T3 Status

Wheat **Coordinated** Agricultural Project

- One of the coordinations has to do with getting the data together in one place to enable more powerful analyses
- We want to make that as easy as possible
- The recurring thorn is line **names**
 - Matching across trials
 - Matching in phenotyping and genotyping trials
 - Matching in phenotyping trials and UASHub images
- Matching takes some effort up front
 - But it simplifies all analyses thereafter

WheatCAP phenotype data in T3 for 2022

	Number of new trials	With phenotype data	With field map
Cornell	1	1	1
Kansas State	5	0	5
Montana	1	0	0
Purdue	3	3	3
TAMU	3	0	3
UC Davis	19	18	19
Idaho	1	1	1
Illinois	56	54	54
ARS Kansas	8	8	0
Utah	7	0	7

Field Trial

Phenotyping projects are public 2 years after they have been loaded into the WheatCAP site. These projects are then moved to wheat.triticeaetoolbox.org.

Show 10 \sim entries							S	Search:		
Trial name	Description	Breeding 🍦 program	∳ Year	Planting 🍦 Date	Harvest 🍦 Date	Has Trial 🍦 Layout	Has Trait Data	Create, Date	Public Date	Transferred
GP502_2022	Genomic selection spring wheat panel @ Aberdeen, ID	University of Idaho	2022	2022-April- 08	2022- August-22	0	0	2022- 09-14	2024- 09-14 D	ata public
22COLKS_TDicQual	TDic Introgressions, Quality Panel	USDA-ARS Kansas	2022				0	2022- 08-27	2024- 08-27	In 2024
22HAYKS_TDicQual	TDic Introgressions, Quality Panel	USDA-ARS Kansas	2022				0	2022- 08-27	2024- 08-27	
22HUTKS_TDicQual	TDic Introgressions, Quality Panel	USDA-ARS Kansas	2022				0	2022- 08-27	2024- 08-27	

Why get more data into T3?

- Carrots
- 1. Larger more powerful analyses
- 2. Genotype imputation
 - 1. Cheap genotyping is relatively low density
 - 2. We have tools to impute up to sequence-level polymorphism
 - 3. These tools get better regularly
- 3. Genomic prediction pipeline
 - 1. Genomic prediction
 - 2. Genomic mate selection
 - 3. Training population design

Discussion: Genomic predictions from T3

- We have a job posting <u>https://academicjobsonline.org/ajo/jobs/22173</u>
- If you have someone good in mind, please direct them there
- At some point, we will have one postdoc
- There are twenty breeding programs
- We can learn from the Sun Grains project what is possible
- Bespoke analyses for each program will be challenging
- What automated analyses would be useful?

How to get more data into T3?

- Get the graduate students involved
- The new WheatCAP students just started
- Amanda Peters and T3 will have a brief training session this fall and a longer workshop Spring 2023 (late February)

Two options

- 1. Manage your breeding program data as you do now
 - 1. When you are ready to upload data
 - 2. Populate T3 templates
 - 3. Upload ensuring matching with existing line data in T3
- 2. Manage some of your breeding program data through T3
 - 1. Your line names are in T3
 - 2. Design phenotyping trials in T3
 - 3. Import trial and traits to Field Book App
 - 4. Collect data on tablet
 - 5. Export from tablet to T3

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The following upload templates will be created for two example trials, each consiting of three reps of ten accessions at two different locations:

- Accessions (10 new accessions)
- Locations (2 new locations)
- Trials (2 RCBD trials with 3 reps, using the same 10 accessions)
- Trait Observations (3 traits observed at both trial locations)

Download Templates (JLJ)

Download each of the upload templates below. Then, follow the upload instructions to upload each data type.

Option 1 T3 Templates



Option 2 Field Book App





Discussion: Getting phenotypes into T3

- What is realistic for you?
- How can we make this process smoother?

UAVHub to T3 pipeline: Ideal

- Trial: design on / upload to T3
- Send images to UAVHub
- UAVHub pulls trial field map from T3
- UAVHub processes images into Level 2 measurements
 - Associates with plots from the field map
- UAVHub pushes measurements to T3
 - The data is ready to download
 - The data is interoperable with all other T3 data

How close are we to this ideal?

- UAVHub has been able to pull trial field maps from T3
- We need to work on pushing the Level 2 measurements back to T3
- Optimistically, the proof of concept is not far off

Is this ideal only mine, or is it also yours?

- Uniform drone phenotypes from 20 breeding programs in one place:
- Cool!

WheatCAP genotype data in T3 for 2022

Genotyping Data Project Search

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Show 10 v entries Search:					ch:
Genotyping Data Project Name	Description	Breeding program	Year	Date in T3 [▼]	Unrestricted as of transferred
GMS_2022_Davis	Genotyping data from Jorge Dubcovsky	UC Davis	2022	2022- 08-23	2024-08-23
GMS_2021_Utah	Genotyping data from Margaret Krause	Utah State University	2021	2022- 03-25	2024-03-25
Watkins Core 2017	Exome capture of Watkins landrace collection. Gardiner et al, Gigascience, 2017 (doi: 10.1101/gr.233551.117)	Designing Future Wheat	2017	2021- 03-08	2023-03-08
WheatCAP_Regulatory	Exome capture of all parents of bi-parental families being used for fine mapping of yield component QTL in the Wheat CAP project	Kansas State University	2019	2021- 02-09	2023-02-09
2019_НарМар	US wheat diversity panel, used for Practical Haplotype Graph	Kansas State University	2020	2020- 11-15	2022-11-15

Genotyping sample tracking with T3 use case

- The lines you will genotype are in T3
- Create barcode labels for the lines
- Plant the lines pots are barcoded
- Scan barcodes as you put tissue into plates (Coordinate app)
- Upload scanned plates to T3
- T3 makes the link with the lines
- T3 creates the template to send to the genotyping lab with the plates

Barcodes from T3

E	R	Ι	E
_		_	_

plot:3001 rw/cl:1/1 rep:1

MEDINA-264

plot:3002

rw/c1:1/2

plot:3003

rw/c1:1/3

rep:1

NA/NA

NA/NA

ERIE plot:3001 rw/c1:1/1 rep:1





MEDINA-264

plot:3002

rw/c1:1/2

rep:1

NA/NA

NA/NA



NA/NA



NA/NA

NY11013-10-15-1312 plot:3003



plot:3001 rw/cl:1/1



NA/NA

rep:1

ERIE

MEDINA-264



NA/NA

rep:1

NY11013-10-15-1312



plot:3003 rw/c1:1/3





NA/NA

rep:1





NY11013-10-15-1312



NA/NA

NA/NA

rep:1

Coordinate app



Coordinate with genotyping labs

Add Genotyping Plate



This workflow will guide you through adding a genotyping plate in the database

Genotyping plates represent 96 or 384 well plates.

Each plate has a globally unique Plate ID.

Each well in the plate has a globally unique tissue sample ID.

The "contents" of each well can be either a tissue sample, plant name, plot name, or accession name. This "source" name must be in the database already. This is useful if you provide a field trial entity (such as a plot or plant or tissue sample name), so that phenotypes and genotypes can be directly compared.

If you choose to submit your genotyping plate to a genotyping facility (Cornell IGD, Intertek, BGI, etc) we can generate the files they require for you. Please be aware of their requirements, such as blank well positions and concentrations.

In addition to sample ID, you have an option to include facility identifier for each well.

Go to Next Step

	01	02	03	04
A	Sample: uniqueKeto95_A01 Accession: AMERICAN_BANNER Source Plot: MasterNut_2015_Ketola_AMERICAN_BANNER_5 Details	Sample: uniqueKeto95_A02 Accession: ARROW Source Plot: MasterNut_2015_Ketola_ARROW_20 Details	Sample: uniqueKeto95_A03 Accession: CAL4PHS-6-271 Source Plot: MasterNut_2015_Ketola_CAL4PHS-6- 271_144 Details	Sample: uniqueKeto95_/ Accession: CALEDONIA Source Plot: MasterNut_2015_Ketola_ Details
В	Sample: uniqueKeto95_B01 Accession: GRANDPRIZE Source Plot: MasterNut_2015_Ketola_GRANDPRIZE_10 Details	Sample: uniqueKeto95_B02 Accession: HOPKINS Source Plot: MasterNut_2015_Ketola_HOPKINS_4 Details	Sample: uniqueKeto95_B03 Accession: IL04-24668-1058 Source Plot: MasterNut_2015_Ketola_IL04-24668- 1058_507 Details	Sample: uniqueKeto95_F Accession: JENSEN-262 Source Plot: MasterNut_2015_Ketola_ 262_139 Details
С	Sample: uniqueKeto95_C01 Accession: NY01066-496 Source Plot: MasterNut_2015_Ketola_NY01066- 496_242 Details	Sample: uniqueKeto95_C02 Accession: NY01066-533 Source Plot: MasterNut_2015_Ketola_NY01066- 533_262 Details	Sample: uniqueKeto95_C03 Accession: NY01066-558 Source Plot: MasterNut_2015_Ketola_NY01066- 558_273 Details	Sample: uniqueKeto95_(Accession: NY01066-572 Source Plot: MasterNut_2015_Ketola_ 572_274 Details
D	Sample: uniqueKeto95_D01 Accession: NY02007-803 Source Plot: MasterNut_2015_Ketola_NY02007- 803_380 Details	Sample: uniqueKeto95_D02 Accession: NY02007-804 Source Plot: MasterNut_2015_Ketola_NY02007- 804_381 Details	Sample: uniqueKeto95_D03 Accession: NY02008-806 Source Plot: MasterNut_2015_Ketola_NY02008- 806_382 Details	Sample: uniqueKeto95_[Accession: BLANK Details

Plate Layout



Genotyping plate uniqueKeto95

Genotyping Project	plotsCald21
Breeding Program	Cornell University
Trial Type	Genotyping Plate
Plate Format	96
Plate Sample Type	DNA
Genotyping Facility	DArT
Description	Please delete
Created By	Jean-Luc Jannink 2022-09-27



SGN trial 9429 (uniqueKeto95)





Discussion: Genotyping sample tracking

- Do you want a workflow like this?
- What is your realistic use case?

Discussion: Quality control analysis

• Do you want pedigree verification functions?

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