linkage map of chickpea using 3430 SNPs was constructed and used to identify QTLs and candidate genes for ascochyta blight resistance in chickpea.**

Abstract Chickpea cultivation in temperate conditions is highly vulnerable to ascochyta blight infection. Cultivation of resistant cultivars in combination with fungicide application within an informed disease management package is the most effective method to control ascochyta blight in chickpeas. Identifying new sources of resistance is critical for continued improvement in ascochyta blight resistance in chickpea. The objective of this study was to identify genetic loci and candidate genes controlling the resistance to ascochyta blight in recombinant inbred lines derived from crossing cultivars Amit and ICCV 96029. The RILs were genotyped using the genotyping-by-sequencing procedure and Illumina® GoldenGate array. The RILs were evaluated in the field over three site-years and in three independent greenhouse experiments. A genetic map with eight linkage groups was constructed using 3430 SNPs. Eight QTLs for resistance were identified on chromosomes 2, 3, 4, 5 and 6. The QTLs individually explained 7–40% of the phenotypic variations. The QTLs on chromosomes 2 and 6 were associated with the resistance at vegetative stage only. The QTLs on chromosomes 2 and 4 that were previously reported to be conserved across diverse genetic backgrounds and against different isolates of *Ascochyta rabiei* were confirmed in this study. Candidate genes were identified within the QTL regions. Their co-localization with the underlying QTLs was confirmed by genetic mapping. The candidate gene-based SNP markers would lead to more efficient marker-assisted selection for ascochyta blight resistance and would provide a framework for fine mapping and subsequent cloning of the genes associated with the resistance.

Introduction

Chickpea (*Cicer arietinum* L.) is the world's second most important grain legume. Multiple pests and diseases significantly affect chickpea productivity. Among the diseases, ascochyta blight caused by the necrotrophic fungal pathogen *Ascochyta rabiei* (Pass.) Lab. is one of the most devastating fungal diseases of chickpea. *A. rabiei* can infect the chickpea plant at any growth stage from plant emergence to seed maturity and produces blight-like symptoms on all above-ground plant parts. The ascochyta blight infection results in lower yield and poor seed quality. Ascochyta blight infection can occur across all major chickpea growing areas globally; however, the frequency of occurrence and severity are much higher in cool and humid growing areas, where several epidemics of ascochyta blight had caused complete crop loss (Kaiser et al. 2000). In North America, management of ascochyta blight is heavily dependent on fungicide applications. This practice has resulted in insensitivity of *A. rabiei* isolates against certain fungicides such as strobilurin (Chung et al. 2007; Wise et al. 2009). To avoid or delay the progress of *A. rabiei* becoming insensitive to fungicides, the use of resistant varieties is considered the most effective and sustainable disease management strategy. Globally,

Communicated by Albrecht E. Melchinger.

Electronic supplementary material The online version of this article (https://doi.org/10.1007/s00122-019-03322-3) contains supplementary material, which is available to authorized users.

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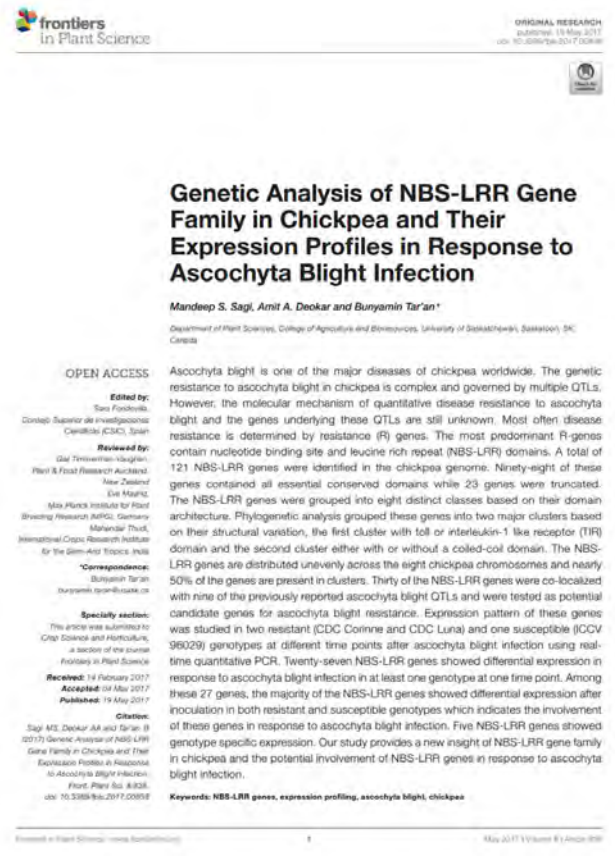

frontiers in Plant Science

ORIGINAL RESEARCH

Genetic Analysis of NBS-LRR Gene Family in Chickpea and Their Expression Profiles in Response to Ascochyta Blight Infection

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OPEN ACCESS

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Specialty section:
This article was submitted to Crop Science and Horticulture, a section of the journal Frontiers in Plant Science

Received: 14 February 2017
Accepted: 04 May 2017
Published: 19 May 2017

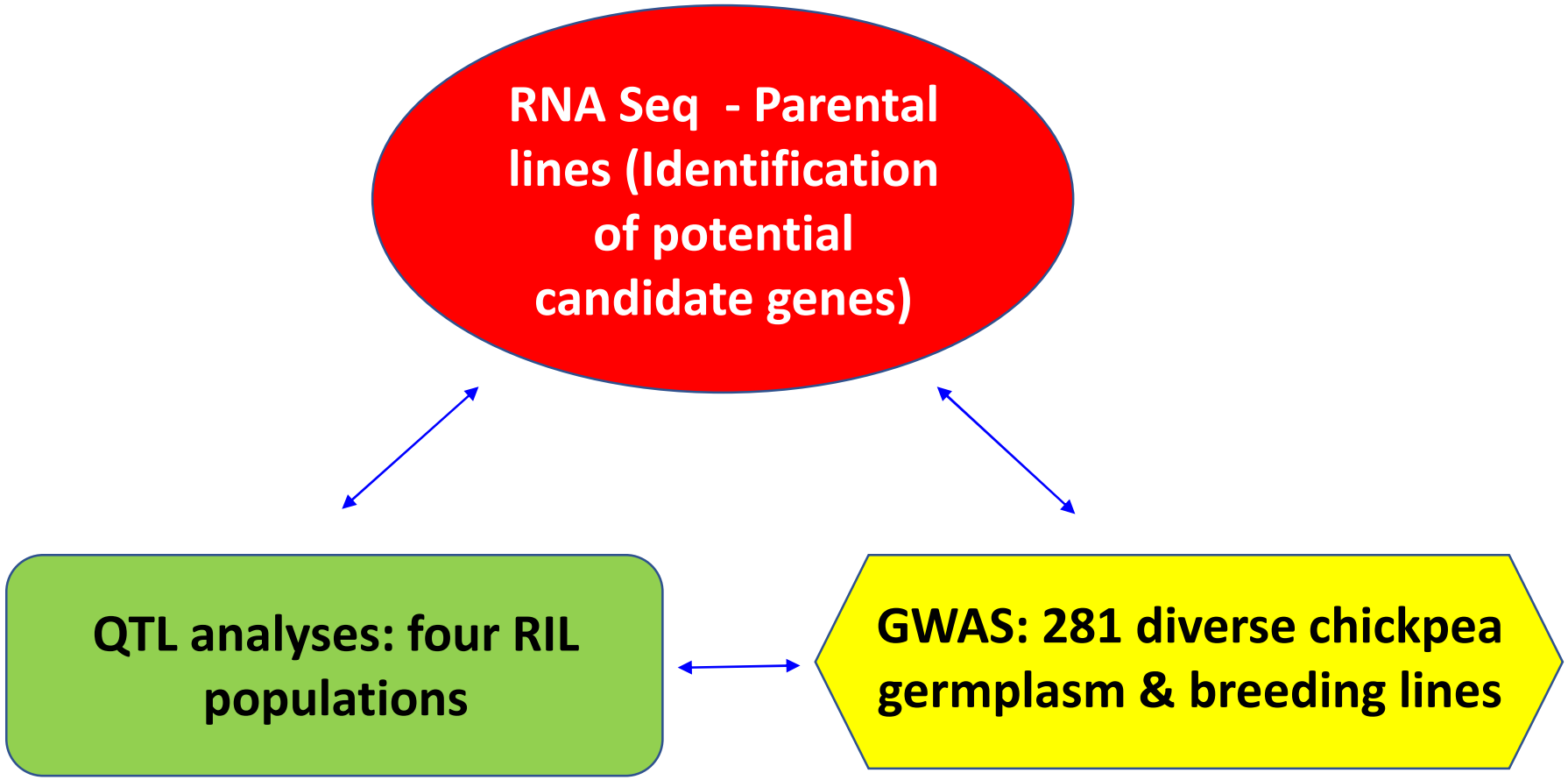
Citation:
Sagi MS, Deokar AA and Tar'an B (2017) Genetic Analysis of NBS-LRR Gene Family in Chickpea and Their Expression Profiles in Response to Ascochyta Blight Infection. Front. Plant Sci. 8:838. doi: 10.3389/fpls.2017.00838

Ascochyta blight is one of the major diseases of chickpea worldwide. The genetic resistance to ascochyta blight in chickpea is complex and governed by multiple QTLs. However, the molecular mechanism of quantitative disease resistance to ascochyta blight and the genes underlying these QTLs are still unknown. Most often disease resistance is determined by resistance (R) genes. The most predominant R-genes contain nucleotide binding site and leucine rich repeat (NBS-LRR) domains. A total of 121 NBS-LRR genes were identified in the chickpea genome. Ninety-eight of these genes contained all essential conserved domains while 23 genes were truncated. The NBS-LRR genes were grouped into eight distinct classes based on their domain architecture. Phylogenetic analysis grouped these genes into two major clusters based on their structural variation, the first cluster with toll or interleukin-1 like receptor (TIR) domain and the second cluster either with or without a coiled-coil domain. The NBS-LRR genes are distributed unevenly across the eight chickpea chromosomes and nearly 50% of the genes are present in clusters. Thirty of the NBS-LRR genes were co-localized with nine of the previously reported ascochyta blight QTLs and were tested as potential candidate genes for ascochyta blight resistance. Expression pattern of these genes was studied in two resistant (CDC Corinne and CDC Luna) and one susceptible (ICCV 96029) genotypes at different time points after ascochyta blight infection using real-time quantitative PCR. Twenty-seven NBS-LRR genes showed differential expression in response to ascochyta blight infection in at least one genotype at one time point. Among these 27 genes, the majority of the NBS-LRR genes showed differential expression after inoculation in both resistant and susceptible genotypes which indicates the involvement of these genes in response to ascochyta blight infection. Five NBS-LRR genes showed genotype specific expression. Our study provides a new insight of NBS-LRR gene family in chickpea and the potential involvement of NBS-LRR genes in response to ascochyta blight infection.

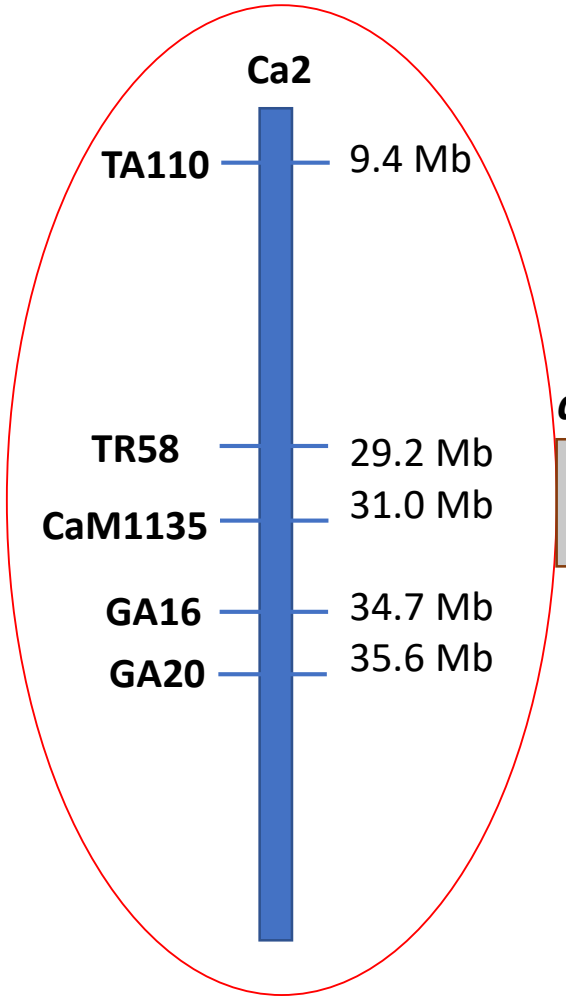
Keywords: NBS-LRR genes, expression profiling, ascochyta blight, chickpea

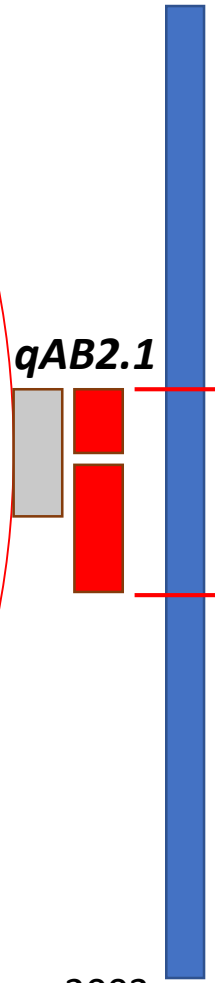
QTLs for resistance to ascochyta blight (in order of importance): Chr4, Chr2, Chr3, Chr5, Chr 8

Identification of potential candidate genes for resistance to ascochyta blight using RNA-Seq, QTL analyses and GWAS.



Conserved QTL across populations





Candidate genes involved in plant defence system located within the QTL region

ABA-R
ERF3
TMV resistance protein-1
Pectinesterase inhibitor
GDSL esterase/lipase-1
GDSL esterase/lipase-2

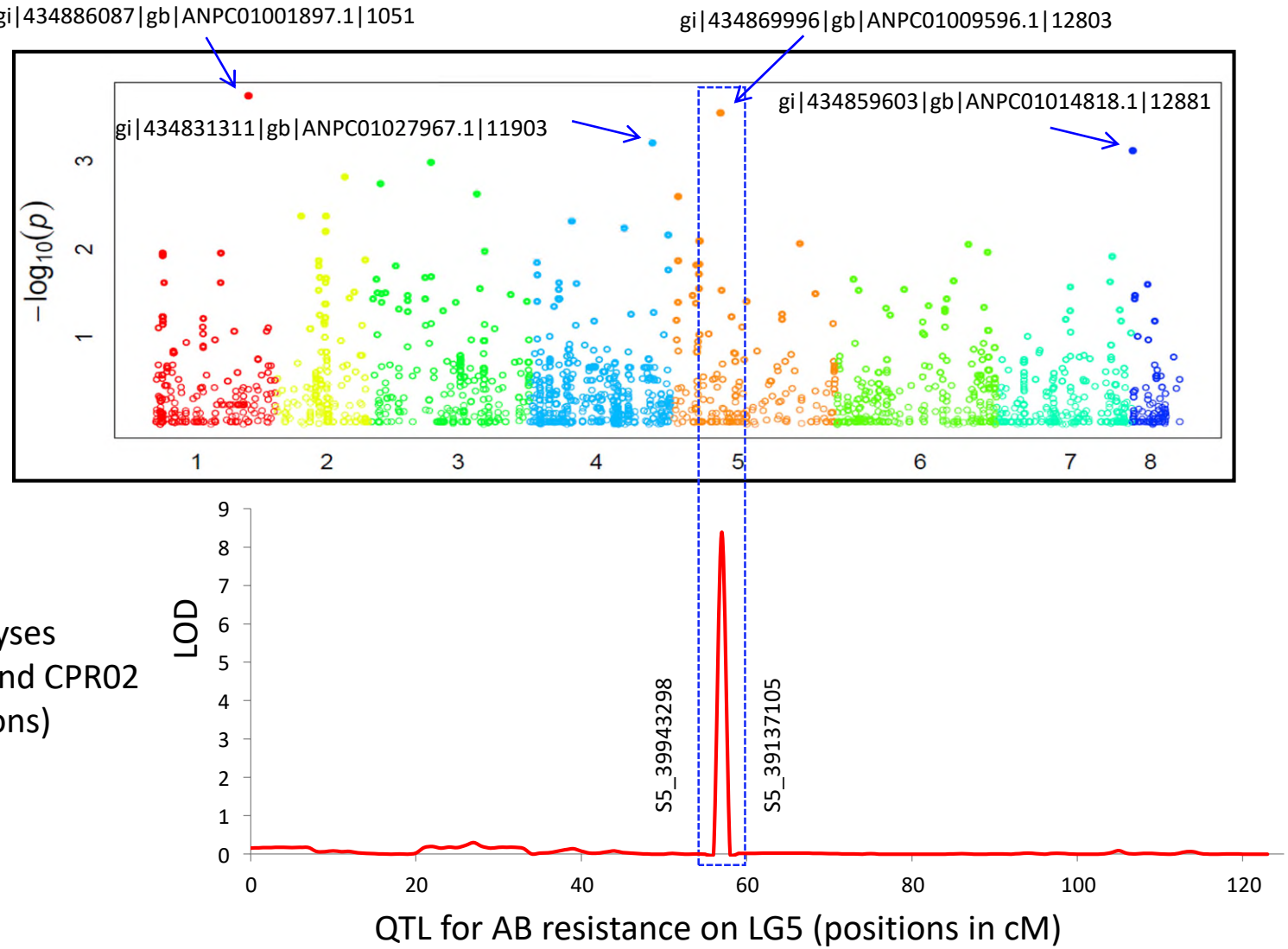
qAB2.1 & qAB2.2
PVE: 10-15
CPR01, CPR02

***ara*1 and *ara*2a** Udupa and Baum 2003,
Thudi et al. 2011, QTLAR3 (Iruela et al 2007)
ABQTL-1 (Varshney et al 2013),
Ar19 (Cho et al 2004)

Identification of genomic region associated with AB using genome wide association analysis and bi-parental mapping populations (QTL analysis)

GWAS

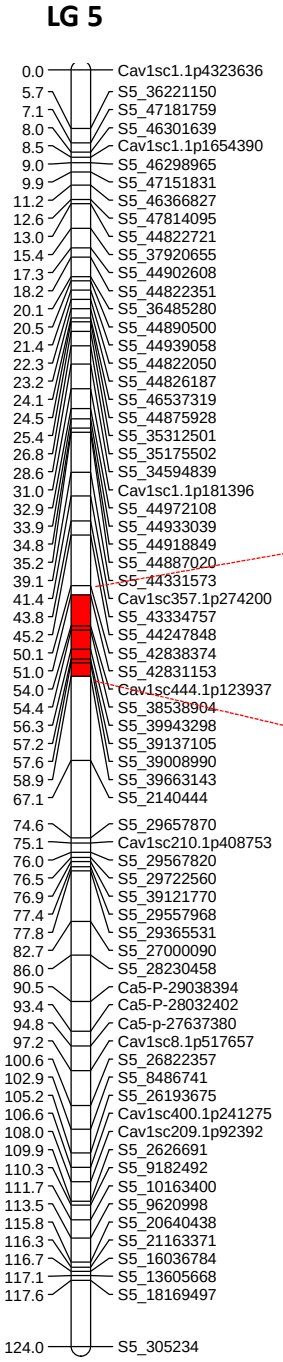
QTL analyses (CPR01 and CPR02 Populations)



Source: Deokar, unpublished data

Integrating transcript profiles with QTL mapping

Genes located in QTL interval and differentially expressed in response to AB infections were selected as potential candidate genes



Physical map

CDC Frontier CaV1.0

Ca5

40 Mb

42Mb

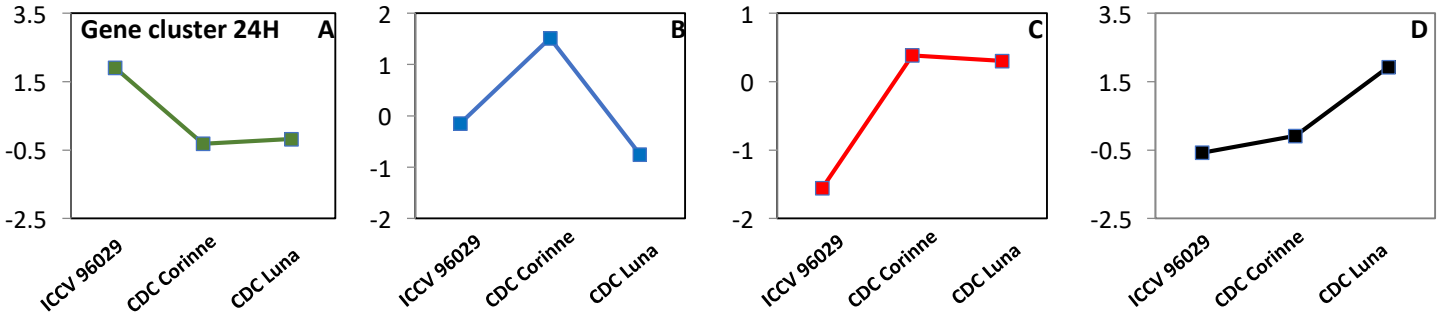
QTL for AB

Field and green house screening

LOD= 4 - 17

PVE (%) = 12-46%

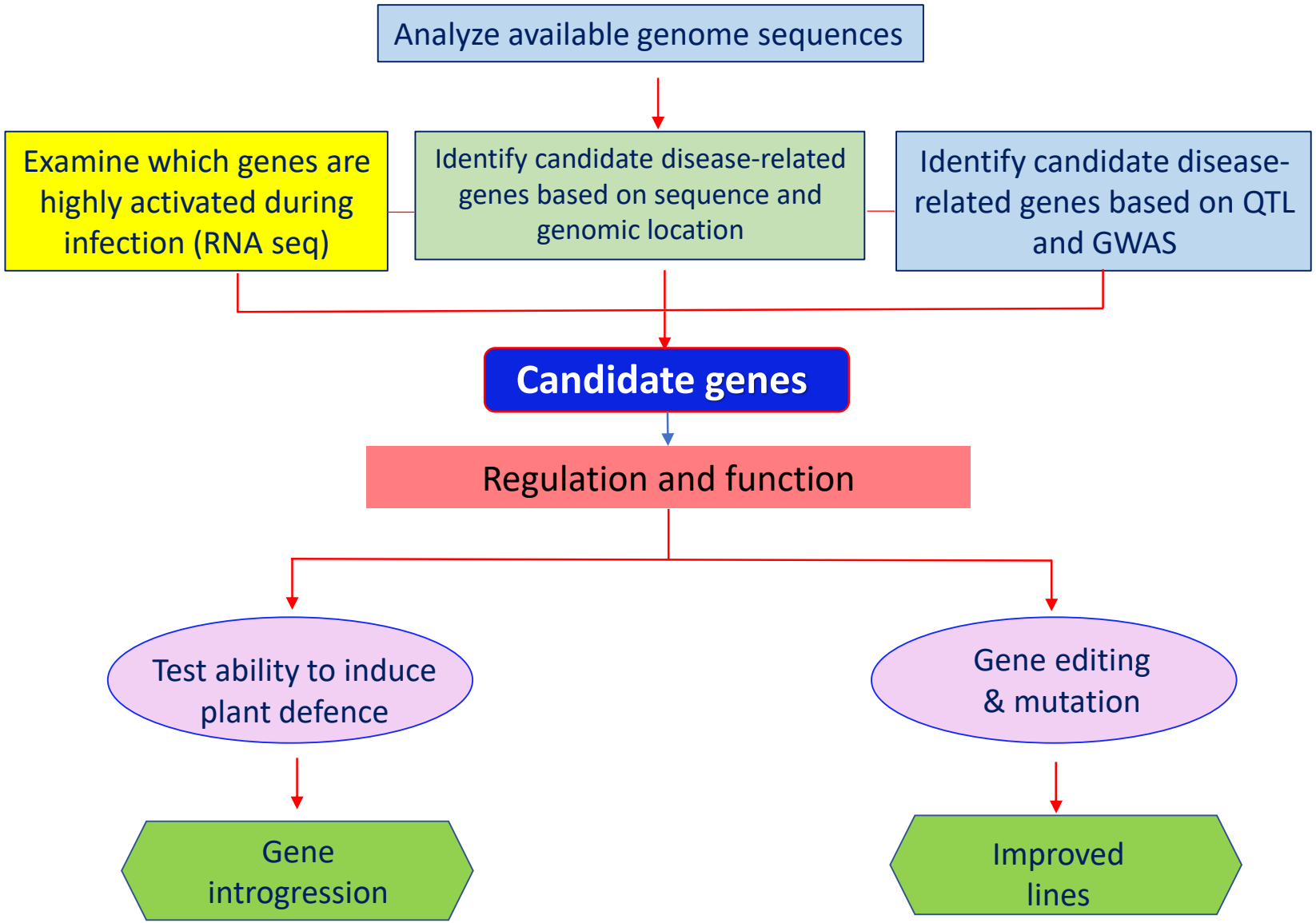
Time	Gene Cluster	Gene ID	Annotation
24H	B	Ca_11396	adenosylhomocysteinase
24H	C	Ca_07411	callose synthase 10
24H	C	Ca_07641	zinc finger protein CONSTANS 9
24H	D	Ca_03876	amino acid permease 3
48H	A	Ca_07425	abhydrolase domain-containing protein
48H	A	Ca_07560	probable serine/threonine-protein kinase
48H	A	Ca_07602	beta-carotene isomerase D27, chloroplastic
48H	A	Ca_11311	small heat shock protein, chloroplastic
48H	A	Ca_12654	aldehyde dehydrogenase
48H	B	Ca_07508	alpha,alpha-trehalose-phosphate synthase
48H	B	Ca_12643	beta-galactosidase 16
48H	B	Ca_12669	gamma-glutamyltranspeptidase 2
48H	D	Ca_07629	repetitive proline-rich cell wall protein 2
72 H	A	Ca_07615	CYSTM1 family protein A
72 H	A	Ca_11408	chalcone synthase 1B



Expression pattern of candidate genes in ICCV 96029, CDC Corinne and CDC Luna

Source: Deokar, unpublished data

Genomic approach to control Ascochyta blight in chickpea



Identifying New Sources of Resistance to Ascochyta Blight in Chickpea

Elizabeth Berenik, Tamanna Jahan, Shweta Kalve, and Bunyamin Tar'an
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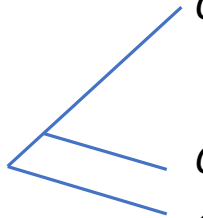


Introduction

Ascochyta blight, caused by the fungus *Ascochyta rabiei* Pass. Lab. is a detrimental disease to chickpea (*Cicer arietinum* L.) causing yield losses of up to 100% under conducive environments (Navas-Cortés et al., 1998). With the emergence of more aggressive fungal populations and varying climatic conditions, stronger and more durable resistance to Ascochyta blight in chickpeas is needed. An abundance of genetic variability is present within the wild chickpea species, including resistance to Ascochyta blight. Previous research has shown strong resistance to Ascochyta blight is present in *Cicer judaicum*, however, no fertile progeny has been recovered from crossing *C. judaicum* and cultivated chickpea. *Cicer pinnatifidum* has successfully been crossed with cultivated species and is being used as a potential bridge species (Mallikarjuna and Jadhav, 2008). An interspecific population consisting of 200 F6 lines derived from a cross between *C. pinnatifidum* x *C. judaicum* were screened for their reaction to Ascochyta blight under field and greenhouse conditions.

Materials and Methods

A total of 200 lines were developed from an interspecific cross of *Cicer pinnatifidum* x *Cicer judaicum*. These lines were increased in the greenhouse to F_6 and screened for resistance to Ascochyta blight. ICCV 96029, as a highly susceptible cultivar was used control. Eight CDC chickpea commercial cultivars were used as resistant checks.
All plant materials were planted in the greenhouse and inoculated with *A. rabiei* isolate AR170-03. Disease progression was rated based on a the Horsfall and Barratt 1- 12 rating scale at 7, 14, and 21 days after inoculation. The plant material is being subjected to disease screening with 2 repeats, each containing 4 replications.

Results

A frequency distribution at 14 days post inoculation (Figure 1) shows the range of disease scores within the lines. This range of scores is significantly different than that obtained from the control plants ($p = 0.04$). Based on a best linear unbiased predictor test, seven lines were deemed as highly resistant through all three rating periods (Figure 2). Based on a box and whisker test (Figure 3) we see that the lines have a wide range of distribution, out competing that of the controls. A closer look of F_6line 62 (Figure 4) we see a slower progression of disease than that of the control included in its pot.

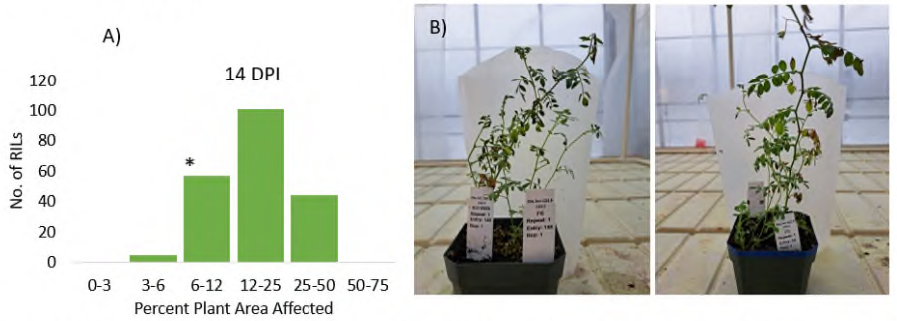


Figure 1. A) Frequency distribution of the mean ratings at 14 days post inoculation under controlled conditions. * indicates the scores of the parental lines. B) Selected F6 lines (RILs # 145 and 62) with control ICCV96029 for use in crossing block as donor for new resistance to ascochyta blight.

References

Mallikarjuna, N., and Jadhav, D.R. (2008) Techniques to produce hybrid between *Cicer arietinum L. x C. pinnatifidum* Jaub. Indian Journal of Genetics and Plant Breeding, 68 (4). pp. 398-405.
Navas-Cortés JA, Pérez-Artés E, Jiménez-Diaz RM, Llobell A, Bainbridge BW, Heale JB, 1998. Mating type, pathotype, and RAPDs analysis in *Didymella rabiei*, the agent of ascochyta blight of chickpea. *Phytoparasitica* 26, 199– 212.

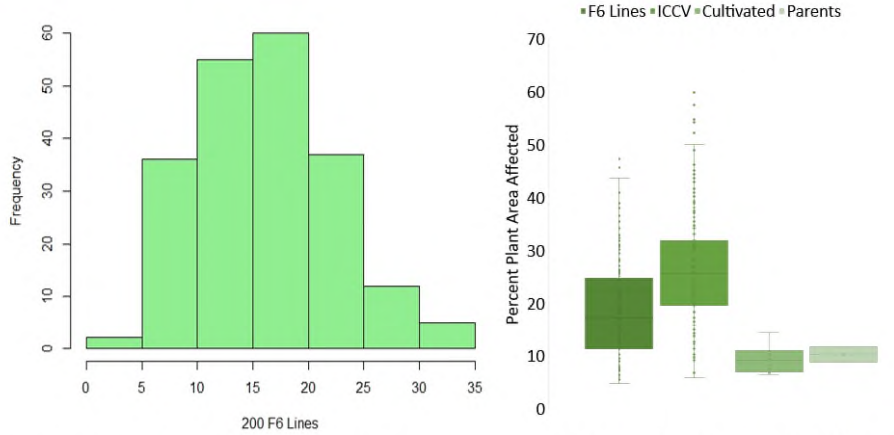


Figure 2. A histogram containing the results of a best linear unbiased predictor test over the three rating periods.

Figure 3. Distributions of the 200 F_6 lines, ICCV 96029, CDC varieties and parental lines.

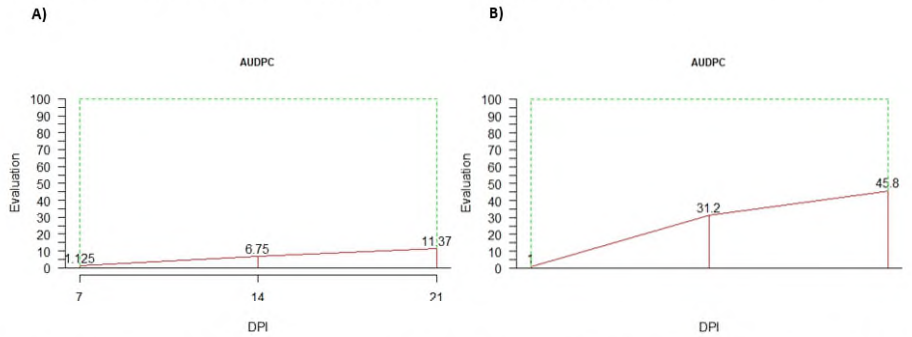


Figure 4. An area under the disease progression curve depicting ascochyta blight development in the greenhouse at 7, 14, and 21 days after inoculation (DPI). A) represents F_6 line 62 B) represents the control included in the pot with line 62.

Conclusions and Future Research

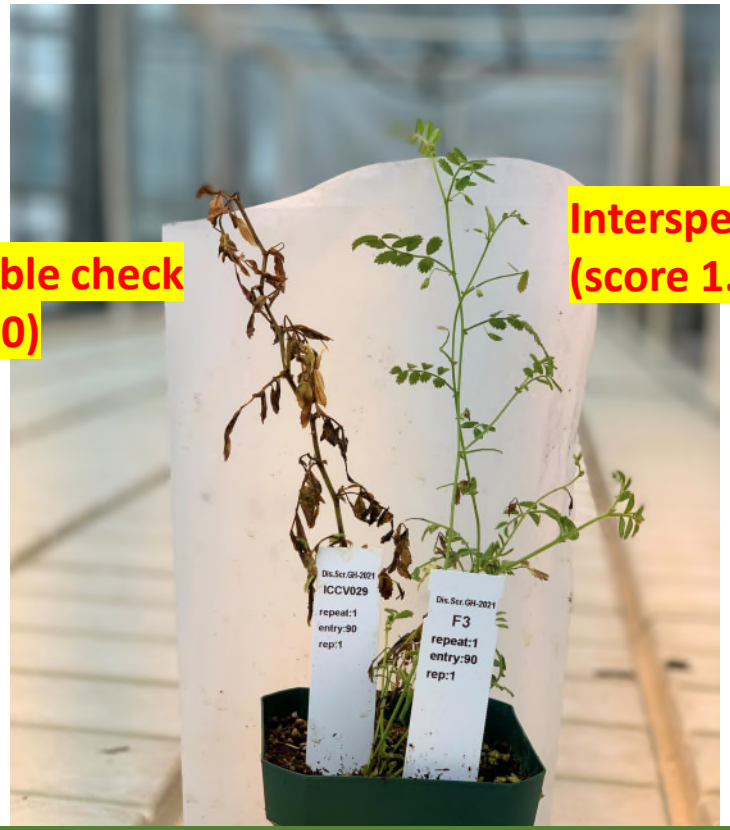
The current greenhouse screening has identified multiple F_6 lines with strong resistance to ascochyta blight. Few lines have resistance levels higher than the parental lines indicating that *Cicer pinnatifidum* and *Cicer judaicum* parents carry different genes for resistance. Selected resistance lines are being used as donor in crossing block to introgress the resistance into cultivated chickpea. To further confirm this resistance, additional screening in the greenhouse and field is needed. Linkage map development and quantitative trait loci (QTLs) analysis will be conducted to identify genomic regions corresponding with the resistance.

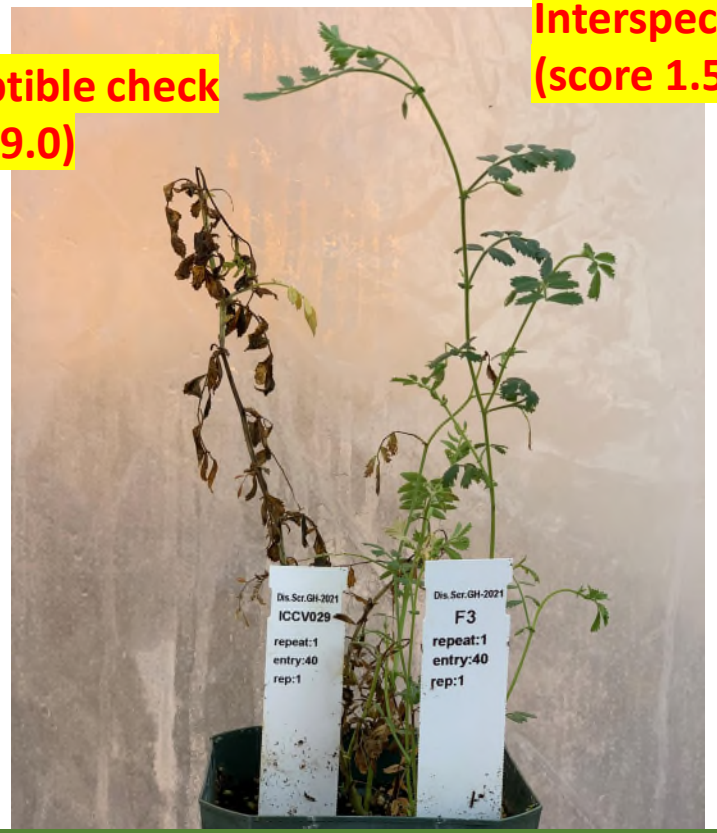
Acknowledgments:

CDC Pulse Crop Breeding Staff
CDC Pulse Pathology Lab
Robert P. Knowles Scholarship

ADF #20200134 Diversifying Sources for Resistance to Ascochyta Blight in Chickpea

(Matching fund: WGRF)





2023 Field evaluation: Moose Jaw, Elrose, Saskatoon (irrigation)

Screening for Ascochyta blight resistance of the progeny from interspecific cross between *Cicer pinnatifidum* and *C. judaicum*

Pictures were taken by Tamanna Jahan and Elizabeth Berenik on June23, 2021

Abiotic Stress Tolerance

"Mining" wild relatives for tolerance to abiotic stresses

C. arietinum x C. reticulatum // *C. arietinum x C. reticulatum*

(CDC Leader) (19 different accessions)

↓

600 lines

↓

F5 (200 lines) ← selected for seed quality and resistance to Ascochyta Blight

↓

Selfing until F8

(200 interspecific lines)

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August 2022

TYPE Original Research
PUBLISHED 19 August 2022
DOI 10.3389/fpls.2022.933277

OPEN ACCESS

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SPECIALTY SECTION
This article was submitted to Plant Breeding, a section of the journal Frontiers in Plant Science

RECEIVED 30 April 2022
ACCEPTED 17 June 2022
PUBLISHED 19 August 2022

CITATION
Kalve S, Gali KK and Tar'an B (2022) Genome-wide association analysis of stress tolerance indices in an interspecific population of chickpea.
Front. Plant Sci. 13:933277.
doi: 10.3389/fpls.2022.933277

Genome-wide association analysis of stress tolerance indices in an interspecific population of chickpea

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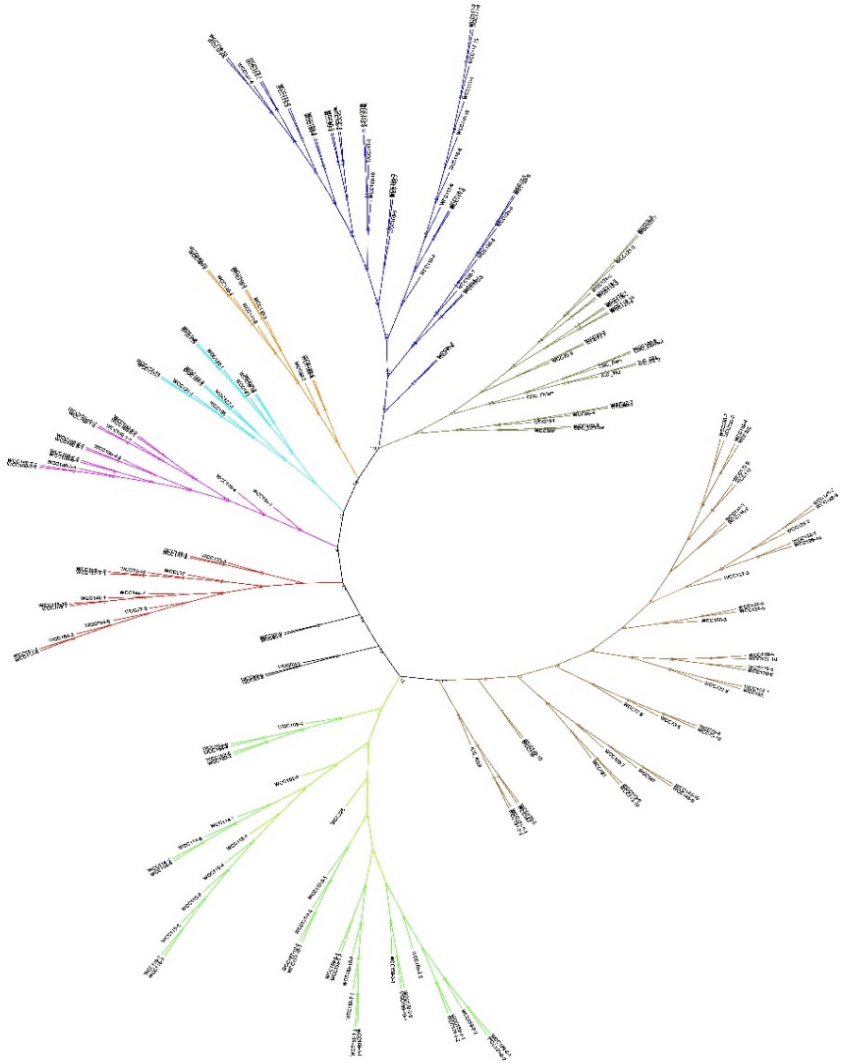
Chickpea is a cool season crop that is highly vulnerable to abiotic stresses such as heat and drought. High temperature during early flowering and pod development stages significantly reduces the crop yield. The wild relatives of chickpeas can be potential donors for the introgression of heat and drought tolerance into cultivated chickpeas for crop improvement. Initially, 600 interspecific lines were derived from crosses between two elite cultivars, CDC Leader (kabuli chickpea) and CDC Consul (desi chickpea), and 20 accessions of *Cicer reticulatum*. The F_5 interspecific lines were tested for agronomic and seed quality traits including reaction to ascochyta blight disease under field conditions at two locations in 2018. A subset of 195 lines were selected based on resistance to ascochyta blight and acceptable seed quality. These lines were evaluated for their performance under suboptimal conditions at Lucky Lake (2019 and 2020) and Moose Jaw (2019), Saskatchewan, Canada, and Yuma, Arizona, United States (2019–2020). The lines were grown and evaluated at two seeding dates, normal (SD1) and late (SD2) seeding dates, at each location and year. The same lines were genotyped using Cicer60K Axiom® SNP chip. The population structure was determined based on 35,431 informative SNPs using fastStructure, and the interspecific lines were clustered at a *k*-value of 15. Significant marker-trait associations were identified for seed yield from SD1 and SD2 seeding dates, and stress tolerance indices (ATI, K_1STI, MP, SSPI, and TOL) using phenotypic values both from individual locations and combined analyses based on BLUP values. SNP marker Ca2_34600347 was significantly associated with yield from both the seeding dates. This and other SNP markers identified in this study may be useful for marker-assisted introgression of abiotic stress tolerance in chickpea.

KEYWORDS

suboptimal conditions, interspecific crosses, marker-assisted introgression, wild chickpea, cultivars, stress tolerance indices



Neighbor-joining tree based on 35,432 SNPs showing the genetic relatedness among the 200 chickpea interspecific inbred lines.

The 200 lines were seeded at two seeding dates (normal and late seeding) at three locations to expose the lines to high temp during flowering

		Max T (°C) at flowering	
Location	Year	Seeding date 1 (normal)	Seeding date 2 (late)
Moose Jaw, SK	2019	25.4	35.4
Lucky Lake, SK	2019	26.9	34.2
Lucky Lake, SK	2020	25.8	34.7
Yuma, AZ, USA	2020	29.4	38.9

RCBD with 3 reps was used at each location and seeding date

TOL (tolerance index) = Yp–Ys (Rosielle and Hamblin, 1981)

MP (mean productivity) = (Yp+Ys)/2 (Rosielle and Hamblin, 1981)

ATI (abiotic tolerance index) = $[(Yp–Ys)/(\bar{Y}p/\bar{Y}s)] \times 100$ (Moosavi et al., 2008)

SSPI (stress susceptibility percentage index) = $[(Yp–Ys)/(2\bar{Y}p)] \times 100$ (Moosavi et al., 2008)

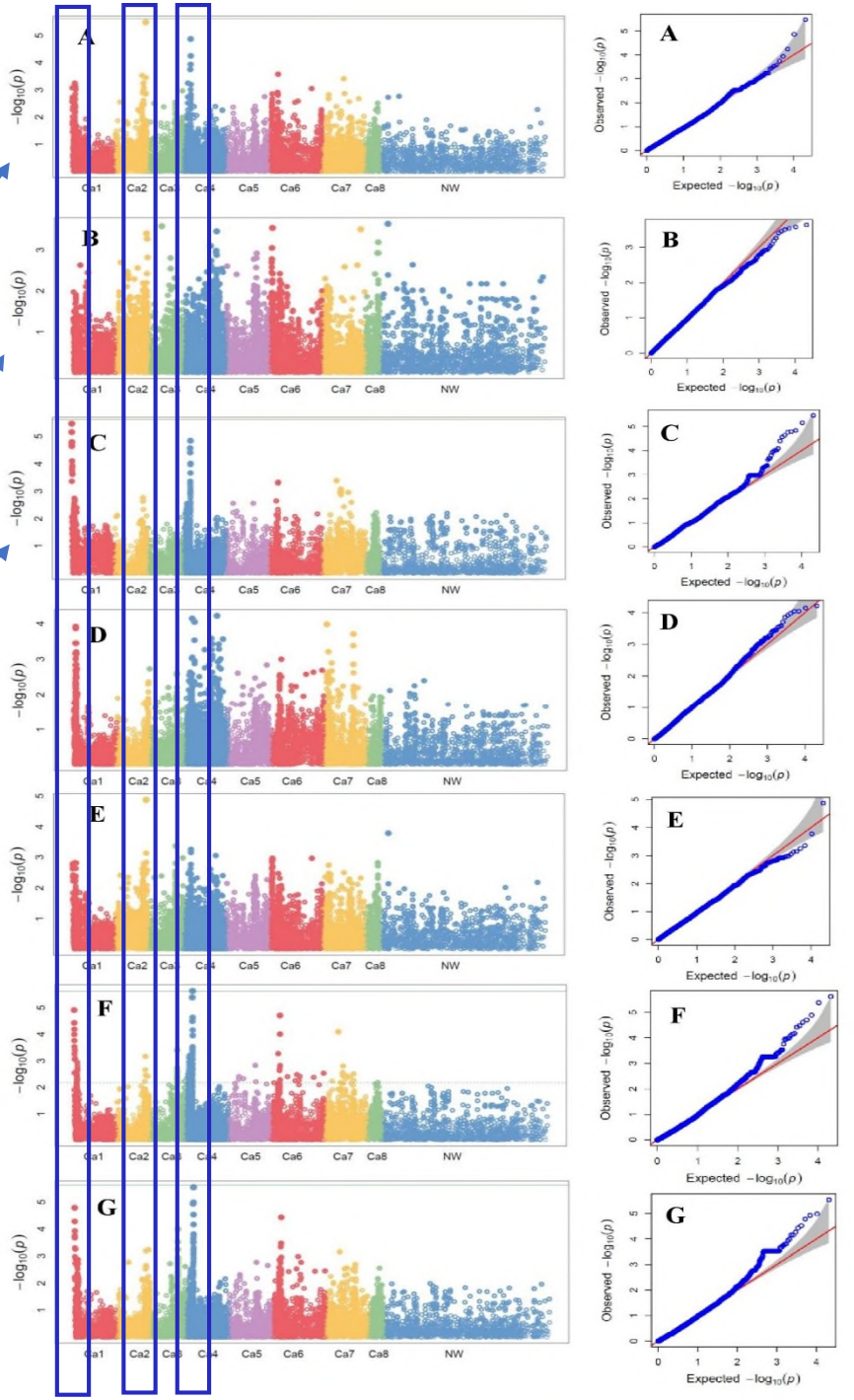
K_1STI (modified stress tolerance index) = $(Yp2/\bar{Y}p2) \times [(Yp+Ys)/\bar{Y}p2)$ (Farshadfar and Sutka, 2003)

- Interspecific population chickpea nursery at Yuma, AZ. March 12, 2020

Location	Yield (g/m²)			
	SD1		SD2	
	Mean	Range	Mean	Range
Lucky Lake, 2019	228	28-443	193	22-395
Moose Jaw, 2019	306	90-486	210	43-385
Yuma 2019-2020	259	5-1638	89	3-282
Lucky Lake 2020	129	6-466	146	9-467

SNP markers associated with different stress indices

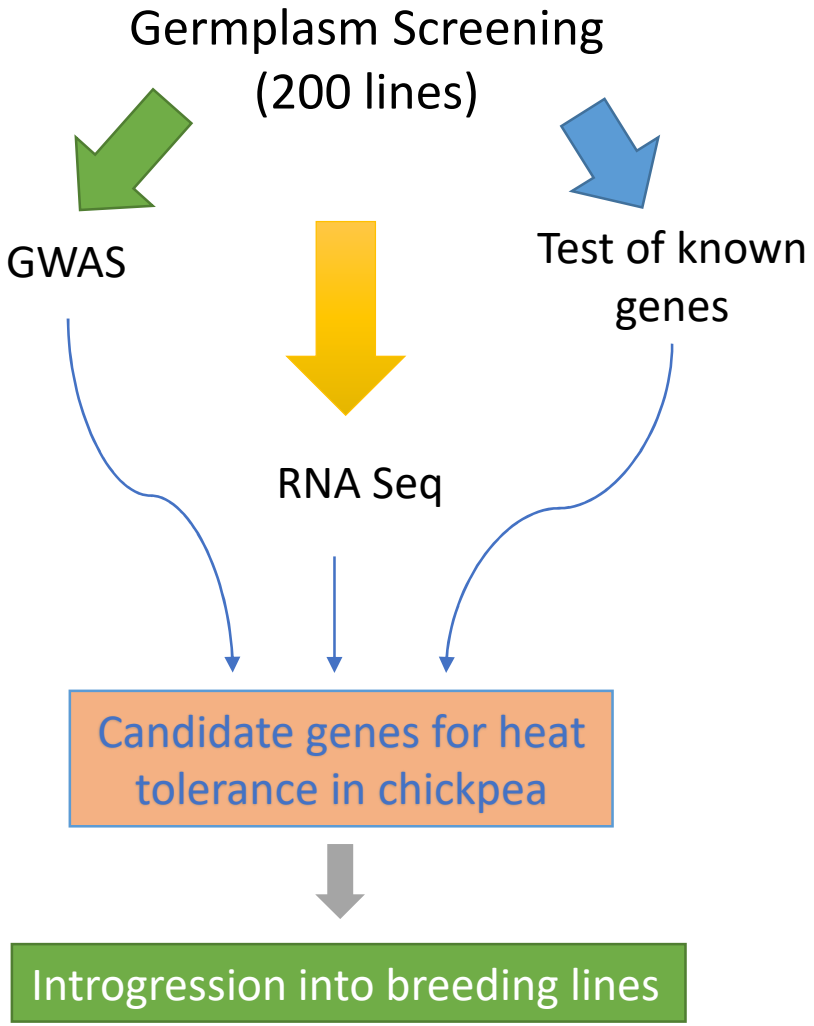
Stress Indices	SNP marker	P-value	MAF
Ys (Seed yield under stress conditions)	NW_9270594	$2.31E^{-04}$	0.31
	Ca3_15304269	$2.61E^{-04}$	0.09
	Ca6_3396299	$2.89E^{-04}$	0.31
	Ca7_43614232	$3.14E^{-04}$	0.41
	Ca4_37419513	$3.47E^{-05}$	0.40
	Ca2_34600347	$3.92E^{-04}$	0.07
Yp (Seed yield under non-stress conditions)	Ca2_34600347	$3.25E^{-06}$	0.07
	Ca4_8694304	$1.35E^{-05}$	0.05
	Ca4_8737135	$5.55E^{-05}$	0.14
ATI (Abiotic tolerance index)	Ca1_47259	$3.42E^{-06}$	0.46
	Ca1_56428	$6.91E^{-06}$	0.46
K_1STI (Modified stress tolerance index)	Ca4_36637574	$6.05E^{-05}$	0.10
	Ca4_8646741	$7.12E^{-05}$	0.16
	Ca4_11276937	$9.00E^{-05}$	0.07
	Ca4_11277513	$9.00E^{-05}$	0.07
MP (Mean productivity)	Ca2_34600347	$1.34E^{-05}$	0.07
SSPI (Stress susceptibility percentage index)	Ca4_8694304	$2.37E^{-06}$	0.05
	Ca4_8313845	$4.17E^{-06}$	0.06
TOL (Tolerance index)	Ca4_8694304	$2.87E^{-06}$	0.05
	Ca4_8670257	$1.04E^{-05}$	0.06
	Ca4_8313845	$1.19E^{-05}$	0.06
	Ca1_47259	$1.66E^{-05}$	0.46



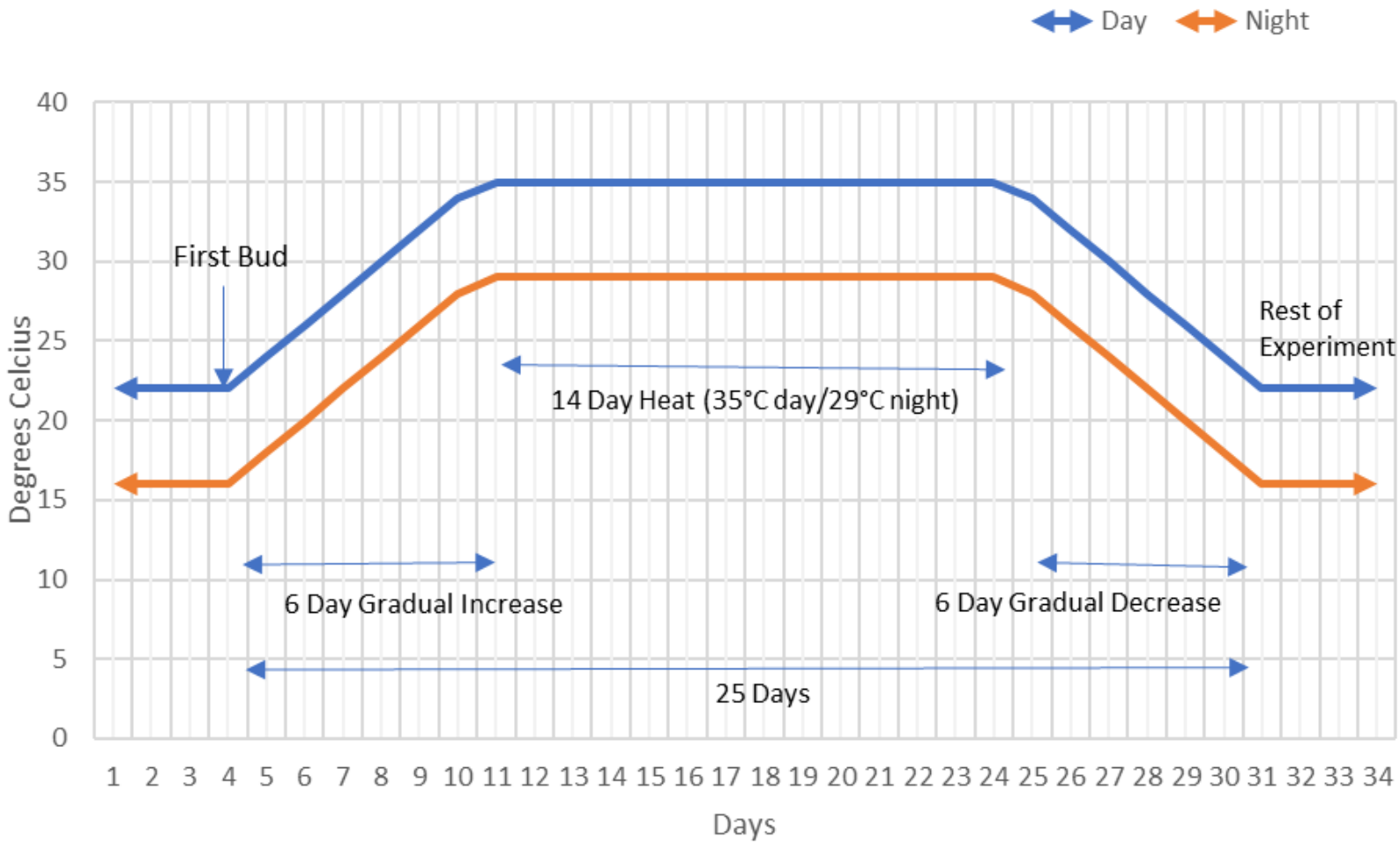
- **Genetic analysis of heat stress tolerance in chickpea**

Sophie Duchesne

(PhD student)



Evaluation for tolerance to heat stress in chickpeas



Seed Quality

Tamanna Jahan (PhD)

frontiers | Frontiers in Plant Science

17 March 2023

TYPE Original Research
PUBLISHED 17 March 2023
DOI 10.3389/fpls.2023.1092493

OPEN ACCESS

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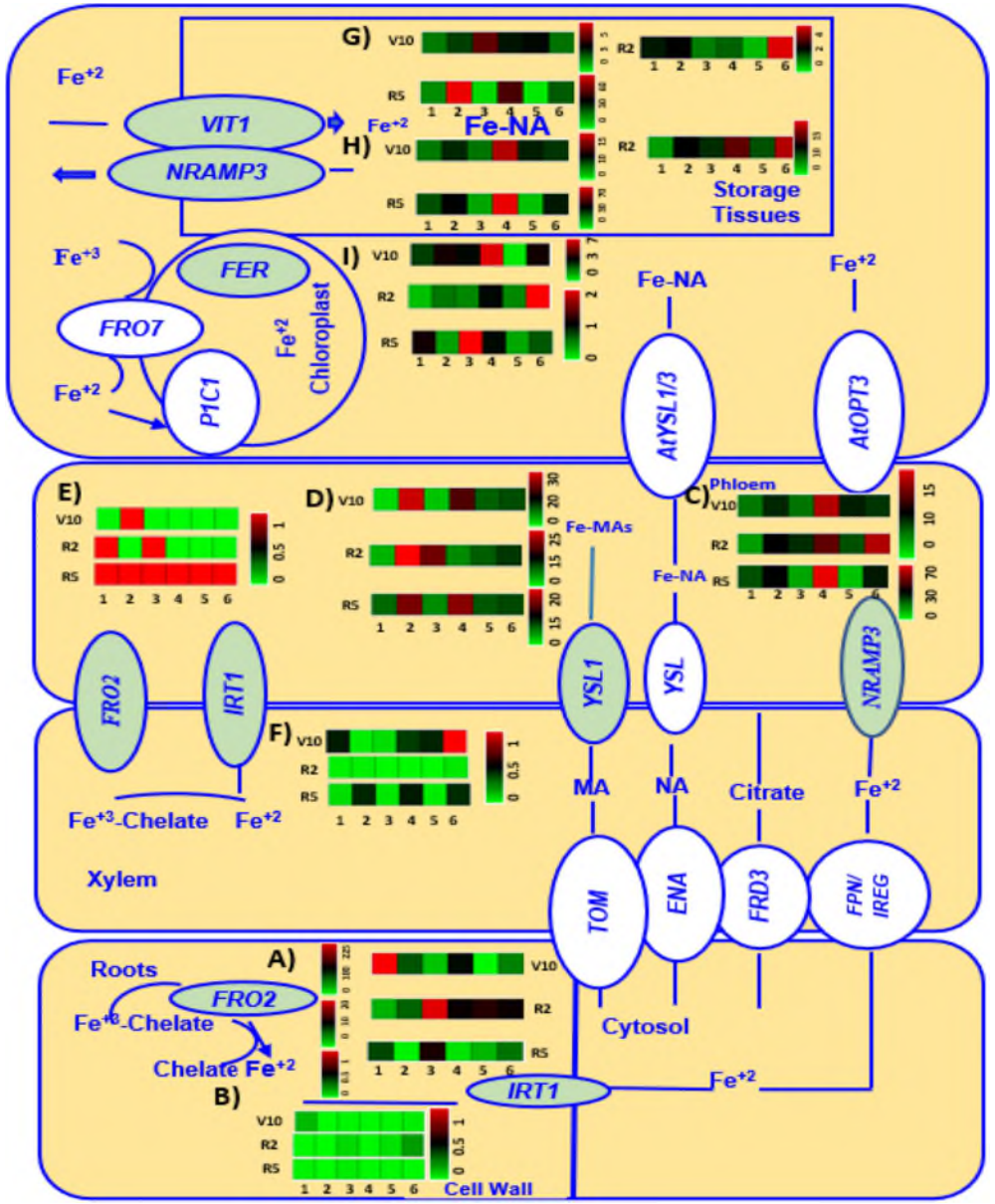
Iron accumulation and partitioning in hydroponically grown wild and cultivated chickpea (*Cicer arietinum* L)

Tamanna A. Jahan[1], Shweta Kalve[1], Zachery Belak[2], Christopher Eskiw[2] and Bunyamin Tar'an[1]*

[1]Department of Plant Sciences, College of Agriculture and Bioresources, University of Saskatchewan, Saskatoon, SK, Canada, [2]Department of Food and Bioproduct Sciences, College of Agriculture and Bioresources, University of Saskatchewan, Saskatoon, SK, Canada

A heatmap analysis showing the gene expression patterns of Fe metabolism related genes FRO2 (A, E), IRT1 (B, F), NRAMP3 (C, H), YSL1 (D), V1T1 (G), and FER3 (I) in roots and leaves of six different genotypes (1 = CDC Verano, 2 = Cermi 075, 3 = FLIP97-677C, 4 = Sarik 067, 5 = Kalka 064, and 6 = CDC 551-1). The data at V10, R2 and R5 growth stages taken only from Fe added (Fe+) conditions. Green and red color represents down-regulation, and up-regulation in the color scale, respectively.

Jahan et al. 2023



Genomics & New Approaches

Genomic Selection

Of Seed Protein and Oil Content

Alanna Orsak
MSc

Training GS Models

Parental lines and germplasm *(Founding alleles; n = 184)*

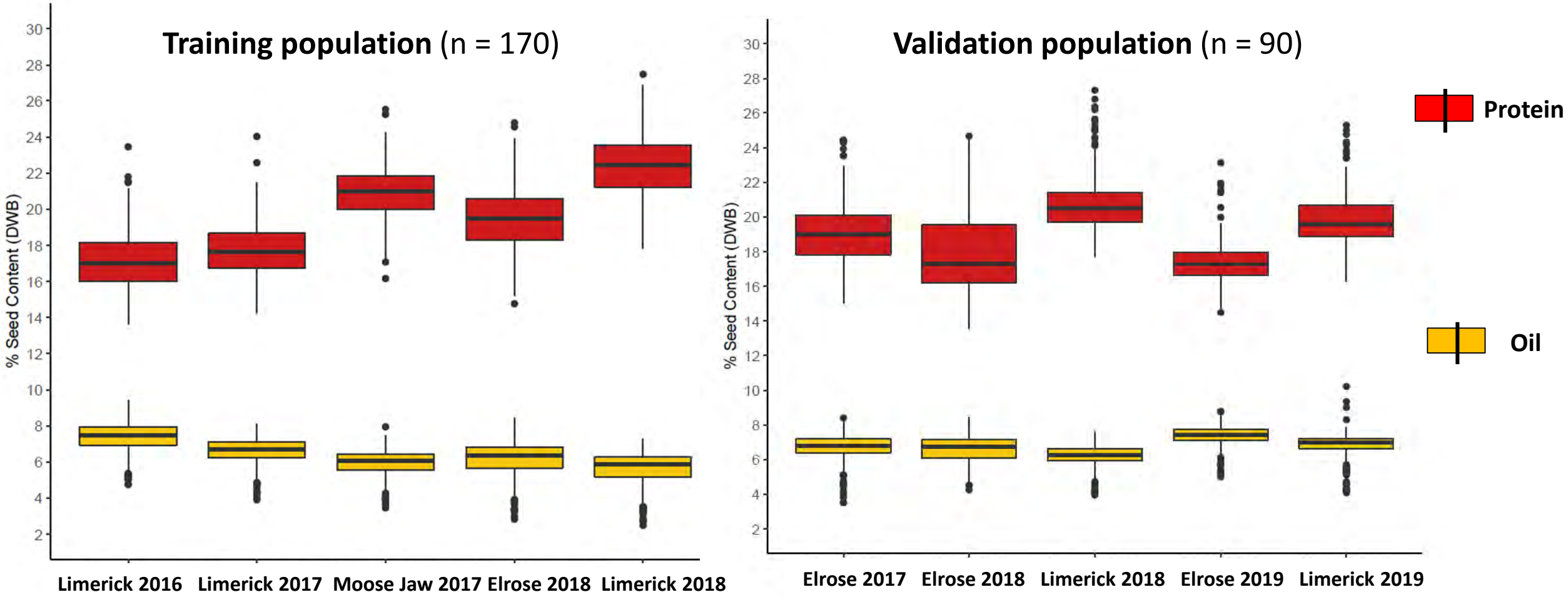
Marker Density:
MAF 5% *(14,971)*
MAF 10% *(11,397)*
LD 0.25 *(1,699)*
LD 0.50 *(2,650)*
LD 0.75 *(3,785)*
All markers (28,177)

Model:
RR-BLUP
G-BLUP
BayesB
BayesCPi

Calculate GEBV

Testing GS Models
Validation population (all elite lines from the CDC breeding program; n= 100)

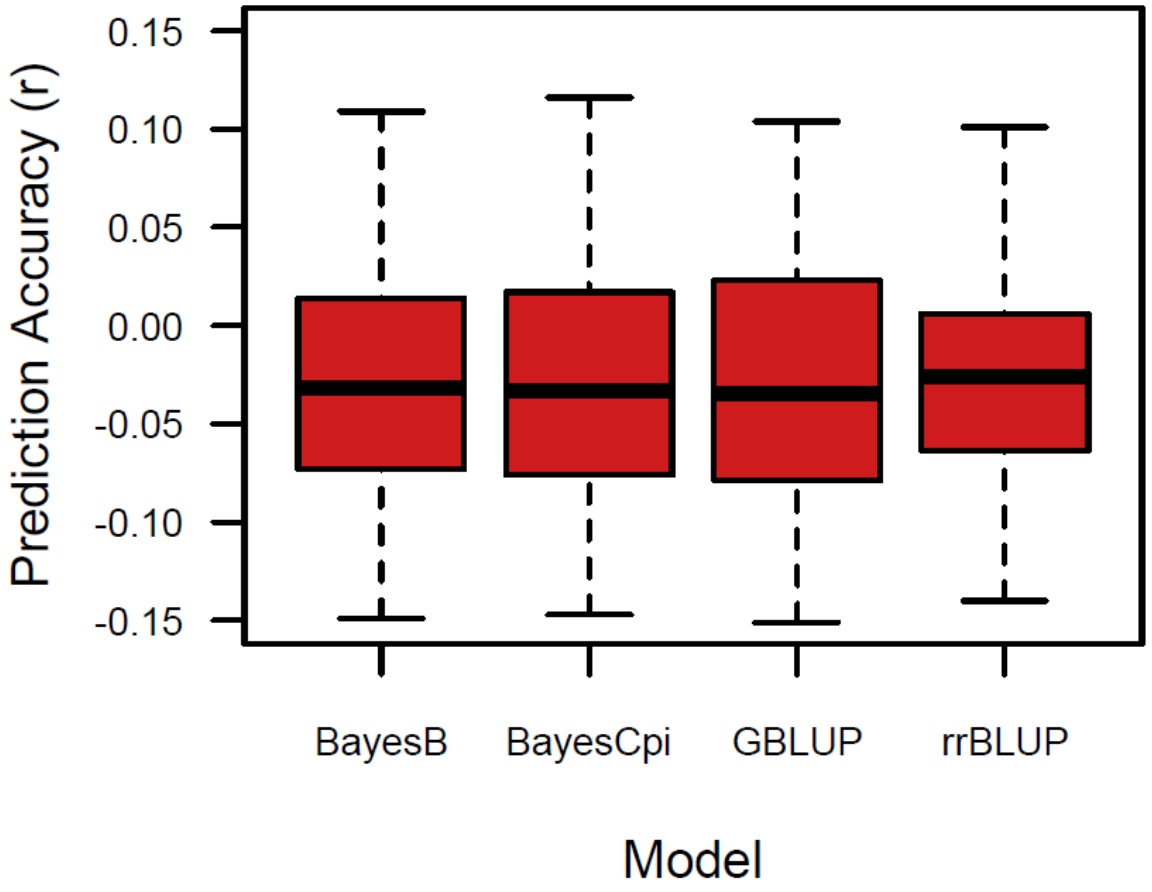
Protein and oil contents of TP and VP at each environment (site-year)

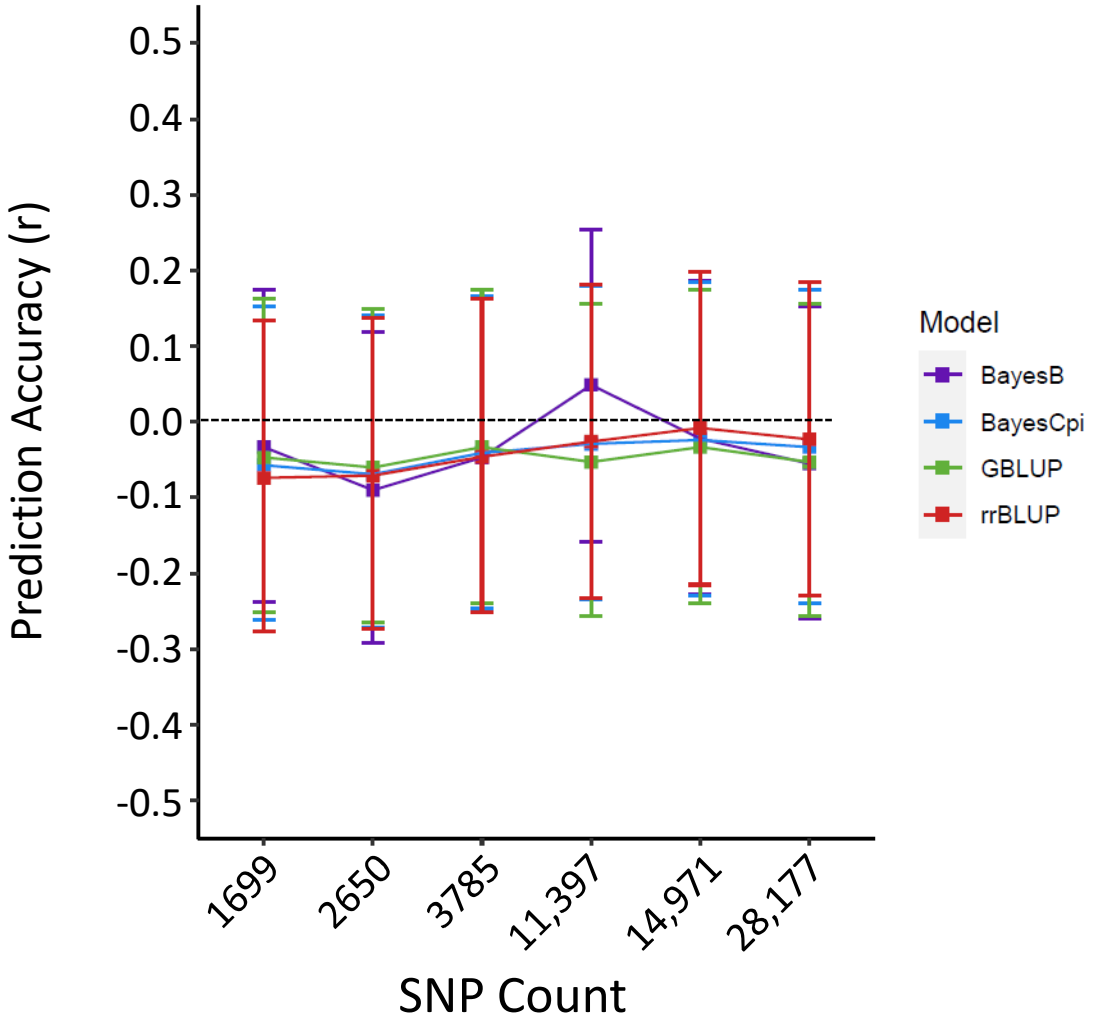


Variable combinations tested for GS

BLUPs		**Cumulative BLUPS**				**Growing Location BLUPS**				**Growing Year BLUPS**			
Predicting BLUPs		Cumulative				Elrose, Limerick, Moose Jaw				2016, 2017, 2018			
Validating BLUPs		Cumulative (Elrose, Limerick, 2017, 2018, 2019)				Cumulative (Elrose, Limerick)				Cumulative (2017, 2018, 2019)			
Model		rrBLUP	GBLUP	BayesB	BayesCπ	rrBLUP	GBLUP	BayesB	BayesCπ	rrBLUP	GBLUP	BayesB	BayesCπ
Full Marker Set		1	2	3	4	5	6	7	8	9	10	11	12
Minor Allele Frequency	5%	13											
	10%	25											
Marker Density based on LD	r^2 <0.75	37											
	r^2 <0.50	49											
	r^2 <0.25	61											**72**

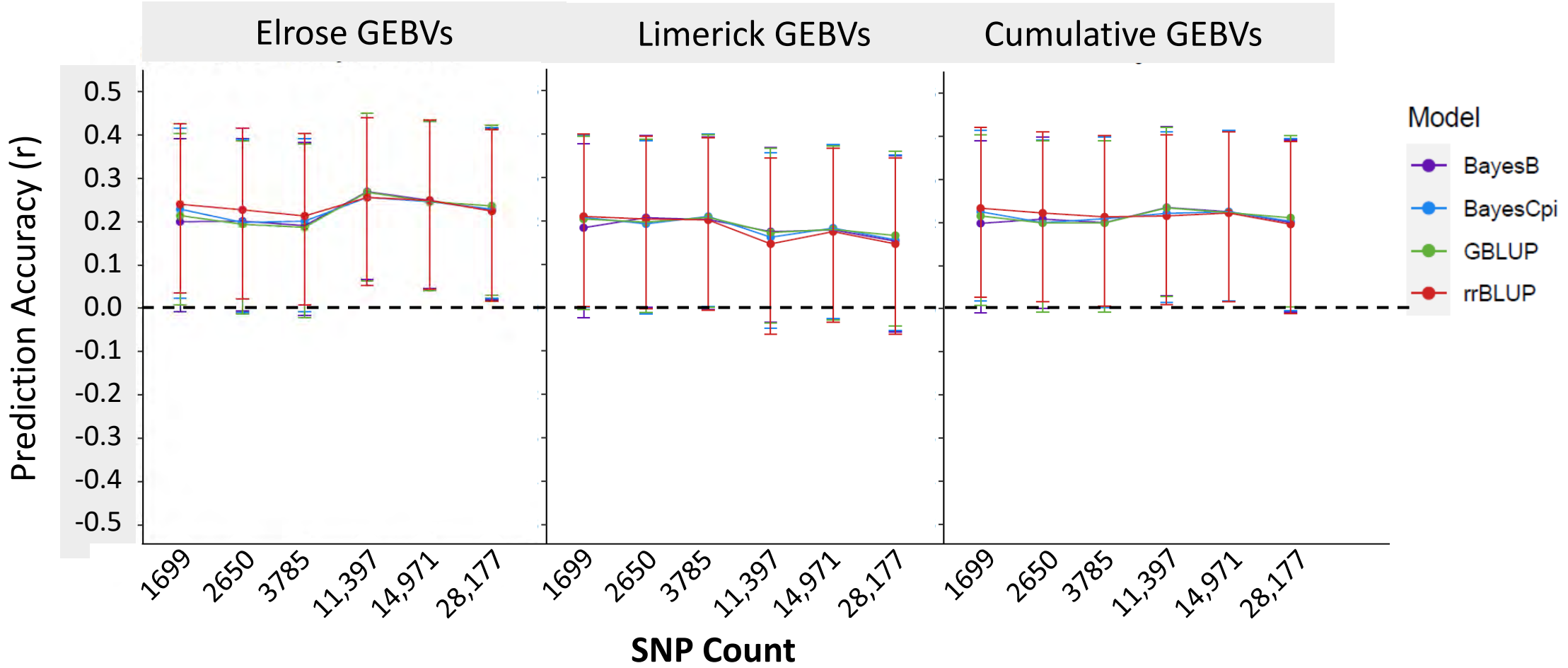
GS for protein → Zero prediction accuracy regardless of GS models and marker density





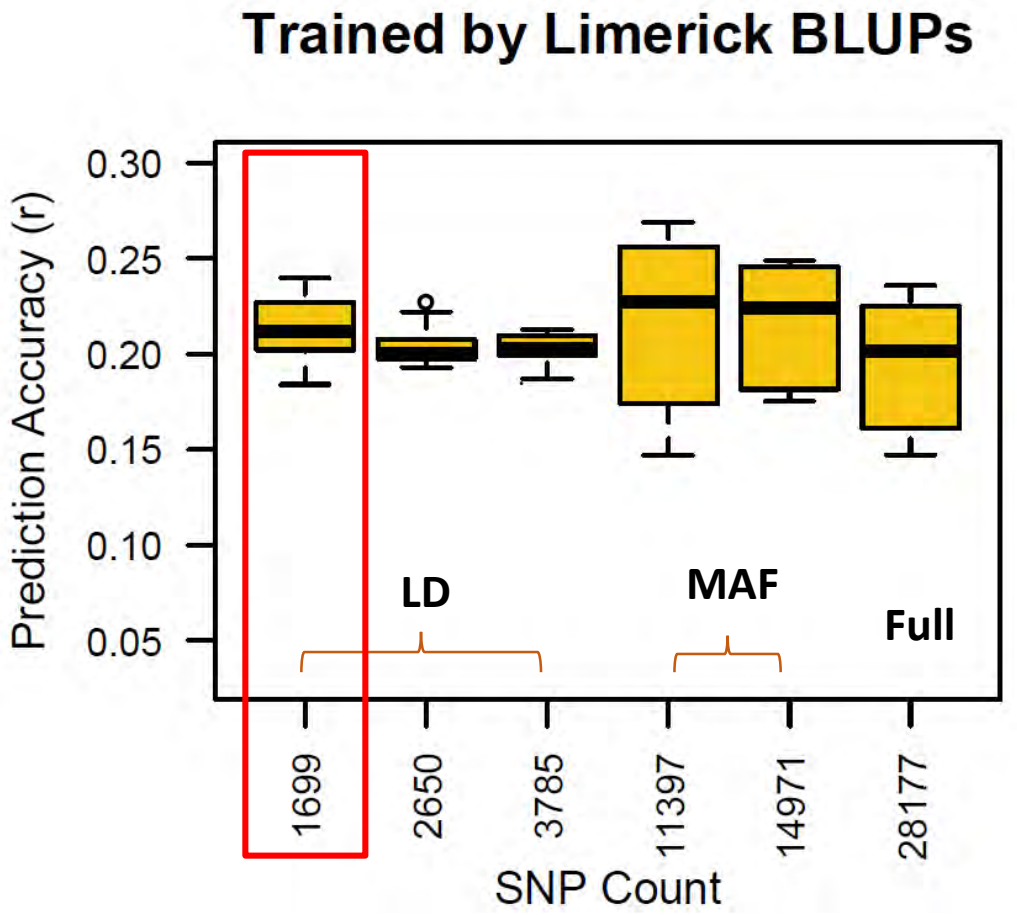
GS for Seed Oil

Oil with Models Trained Using Location BLUPs



Oil Prediction Models Accuracies

Limerick BLUPs predicting cumulative GEBVs at various SNP densities



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Article | Open Access | Published: 10 November 2021

A chickpea genetic variation map based on the sequencing of 3,366 genomes

Rajeev K. Varshney ✉, Manish Roorkiwal, Shuai Sun, Prasad Bajaj, Annapurna Chitikineni, Mahendar Thudi, Narendra P. Singh, Xiao Du, Hari D. Upadhyaya, Aamir W. Khan, Yue Wang, Vanika Garg, Guangyi Fan, Wallace A. Cowling, José Crossa, Laurent Gentzbittel, Kai Peter Voss-Fels, Vinod Kumar Valluri, Pallavi Sinha, Vikas K. Singh, Cécile Ben, Abhishek Rathore, Ramu Punna, Muneendra K. Singh, Bunyamin Tar'an, Chellapilla Bharadwaj, Mohammad Yasin, Motisagar S. Pithia, Servejeet Singh, Khela Ram Soren, Himabindu Kudapa, Diego Jarquín, Philippe Cubry, Lee T. Hickey, Girish Prasad Dixit, Anne-Céline Thuillet, Aladdin Hamwieh, Shiv Kumar, Amit A. Deokar, Sushil K. Chaturvedi, Aleena Francis, Réka Howard, Debasis Chattopadhyay, David Edwards, Eric Lyons, Yves Vigouroux, Ben J. Hayes, Eric von Wettberg, Swapan K. Datta, Huanming Yang, Henry T. Nguyen, Jian Wang, Kadambot H. M. Siddique, Trilochan Mohapatra, Jeffrey L. Bennetzen, Xun Xu & Xin Liu ✉ -Show fewer authors

Nature (2021) | Cite this article

Metrics

With Rajeev Varshney
Senior author

Highlights of the paper:

Developed Haplotype map in chickpea based on whole genome sequencing of 3,366 chickpea germplasm accessions including 195 accessions from seven wild species of the primary, secondary and tertiary gene pools

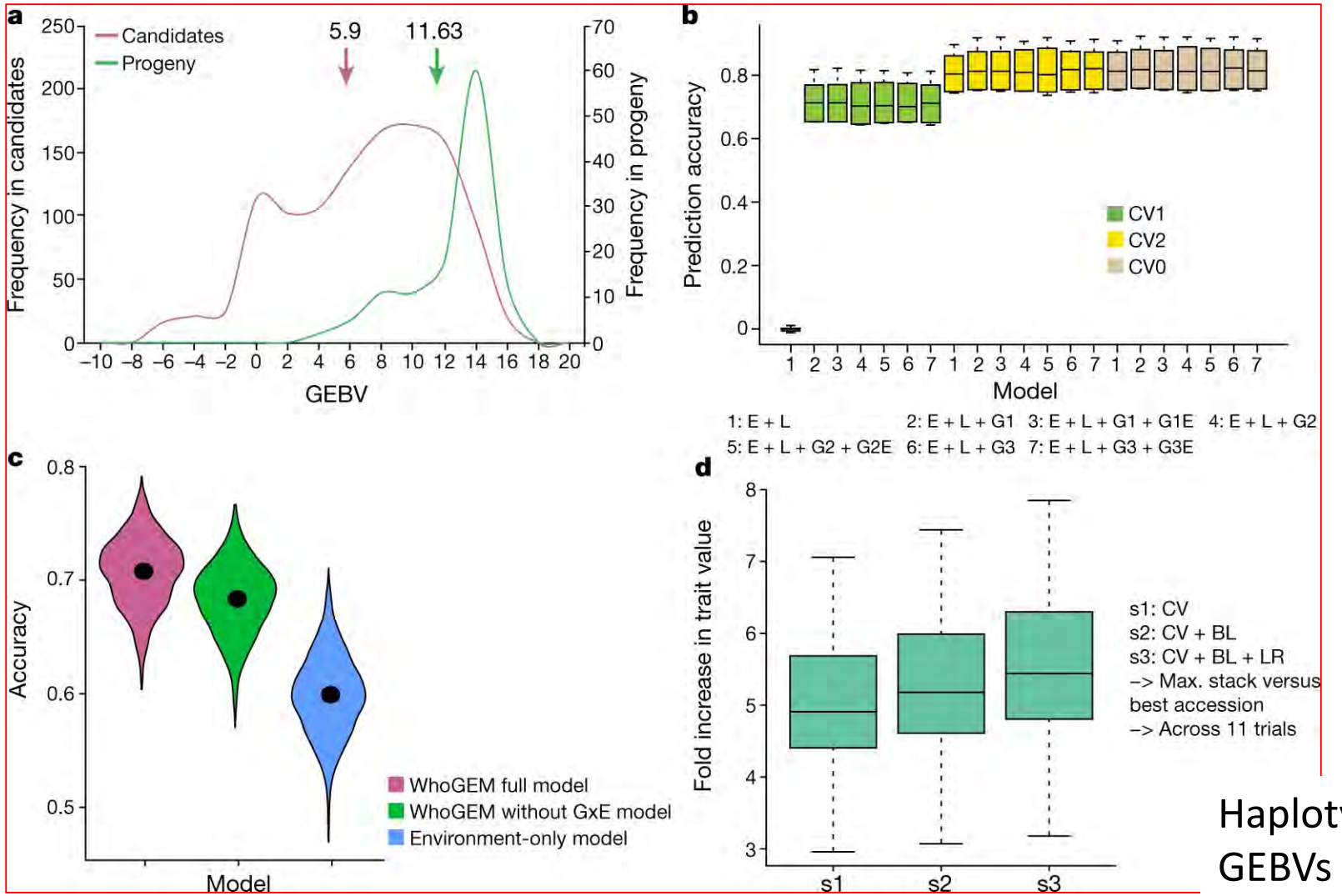
Developed Cicer pangenome based on the largest number of genotypes

Developed and optimized genomic breeding approaches, haplotype-based breeding, genomic prediction, and optimal contributions selection for developing tailor-made high yielding and climate resilient chickpea varieties.

Different strategies of genomic breeding for improving 100-seed weight in chickpeas.

Mean GEBV →23% increase in one generation for seed size.

A general linear model using the WhoGEM prediction machine →highest prediction accuracies for the full model (*n* = 1,500; 300 replicates of a fivefold cross-validation).



GEBV based on Bayesian generalized linear regression (BGLR) → highest prediction accuracy (*n* = 2,980 cultivated accessions).

Haplotype-based local GEBVs that are suggested to provide a fivefold gain over GEBV

Varshney et al. Nature (2021)

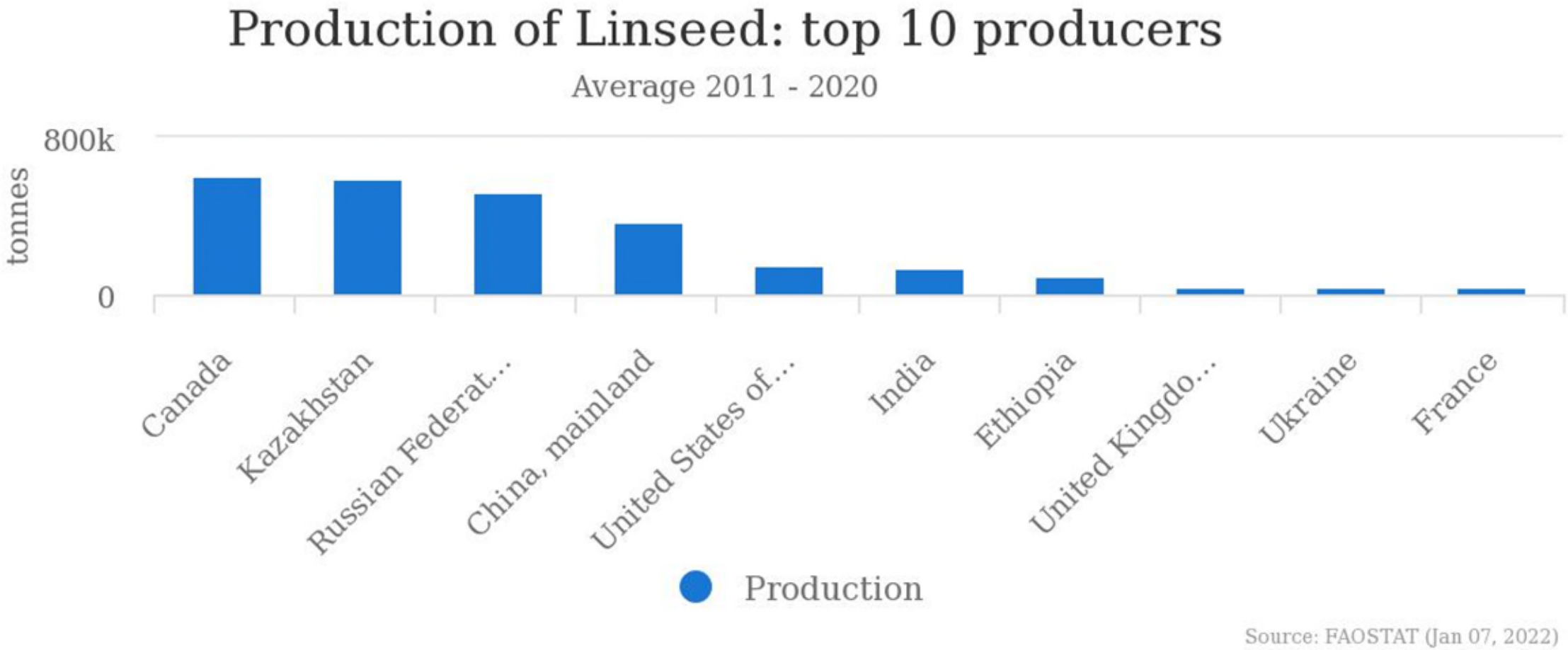
Flax Breeding and Genetics

Breeding objectives and goals:

- Yield
- Early maturity
- Disease resistances (maintenance and improvement)
- Straw management
- Lodging resistance
- Acceptable seed quality
- Abiotic stress tolerance

- Total oil Content ~50%,
- ALA: 60 - 70% of oil,
- High seed protein ~30% DSW (>60% of Meal)
- Plant stature

- Reducing anti-nutritional compounds (e.g. low **cyanogenic glycosides**)
- Low cadmium

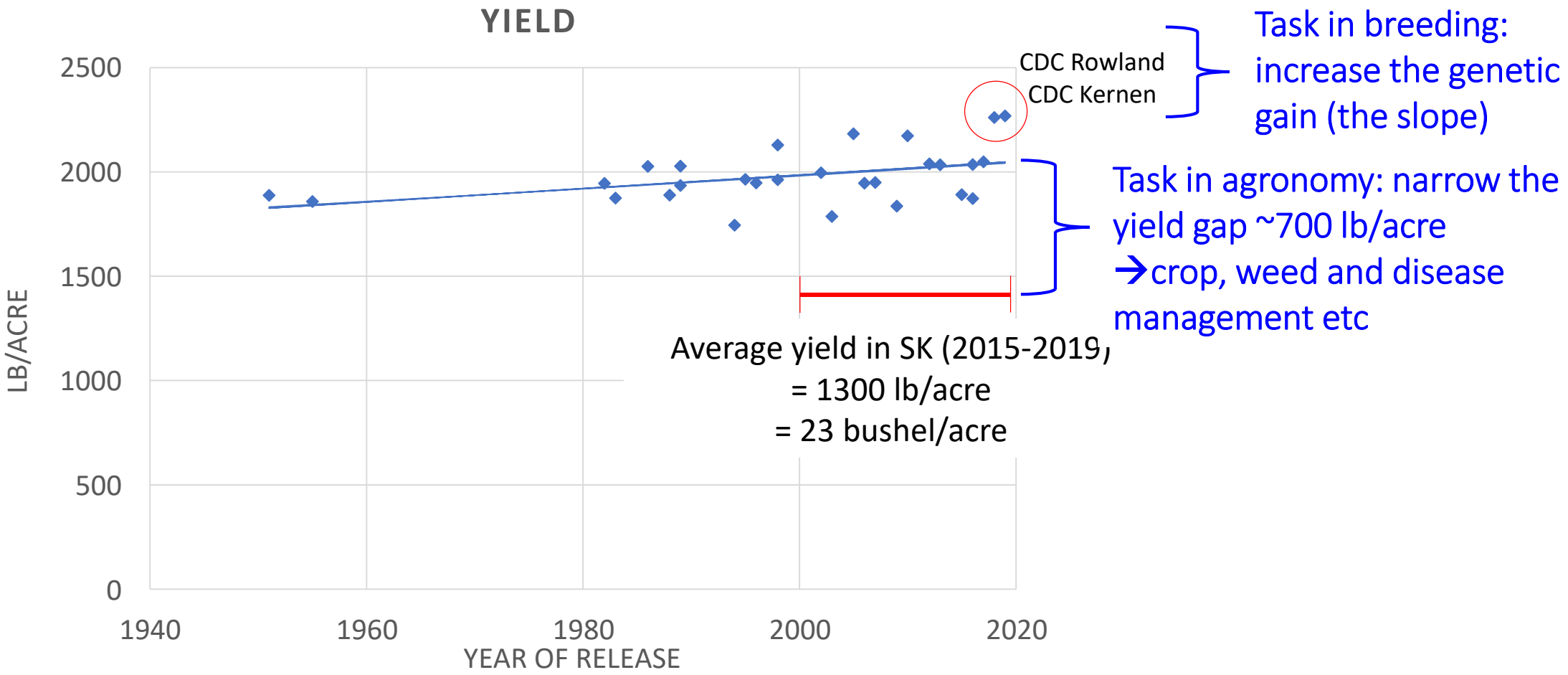

Production of Linseed: top 10 producers
Average 2011 - 2020
800k
tonnes
0
Canada
Kazakhstan
Russian Federat...
China, mainland
United States of...
India
Ethiopia
United Kingdo...
Ukraine
France
Production
Source: FAOSTAT (Jan 07, 2022)

Country	Average yield 2015-2020	
	(kg/ha)	(lb/acre)
Canada	1474	**1315**
China	1311	1170
United States of America	1289	1150
Russian Federation	868	774
Kazakhstan	823	734
India	540	482

→ Ideally: 1800 lb/acre

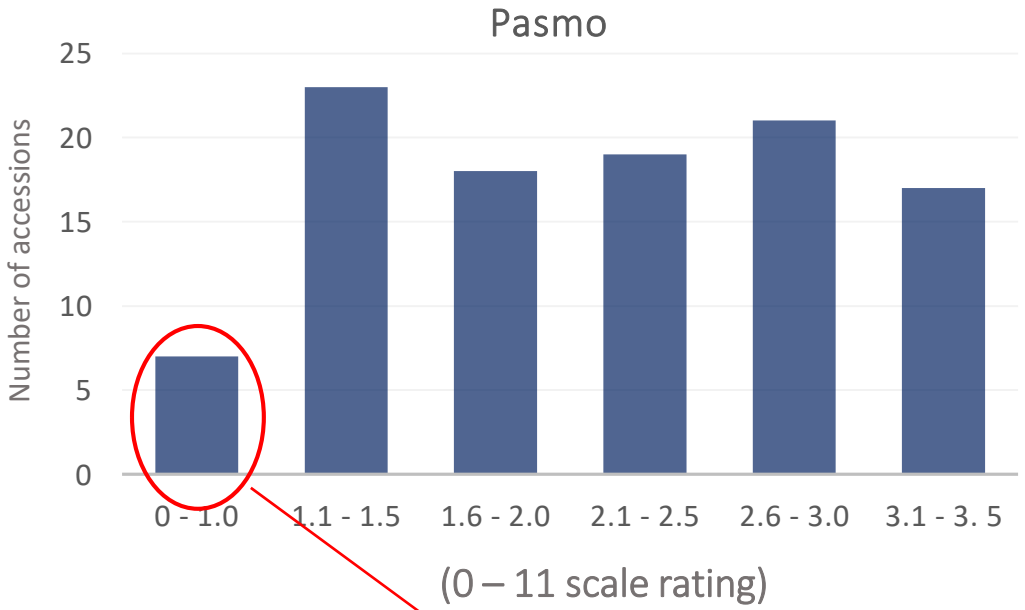
Source: FAOSTAT Jan 07, 2022

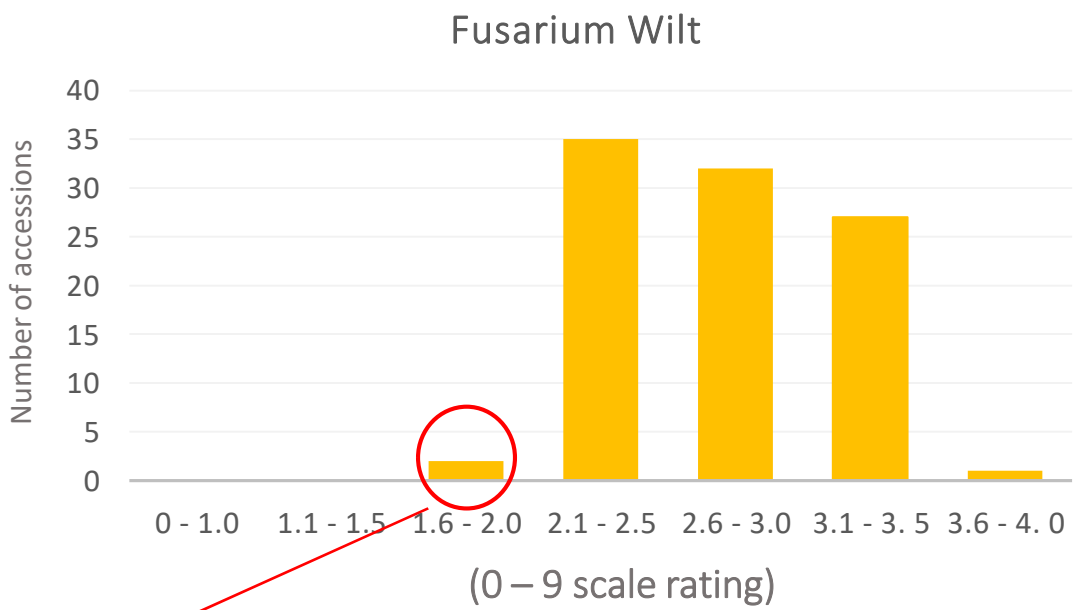
Average yield of the old and newer flax cultivars vs Average yield at farms in SK



Improvement of resistance to pasmo and fusarium wilt in flax (Q 2)

Frequency distribution of top 100 flax accessions from PGRC for their reaction to pasmo and fusarium wilt (average of 2014-2019 trials)





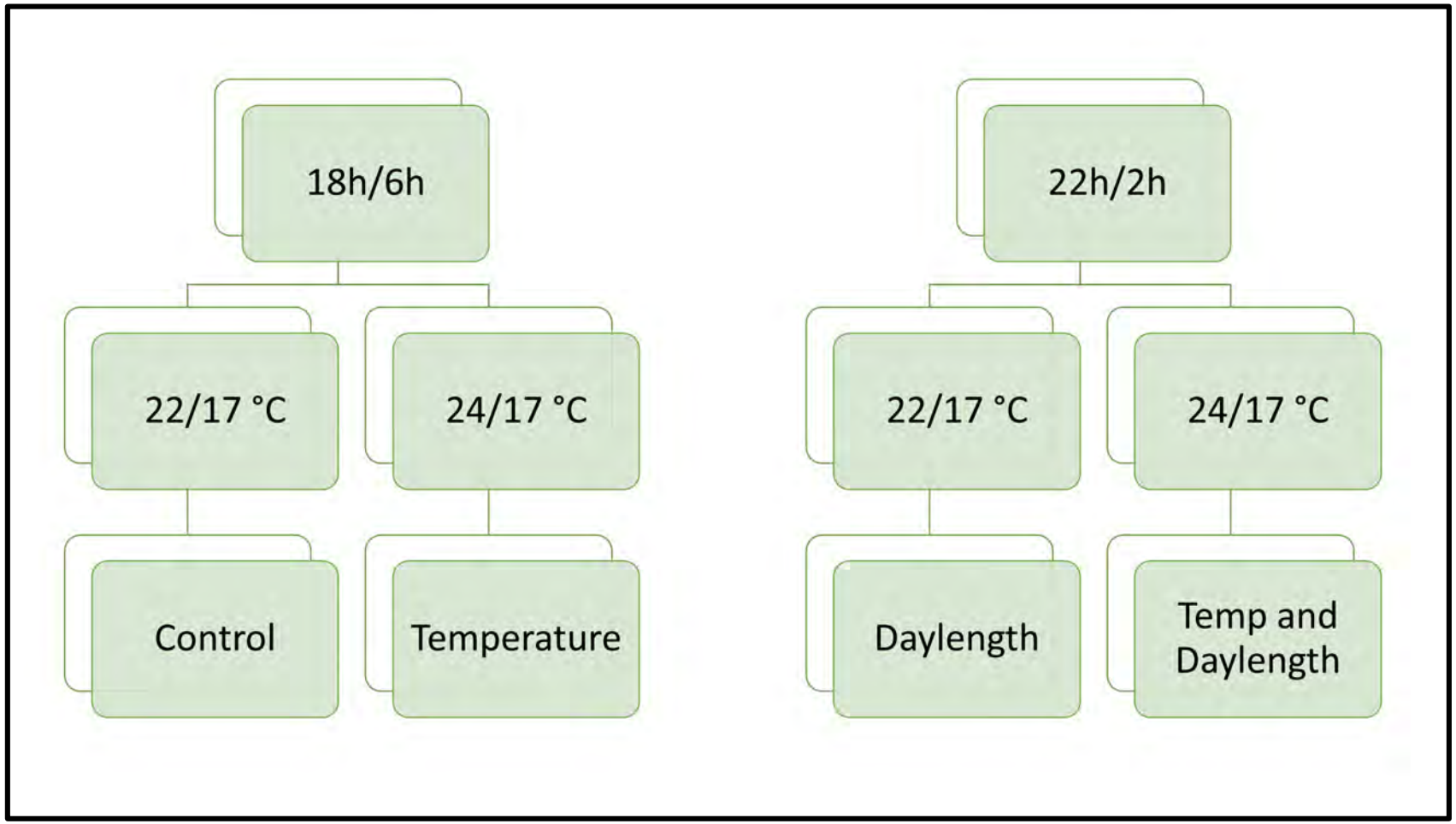
2020 crossing block

Pasmo: 65 populations
Fusarium wilt: 68 populations
2023: F4/F5 populations (KCRF)

Pasmo and fusarium wilt screening was done by the CDC Flax Pathology program (Dr. Randy Kutcher)

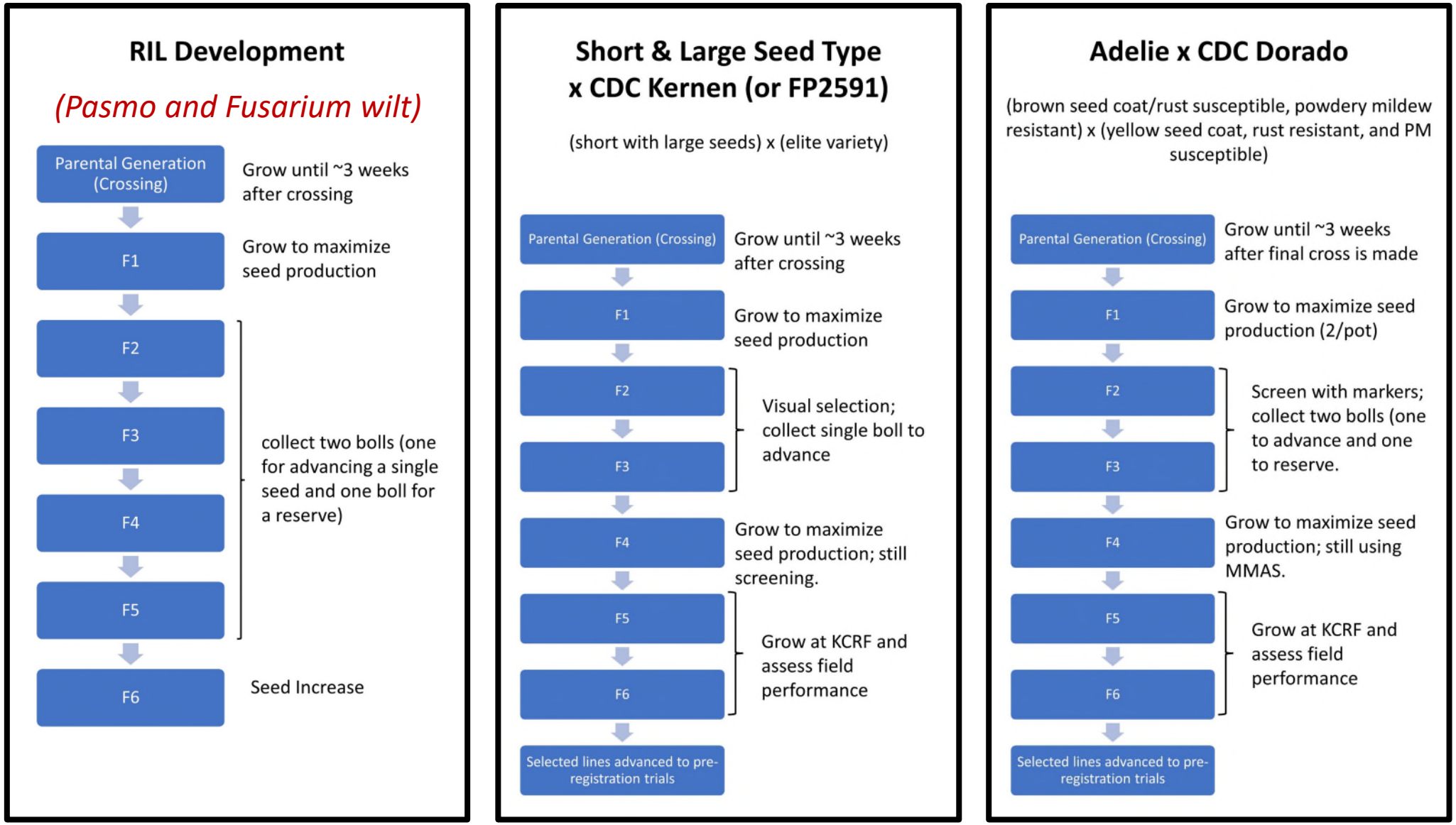
ADF#20210948 Accelerated Breeding Strategy for Flax Improvement (Matching funds: WGRF, SaskFlax, MCA)

Dr. Megan House
Research Officer



System optimization

ADF#20210948 Accelerated Breeding Strategy for Flax Improvement



Quick population development

Integration with phenotypic selection

Integration with MMAS

Mining wild relatives

Fiber → Seed

Seed

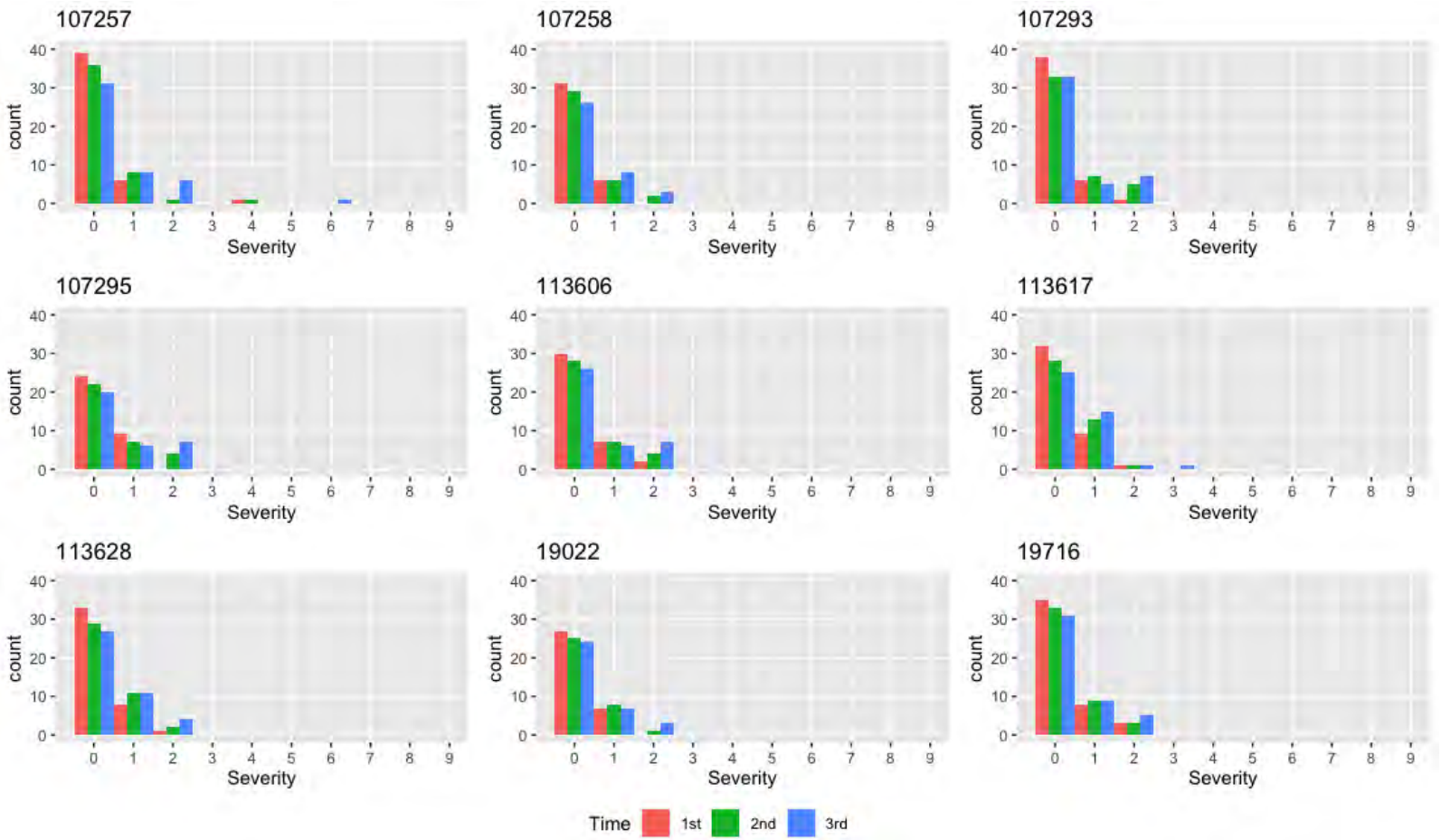
The Use of Wild *Linum* Species for Genetic Improvement of Resistance to Pasmo in the Cultivated Flax

- Expand germplasm base/increase diversity
- Source for disease resistance (pasmo)
- Source for abiotic stress tolerance
- Source for yield component improvement

Xinjie Yu
(PhD student)

Reaction to pasmo across 9 interspecific populations (2022 Field Trial)

- Source: Xinjie Yu (2023)



Boll dehiscence

- *L. bienne*

L. bienne

Accessions	Origin	Dehiscent Level
PGRC CN 107293	unknown	6
PGRC CN 113617	Turkey	7
PGRC CN 19022	Germany	7
PGRC CN 107295	Greece	8
PGRC CN 107258	unknown	8
PGRC CN 19716	Greece	8
PGRC CN 113628	Turkey	8
PGRC CN 113606	Turkey	8
PGRC CN 107257	unknown	9

- CDC Bethune

Rating scale:

Indehiscent

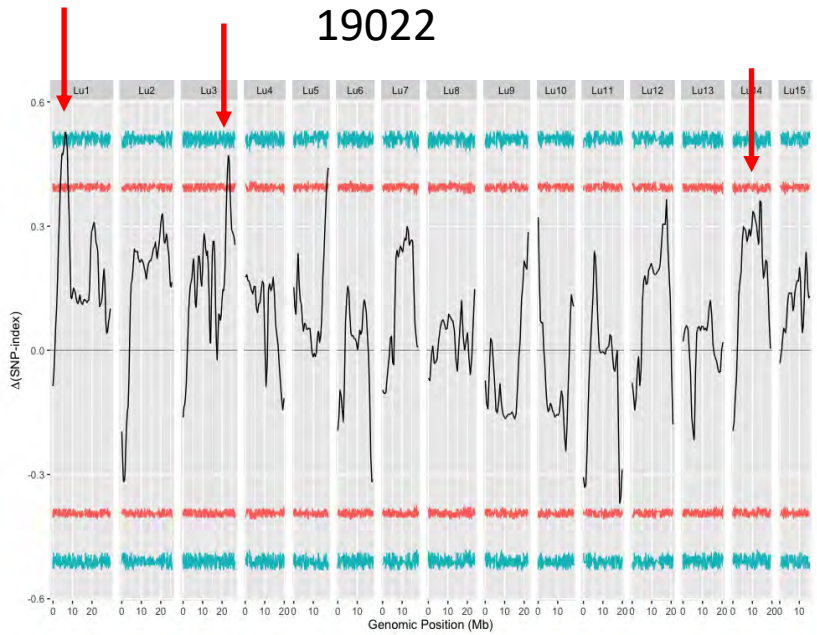
Dehiscent

1 → 10

Source: Xinjie Yu (2023)

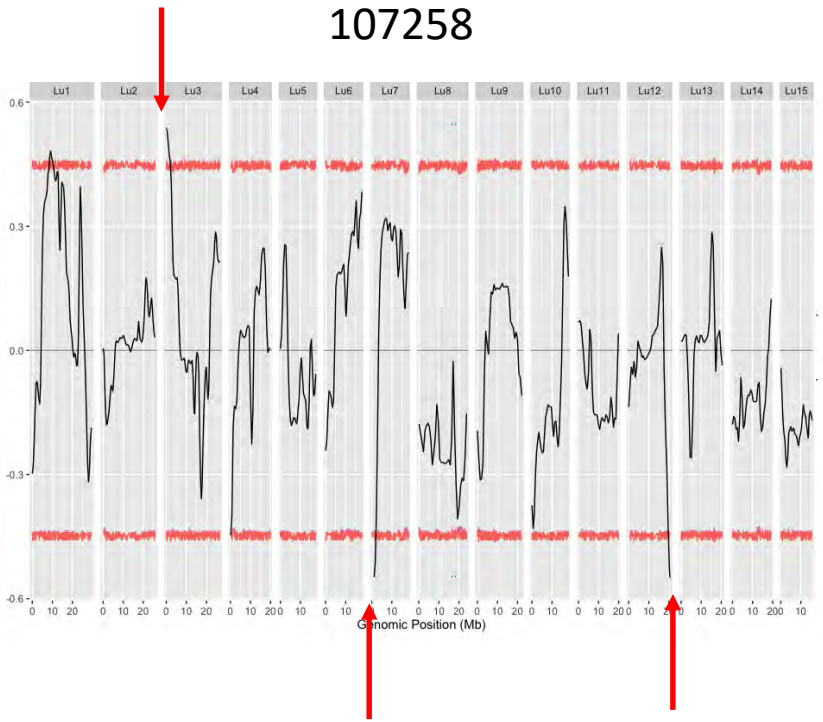
QTLs associated with boll dehiscence identified using bulked segregant sequencing

19022



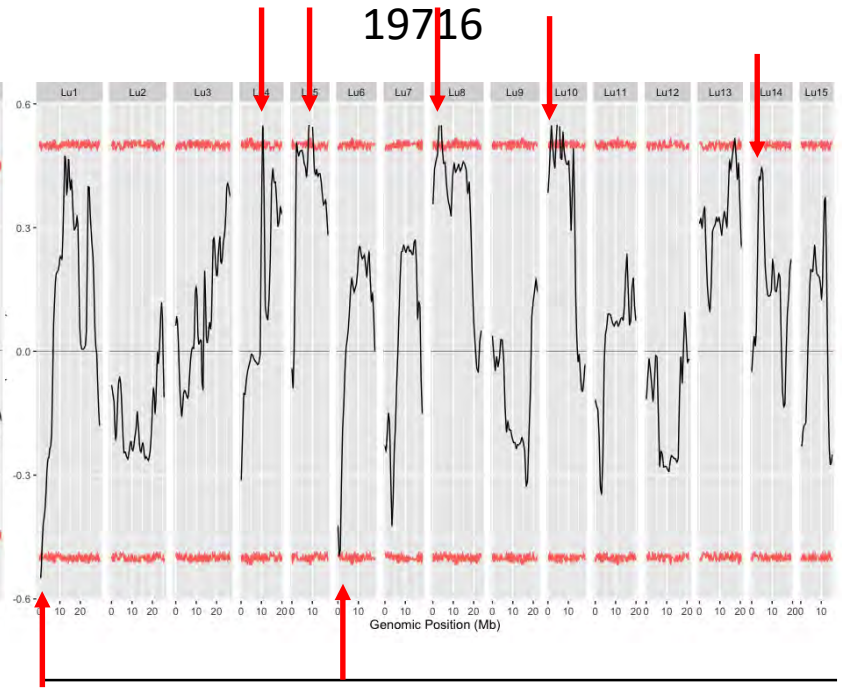
CHR	Start	End	Length
Lu1	4093034	7472902	3379868
Lu3	22519712	23959006	1439294
Lu14	13836257	14021155	184898

107258



CHR	Start	End	Length
Lu3	19754	872281	852527
Lu7	3623	1699825	1696202
Lu12	20132127	20887091	754964

19716



CHR	Start	End	Length
Lu1	619	3119648	3119029
Lu4	10210827	11409814	1198987
Lu5	1763828	14573220	12809392
Lu6	19257	1653184	1633927
Lu8	89398	7074836	6985438
Lu10	29193	10981877	10952684
Lu14	3600049	5885995	2285946

Source: Xinjie Yu (2023)

Breeding objectives

Coriander *Coriandrum sativum*

- Cultivated types can be divided into two classes on basis of seed size: small and large seeded. Small seeded type are highly aromatic vs less aromatic in large seeded type

Germplasm base development

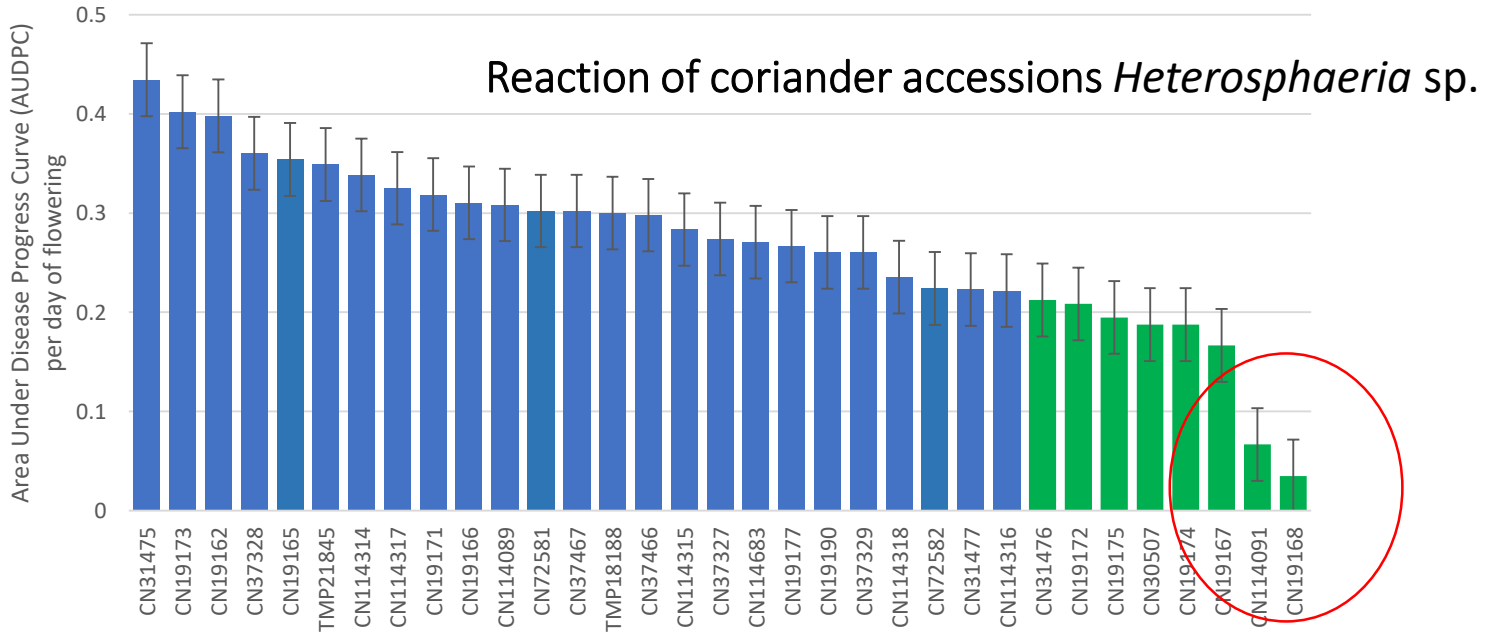
Improve resistance to blossom blight disease and yield

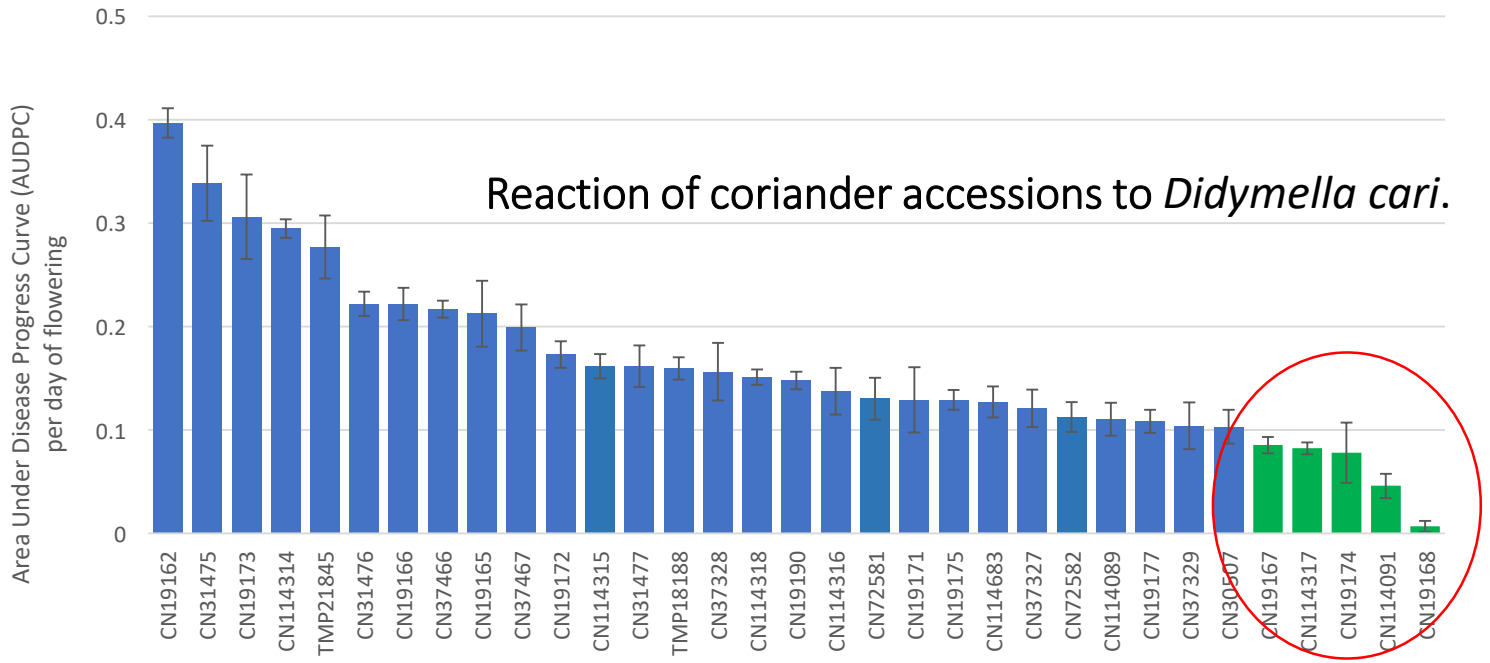
Essential oil content

Caraway *Carum carvi*

Development of germplasm base through mutation breeding

Genetic improvement of disease resistance in biennial caraway



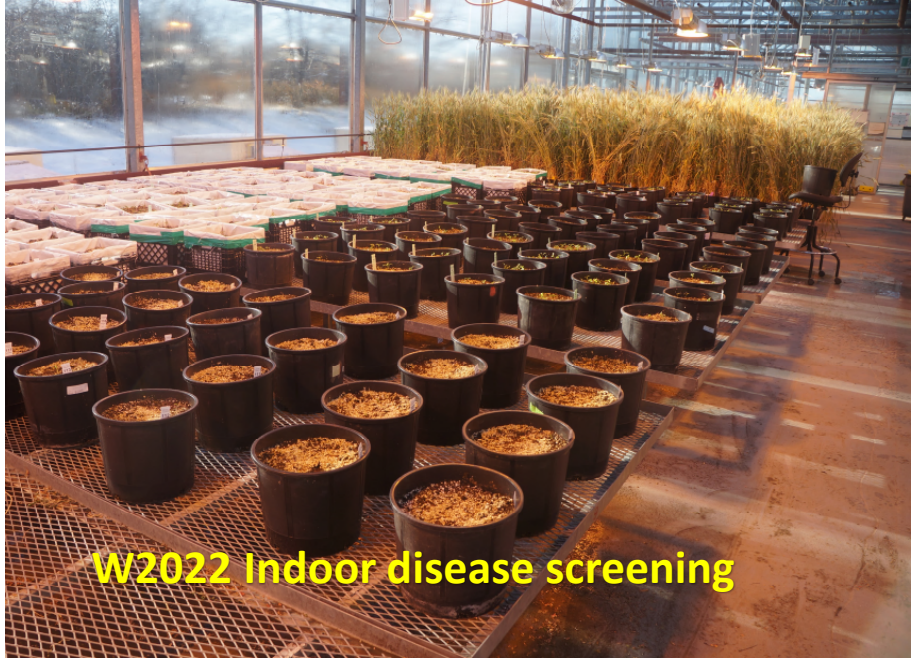


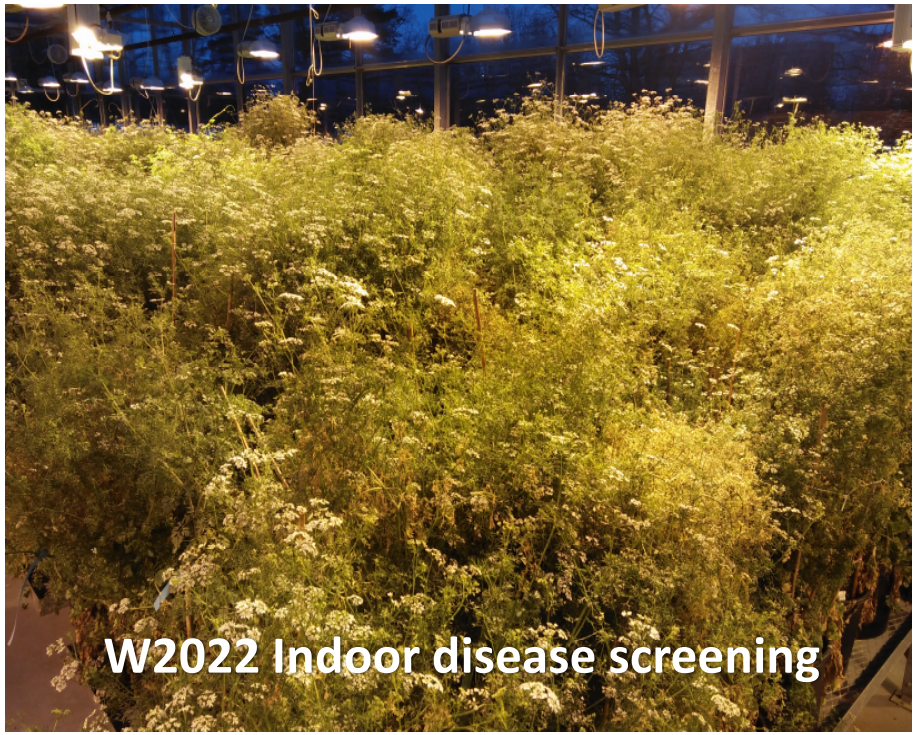
Crosses with current cultivars

Source: Armstrong-Cho, 2019

- Coriander crossing block
cross pollinated diploid species
(2n = 2 x = 22)


2021 disease screening

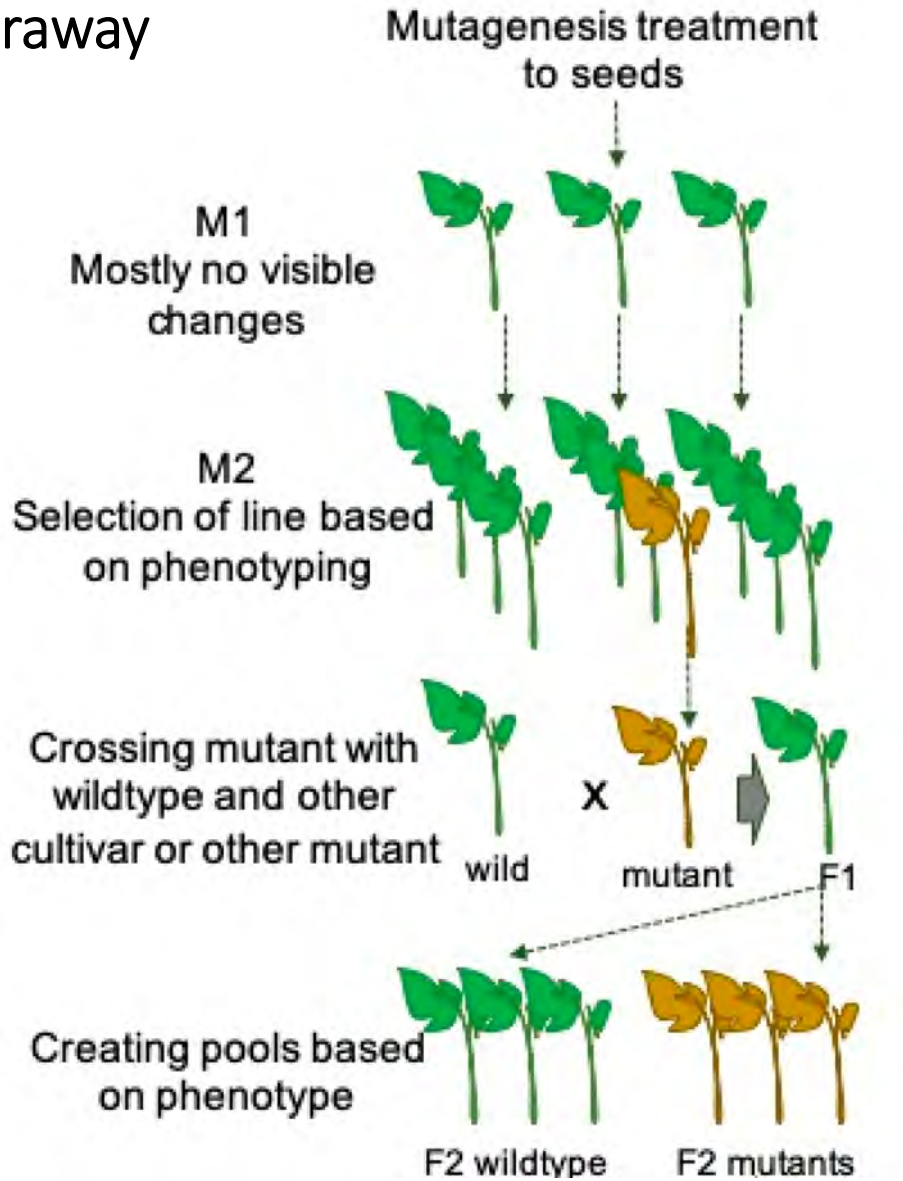

W2022 Indoor disease screening


W2022 Indoor disease screening


2022 Coriander disease screening : 300 Progeny Rows

Mutation breeding and pedigree selection for genetic improvement of disease resistance in biennial caraway

- Caraway (*Carum carvi* L., 2n = 2x = 20)
- Family: Apiaceae family (syn. Umbelliferae).



Caraway M1 population

(Photo taken 3 Dec 2021)

Acknowledgements

Saskatchewan

SASKATCHEWAN pulse Growers

WGRF
Advancing Agriculture through Research

SaskFlax

SeCan
Canada's Seed Partner

DFCC
DIVERSE FIELD CROPS CLUSTER

MANITOBA CROP ALLIANCE

Agriculture and Agri-Food Canada

Thank You !

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