Yield10 BIOSCIENCE

www.yield10bio.com

NASDAQ: **YTEN**

Strategies for Increased Seed Oil in Camelina

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2023 AOCS Annual Meeting & Expo

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Sustainable Growth Starts with a Seed

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*Under the Private Securities Litigation Reform Act of 1995

Yield10's Trait Factory

From Crop Science to Market

Technology Platform - "Trait Factory"[1]

GRAIN 3.0

CRISPR editing

Camelina

Genetic Engineering

GMO

Camelina Seed Products

1. **Feedstock Oil (Biofuel)**
2. **Omega-3 Oil (EPA+DHA)**
3. **PHA Bioplastics**

[1]21 Patent Families Pending

Why Camelina?

- Promising oilseed crop
  - Seed oil levels ~ 40% of seed weight
- Both spring and winter varieties
  - Winter varieties, potential use as cover crop for corn and soybean acres
- Doesn't outcross with canola
- Excellent platform crop for novel high value seed products - value proposition for farmer

Greenhouse grown Camelina

Camelina field plots at flowering

Large scale winter Camelina growth

Yield10 Camelina Review: *Camelina sativa*, an oilseed at the nexus between model system and commercial crop. Malik et al., Plant Cell Rep., 2018

Camelina Based Biofuel Feedstocks

The Potential of the Camelina Crop for Biofuel Feedstocks is Driven by:

Grower adoption – Weed control and seamless integration into crop rotations

Grower adoption & business success – Revenue - increasing harvest value for biofuel feedstocks

- Camelina grain (seed) yield per acre, oil as a percent of seed weight (oil/acre)
- Carbon intensity (CI) score of the oil **(carbon score as a trait target?)**
- Improved protein meal value

Grower adoption & business success – Partnerships across the biofuel value chain

Yield10 has pipeline of Camelina lines and proprietary gene traits to increase value of Camelina

Priority 1: Herbicide tolerant Camelina to enable seamless integration into grower crop rotations

Priority 2: Seed yield and seed oil content to increase the harvest value for biofuels

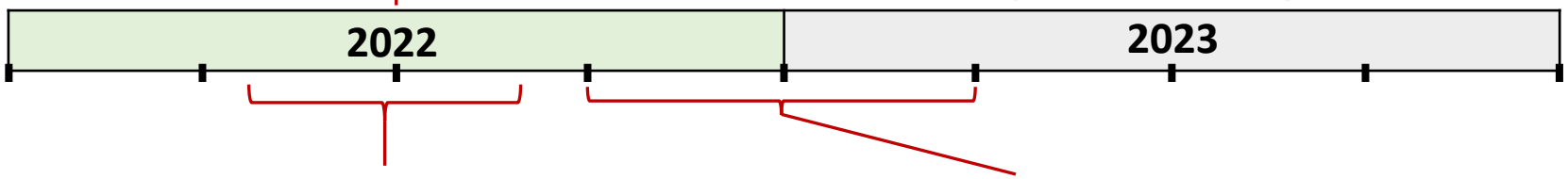
Priority 3: Meal quality traits to improve meal value

Over-the-top Broad Leaf Weed Control for Camelina

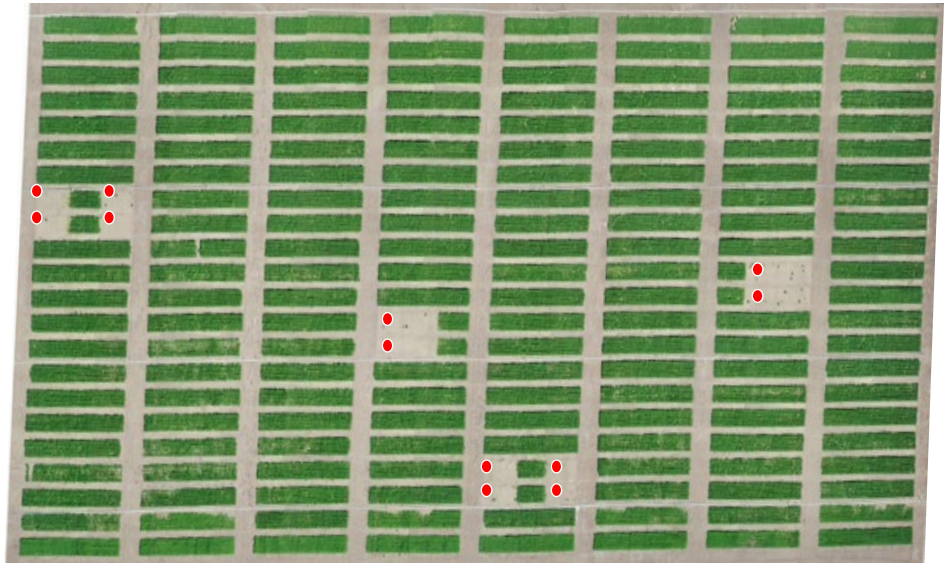
Yield10 is developing elite Camelina containing a robust weed control package for farmers

✓ Filed USDA-APHIS Regulatory Status Review (RSR)

Multi-site spring trials and seed increase of lead event



✓ Spring research field trial – *robust herbicide tolerance*

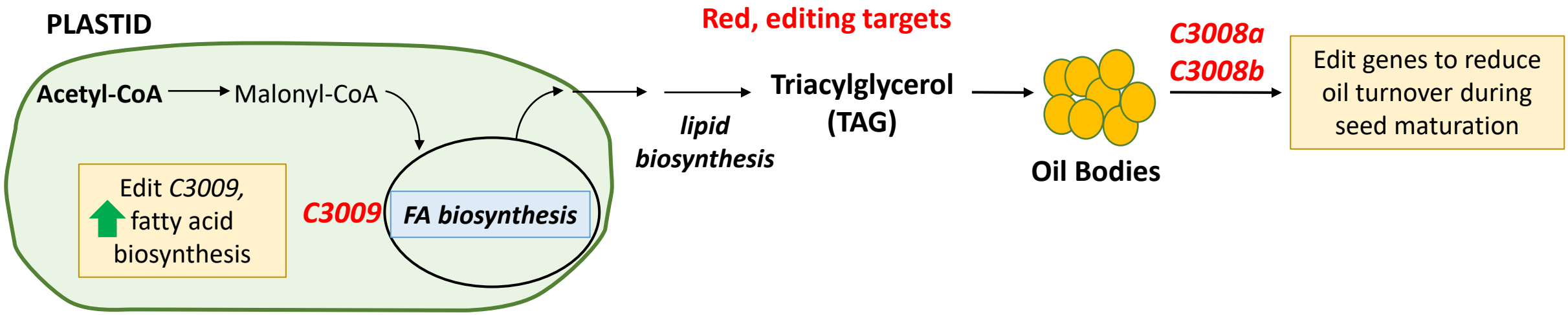


Red dots: control plots that died with herbicide application

✓ Contra-season trial: *robust herbicide tolerance of lead event*

Gene Combinations to Increase Oil Content

Strategy 1: Increase oil biosynthesis and prevent oil turnover[1]



1. C3009 - transcription factor target to upregulate fatty acid biosynthesis

— regulation of embryo fatty acid biosynthetic genes, + regulation of genes responsible for pigment in seed coat

2. C3008a and C3008b - gene targets to reduce oil turnover during seed maturation

C3008a and C3008b, oil body associated lipases

[1]Editing work supported in part by U.S. Department of Energy BETO, Grant No. DE-EE0007003

Multiplex Genome Editing of Three Genes in Camelina

Editing of lipase genes (*C3008a, C3008b*) and transcription factor gene (*C3009*)

- Identified best Camelina orthologs to Arabidopsis genes based on homology
- Simultaneous editing of 9 genes (3 target genes present in 3 copies each) using CRISPR
- Lines with different combinations of edits obtained and characterized
  - *Very difficult to get all 9 gene copies edited in same line, only one line obtained with all 9 genes edited*

- Fully edited *C3009* gene, loss of pigmentation in seed coat
  - ***Unique distinction to track edited seed***

Wild-type control

C3009 100% edited *(yellow seeded)*

Field Tests of E3902 Edited Line

Received 2018 confirmation[1] that USDA-APHIS does not consider lines to be regulated[2]

2019 field test of edited lines at site in US

(randomized complete block design, lines replicated 6 times)

- E3902 oil trait stable in 2019, 2020 and 2021 field trials
- Completed multi-site 2022 field tests
- E3902 is germplasm background for our herbicide tolerant line

2019 Field Data for E3902

% Increase, oil per individual seed (mgs)	% Increase, individual seed weight *(mgs)*	% Increase, seed yield *(calculated kg seed per hectare)*	% Increase, seed oil content *(% of seed weight)*	% Increase, number of seeds harvested	% Increase, calculated total oil produced per hectare
11.8*	8.7*	9.7	4.7*	- 3.7	15.0

Patent pending

**statistically significant (t-test)*

[1]Former USDA-APHIS "Am I Regulated Process"; [2]Pursuant to 7 CFR part 340*

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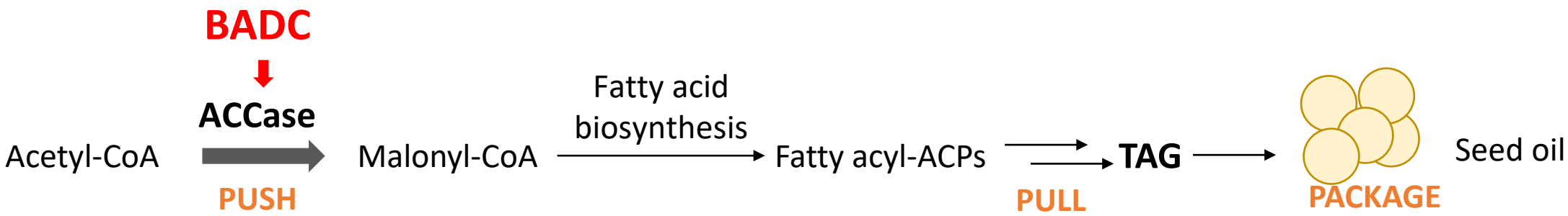
Gene Combinations to Increase Oil Content

Strategy 2: Edit a negative regulator of acetyl-CoA carboxylase (ACCase)

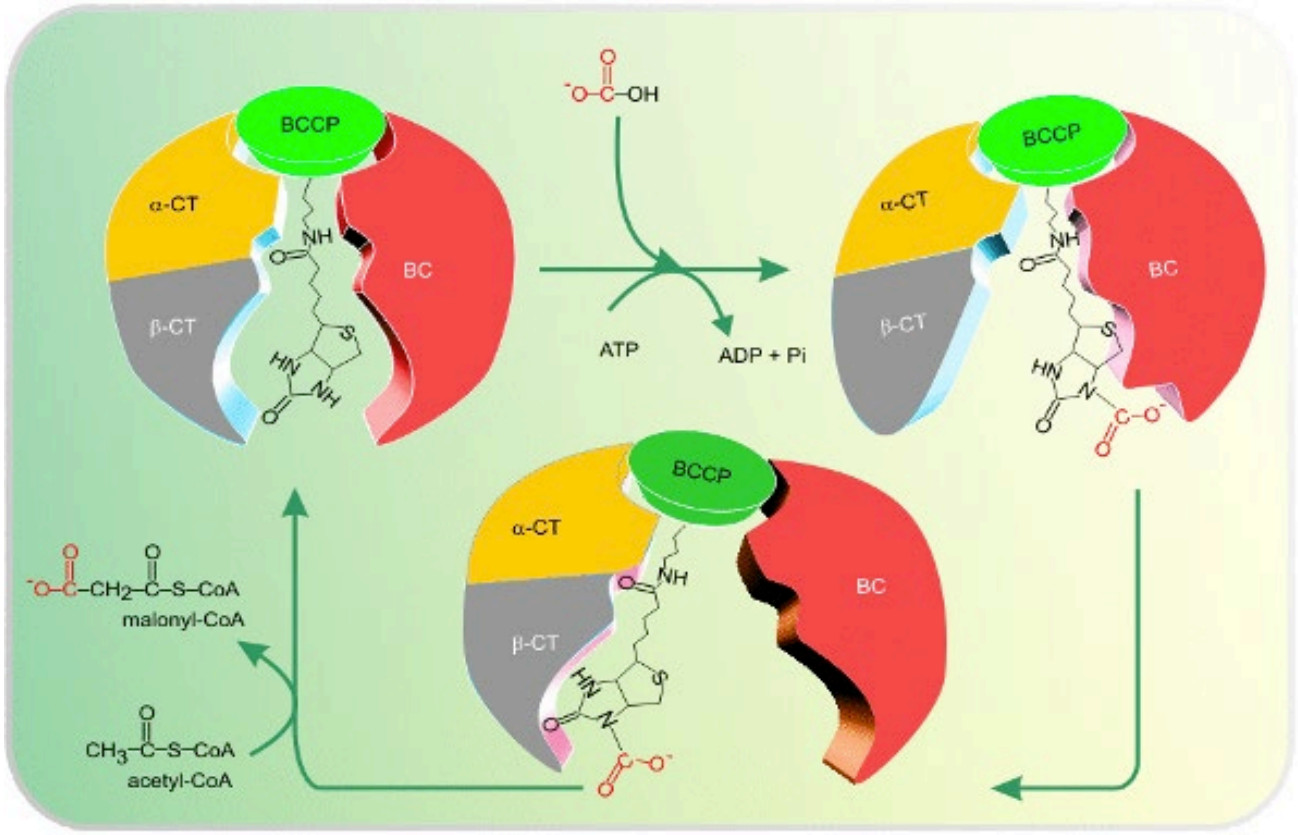
- ACCase - considered to be rate-limiting step in fatty acid biosynthesis
- **Jay Thelen** (University of Missouri) identified role for BADC as a novel negative regulator of the heteromeric ACCase



C3007 (BADC) trait in-licensed from University of Missouri

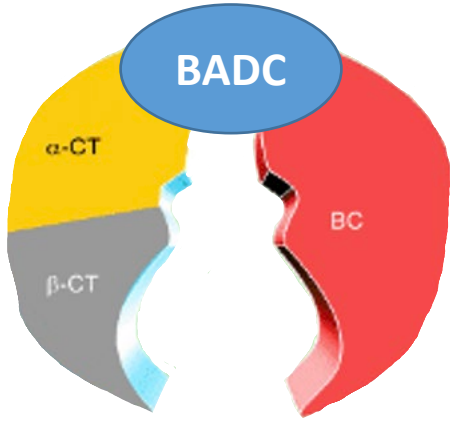
BADC can displace BCCP, but lacks active site motif

Active heteromeric ACCase with BCCP and biotinylation motif in active site



Li-Beisson Y et al., (2013) Acyl-lipid metabolism. Arabidopsis Book 11: e0161

Inactive heteromeric ACCase, BCCP displaced by BADC



No biotinylation motif essential for ACCase enzyme activity

Reduce/eliminate BADC with genome editing to increase ACCase activity

BC: biotin carboxylase; **BCCP: biotin carboxyl carrier protein;** α-CT: α-carboxyltransferase; β-CT: β-carboxyltransferase

Genome Editing of *badc* Genes

Species	Ploidy/genome	# of BADC homologs
Arabidopsis	2n=2x, diploid	**3** *(badc1, badc2, badc3; Salie et al.)*[1]
Camelina	**2n=6x, hexaploid (Cs-G1, -G2, -G3)**	**9 (3 *badc1*, 3 *badc2*, 3 *badc3*) (1 copy on each subgenome; *Yield10*)**[2]

Work at Yield10 to edit *badc* in Camelina

- Identified 3 Camelina *badc* genes (9 alleles total)
- Obtained stable edits for select *badc* genes/gene combinations
  - **Complete editing of all alleles was not obtained, possibly lethal**
- Crossed lines edited in all 3 copies of *badc1* with lines containing combinations of *badc2* or *badc3* edits
- Field trials completed in 2022

[1]**Salie et al**., 2016, Plant Cell, 28, 2312. [2]Camelina genes identified at Yield10

Field Trial of Edited *badc* Lines

Lines tested in field trial

Entry	*badc1*	*badc2*	*badc3*
E4757	X X X		
E4724-C	X X X		
E4806-B	X X X		
E4816-A	X X X		
WT43-F	_ _ _	_ _ _	_ _ _
E6146	X X X	X X _	
E6154	X X X	X X _	
E6119	X X X		X X _
WT43-G	_ _ _	_ _ _	_ _ _

" X " denotes gene is edited; " _ " denotes wild-type gene; Control line.

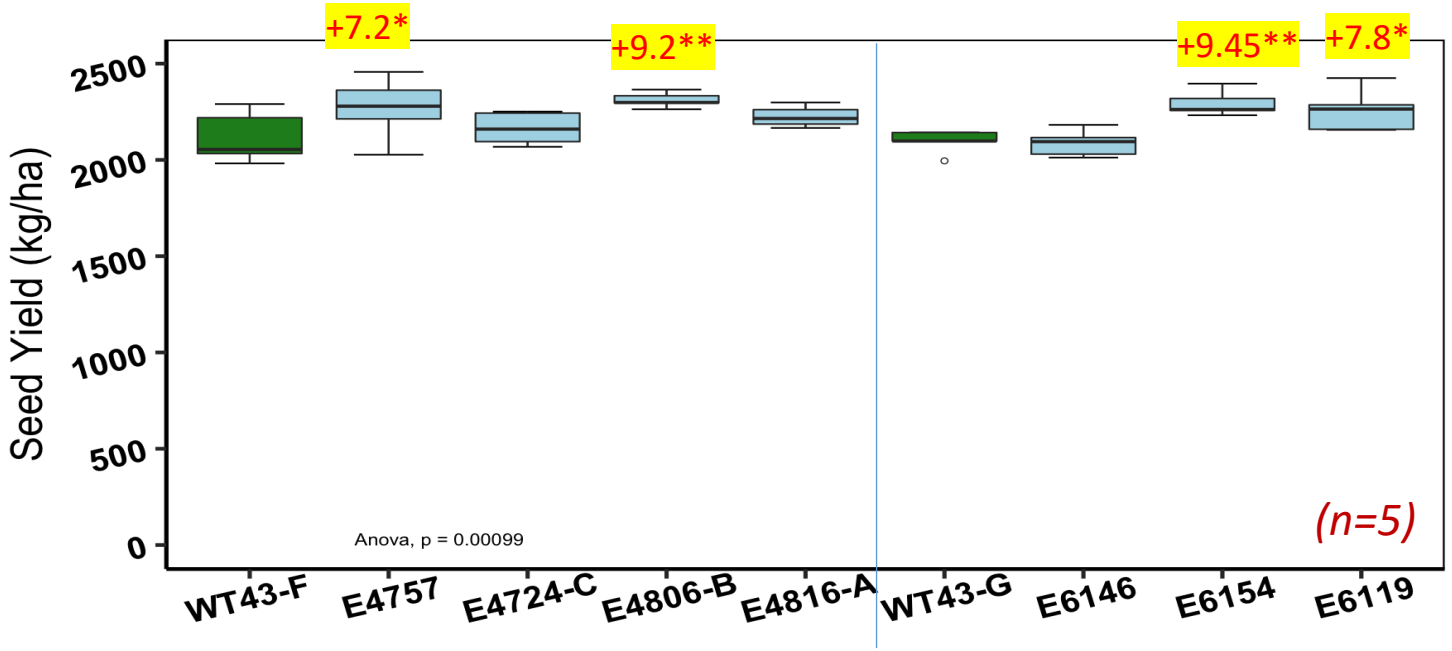
US field site (July 14, 2022)

plots (63 days old)

Field trial drone photo

Spring 2022 Camelina C3007 Field Trial – Seed Yield

Seed Yield of C3007 Edited Lines, Measured in Replicated Plots



T-test. *, $p < 0.05$; **, $p < 0.001$.

Lines tested in field trial

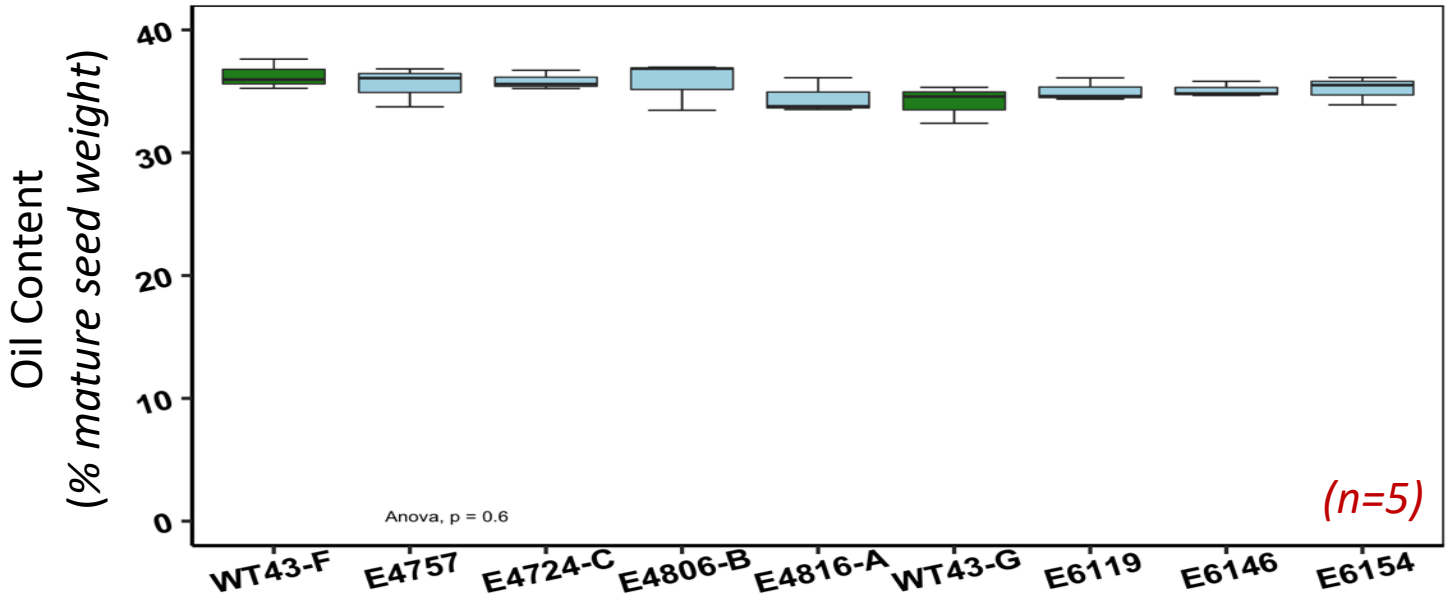
Entry	BADC1	BADC2	BADC3
E4757	X X X		
E4724-C	X X X		
E4806-B	X X X		
E4816-A	X X X		
WT43-F	_ _ _	_ _ _	_ _ _
E6146	X X X	X X _	
E6154	X X X	X X _	
E6119	X X X		X X _
WT43-G	_ _ _	_ _ _	_ _ _

" **X** " denotes gene is edited; "_" denotes wild-type gene; Control line.

Significant yield increase observed for four C3007 (*badc*) edited lines

Spring 2022 Camelina C3007 Field Trial – Seed Oil Content

Seed Oil Content of C3007 Edited Lines, Measured from Replicated Plots



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Lines tested in field trial

Entry	BADC1	BADC2	BADC3
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E4806-B	X X X		
E4816-A	X X X		
WT43-F	_ _ _	_ _ _	_ _ _
E6146	X X X	X X _	
E6154	X X X	X X _	
E6119	X X X		X X _
WT43-G	_ _ _	_ _ _	_ _ _

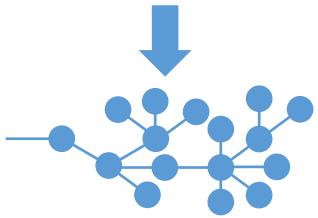
" X " denotes gene is edited; "_" denotes wild-type gene; Control line.

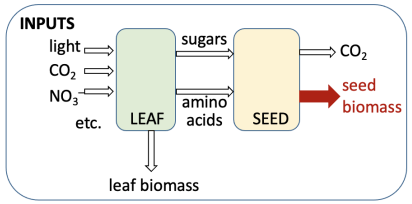
- **No significant change in oil content observed in C3007 (*badc*) edited lines**
- ***badc* edits analyzed increase seed yield but not seed oil content**
- **Field trials to be repeated in spring 2023**

GRAIN 3.0: Identify Unique Gene Combinations for a Trait

How do you move beyond known genes and identify new combinations?

CROP SPECIFIC GENOMICS DATA

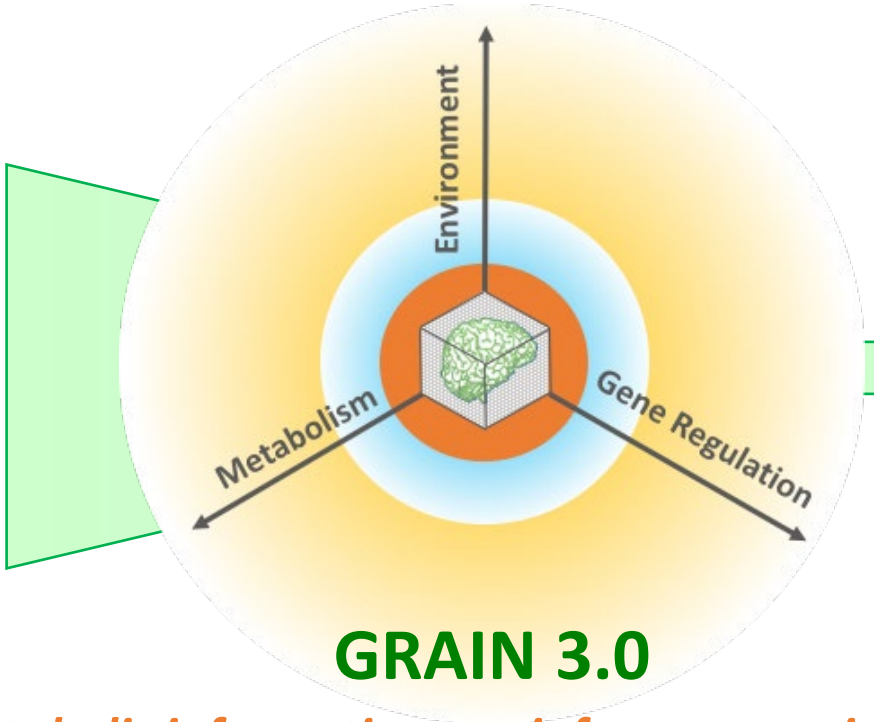




REGULATORY MODELING

METABOLIC MODELING

FAST FIELD TESTING



Actionable gene modifications leading to valuable, novel yield traits

Metabolic information can inform genomic decisions

Yield10 Review Paper on Metabolic Engineering in Plants: Skraly et al., Metabolic engineering to increase crop yield: From concept to execution, 2018, Plant Science

GRAIN Identified New Gene Targets: C3019 –C3022

GRAIN - Search for transcription factors (TFs) to increase seed oil content in Camelina

Ranked List of Gene Targets

211 Identified TFs	
TF1 = WRI1	TF9
TF2 = WRI1	TF10
TF3 = WRI1	TF11
TF4 = MYB56	TF12
TF5	TF13
TF6	TF14
TF7	TF15 = MYB56
TF8	TF16 ….

Proprietary ranking procedures

25 TFs

Most relevant, least studied

4 TFs

Overexpression of TFs

Trait	Effect
C3020	+10% oil
C3019	Negative
C3021	Negative
C3022	Negative

- Ranked list of TFs obtained - Includes known genes in top spots validating approach (WRI1, MYB56)
- Many uncharacterized genes identified, IP white space
- Overexpression of C3020 increases seed oil content by up to 10%, validated in 2021 and 2022 field seasons.
- Genes overexpressed giving a negative phenotype are good editing targets C3019, C3021 and C3022
- Editing of C3021 is completed, data analyses in progress

- Yield10 now has ~10 Camelina gene targets for combinatorial editing to achieve step change increases in oil

Camelina Based Biofuel Feedstocks

Yield10 is Harnessing The Potential of Camelina for Biofuel Feedstocks

Grower adoption – Weed control

- → *Developed and field-tested herbicide tolerant lines for over-the-top spray weed control*
- → *Field trials of next generation stacked herbicide tolerance lines (over-top-spray & soil residue tolerance) in spring 2023*

Grower adoption & business success – Revenue – increased harvest value for biofuel feedstocks

- → *Edited E3902 line has ~5% increase in oil in multiple years of field trials*
- → *Additional testing of badc edited lines that have shown increased seed yield in the field - in progress*
- → *GRAIN modeling has identified additional genes to increase oil content*
- → *Improved protein meal value: Gene editing targets have been identified*

Grower adoption & business success – Partnerships across the biofuel value chain

- → *Discussions with potential partners in progress*

Establishing the Camelina Biofuel Value Chain

Elite Camelina Variety Development- Contract Farming → **Logistics/ Crushing** → **RD or SAF Production**

Vision for the Business

- Gain leadership position for Camelina as a low-carbon feedstock oil
- Contract with growers for large scale production
- Build a network of alliances for contract offtake for biofuels and feed

Development Highlights and Milestones

- Marathon Petroleum LOI to produce Camelina for feedstock oil offtake
- Mitsubishi Corp MOU for feedstock oil supply for biofuel
- American Airlines MOU to develop value chain for Camelina in SAF
- Signed offtake agreement with privately owned crusher/biorefiner in a target growing region providing a customer for Camelina grain
- Engaged with additional players in biofuels supply chain
- Progressing early commercialization

Mitsubishi Corporation

American Airlines

MARATHON

Privately owned offtake partner for Camelina grain in key growing region

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Thank you!

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