

BREEDDBASE

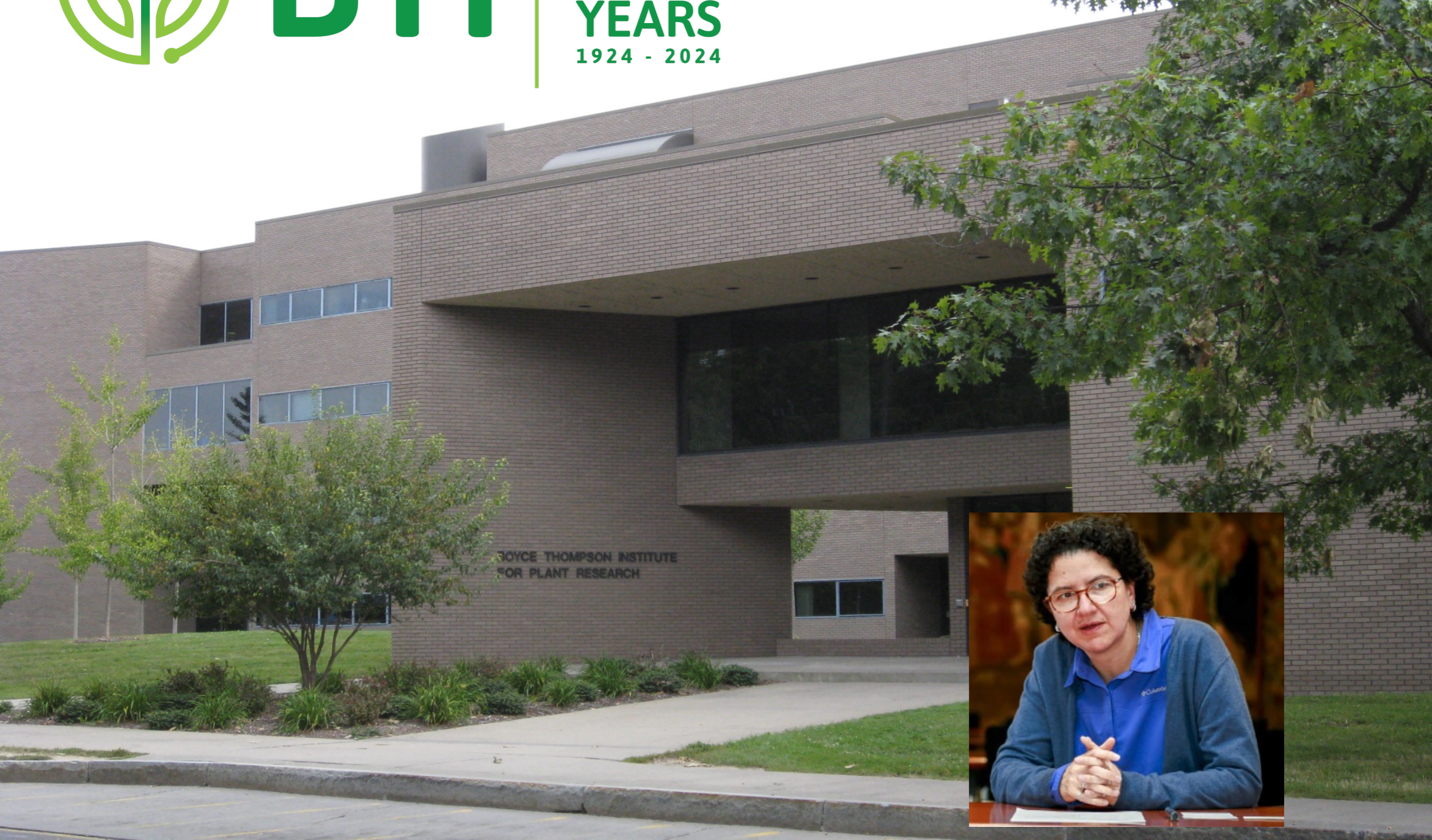


The Digital Ecosystem for Breeding



BTI

CELEBRATING
100
YEARS
1924 - 2024



<https://btiscience.org/>

Prof Silvia Restrepo

FAIR Data

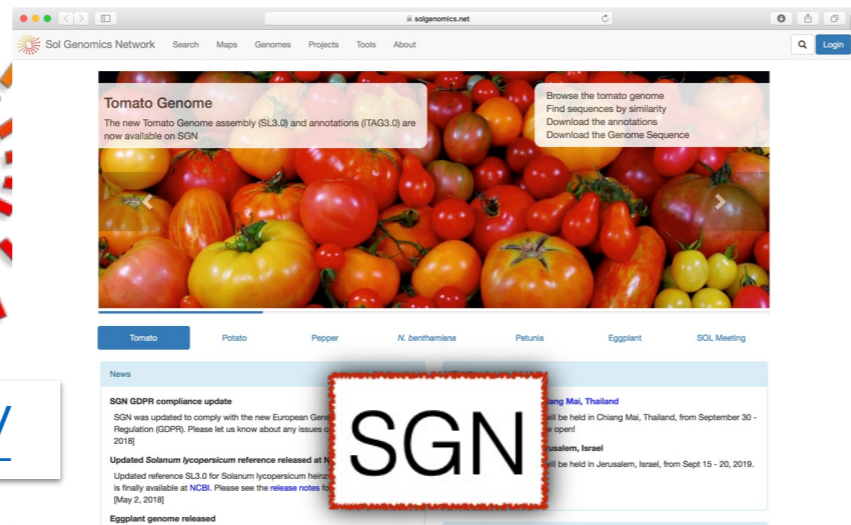
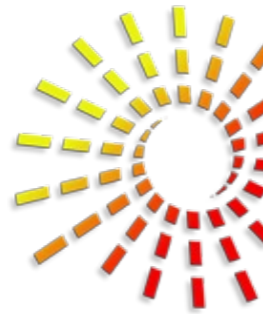
- Findability
- Accessibility
- Interoperability
- Reuse

<https://www.go-fair.org/fair-principles/>

BREEDDBASE FAIR implementation

- Cloud-based, open source system (Accessible)
- Identifiers (Findable)
 - Well defined and curated id spaces
- BrAPI (Accessible, Interoperable)
 - Peter Selby
- Ontologies (interoperable, Reusable)
 - CropOntology
 - Elizabeth Arnaud, Marie-Angelique Laporte





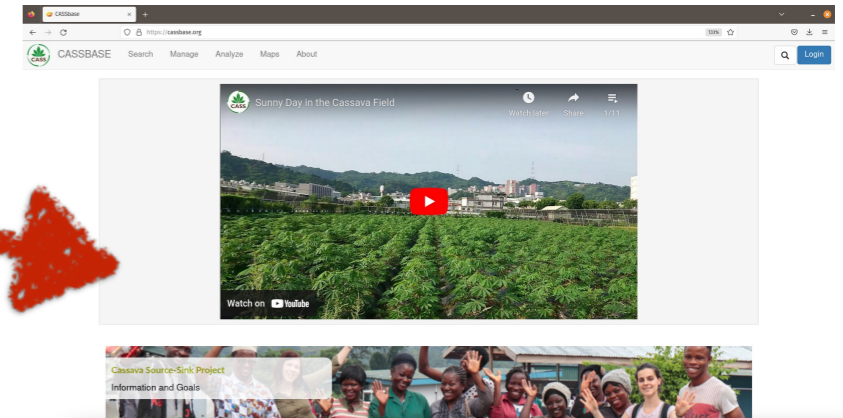
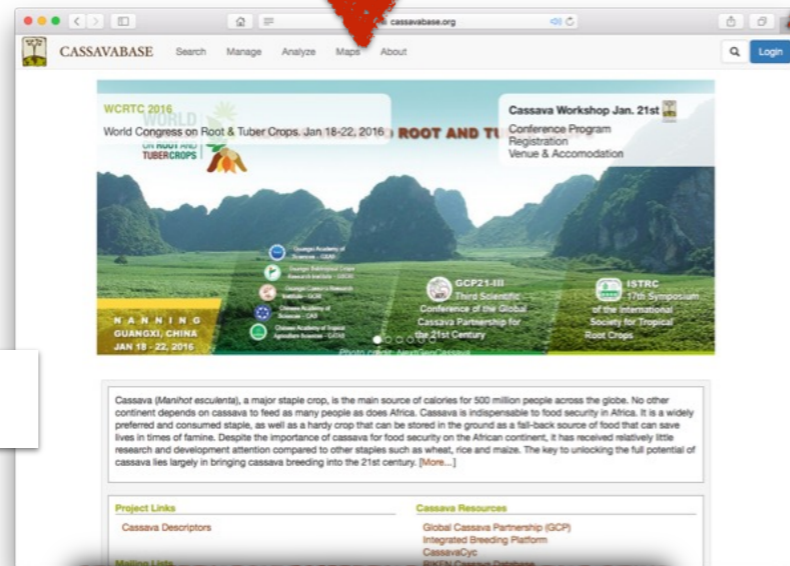
<https://solgenomics.net/>

<https://github.com/solgenomics>



CASSAVABASE

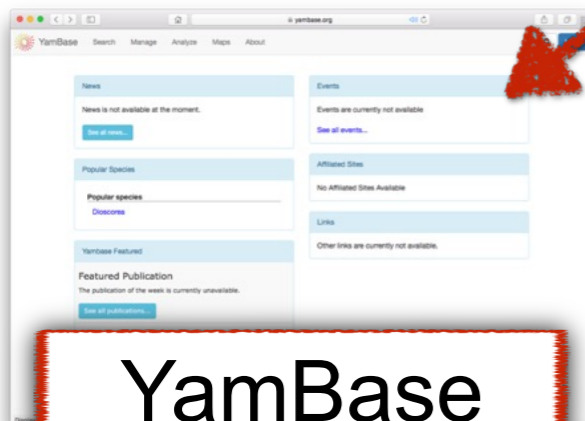
<https://cassavabase.org/>



CitrusGreening.org

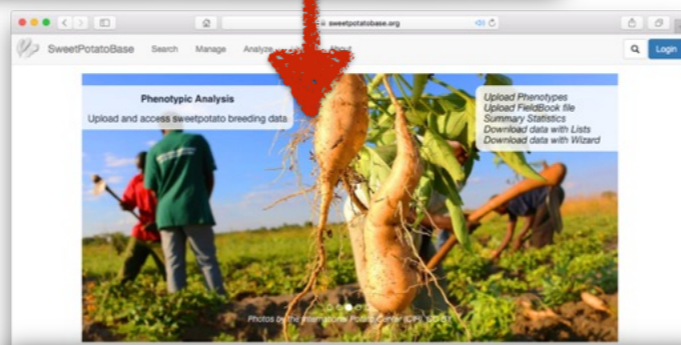
CassavaBase

<https://fernbase.org/>
<https://hornwortbase.org/>
<https://erysimum.org/>
<https://milkweedbase.org/>



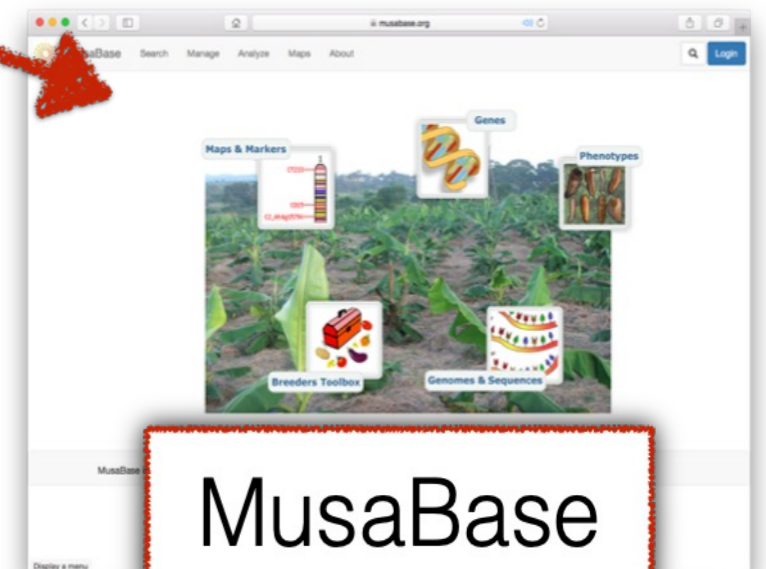
YamBase

<https://yambase.org/>



Sweetpotatobase

<https://sweetpotatobase.org/>

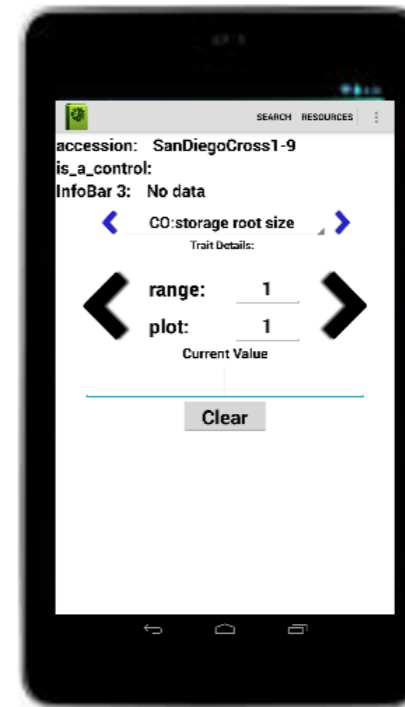


MusaBase

<https://musabase.org>

BREEDBASE

“Digital Ecosystem”



Fieldbook

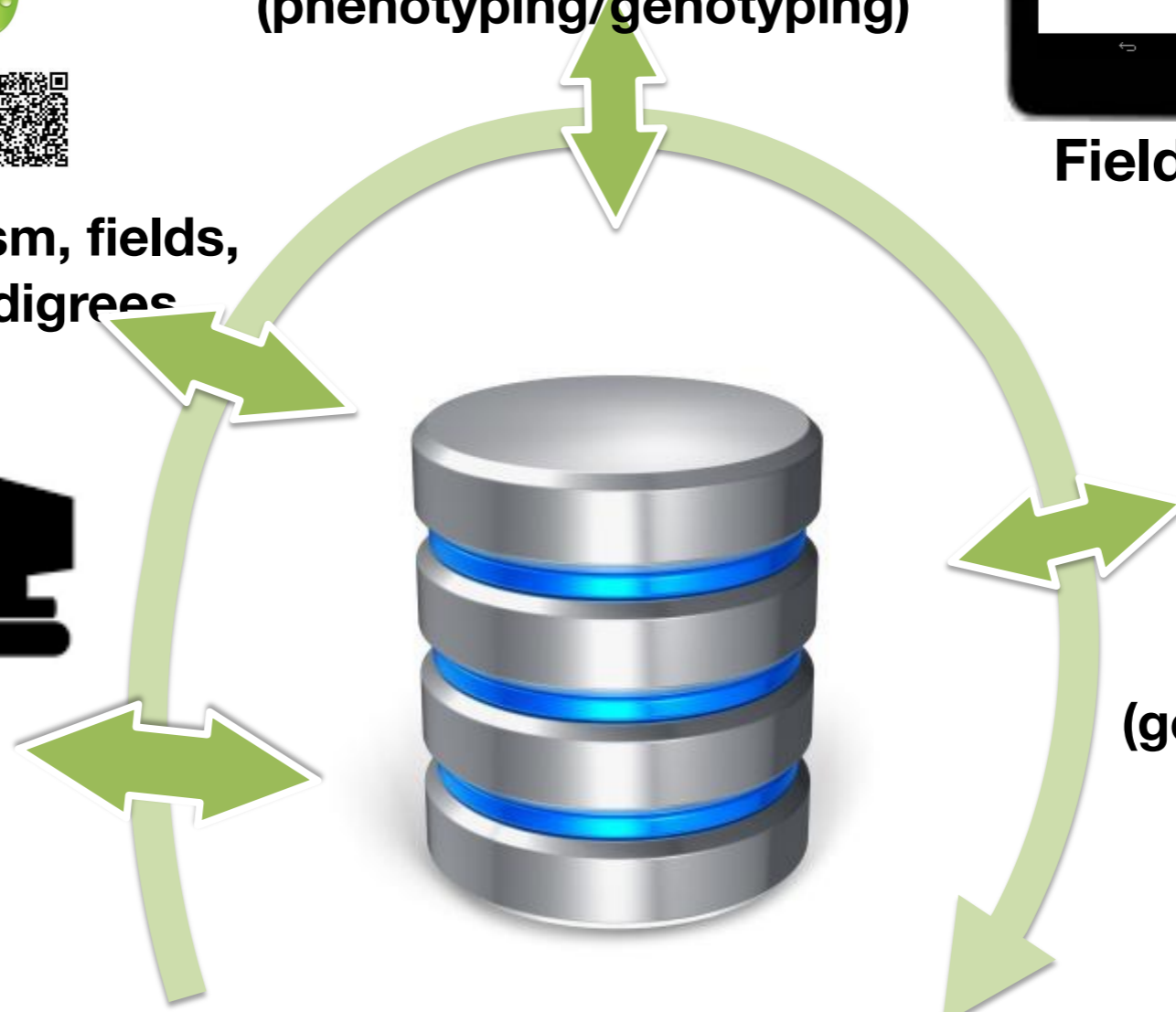
**collect data, evaluate progeny
(phenotyping/genotyping)**



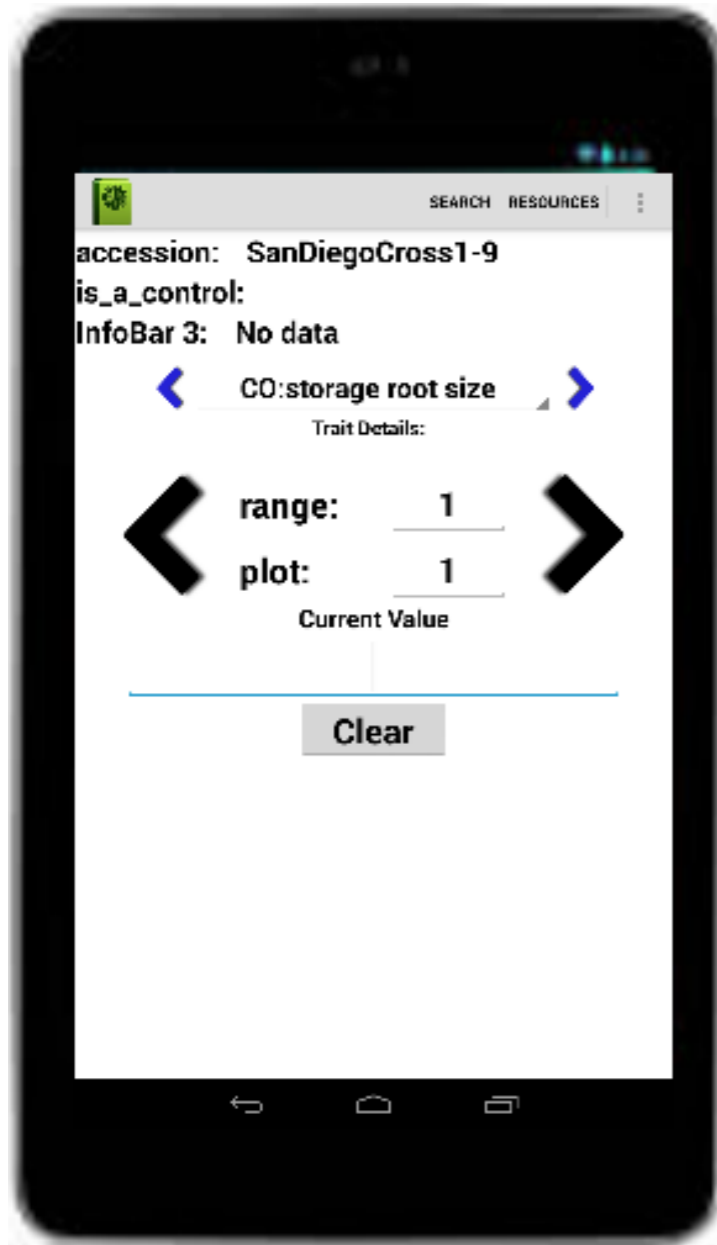
**manage germplasm, fields,
inventory, & pedigrees**



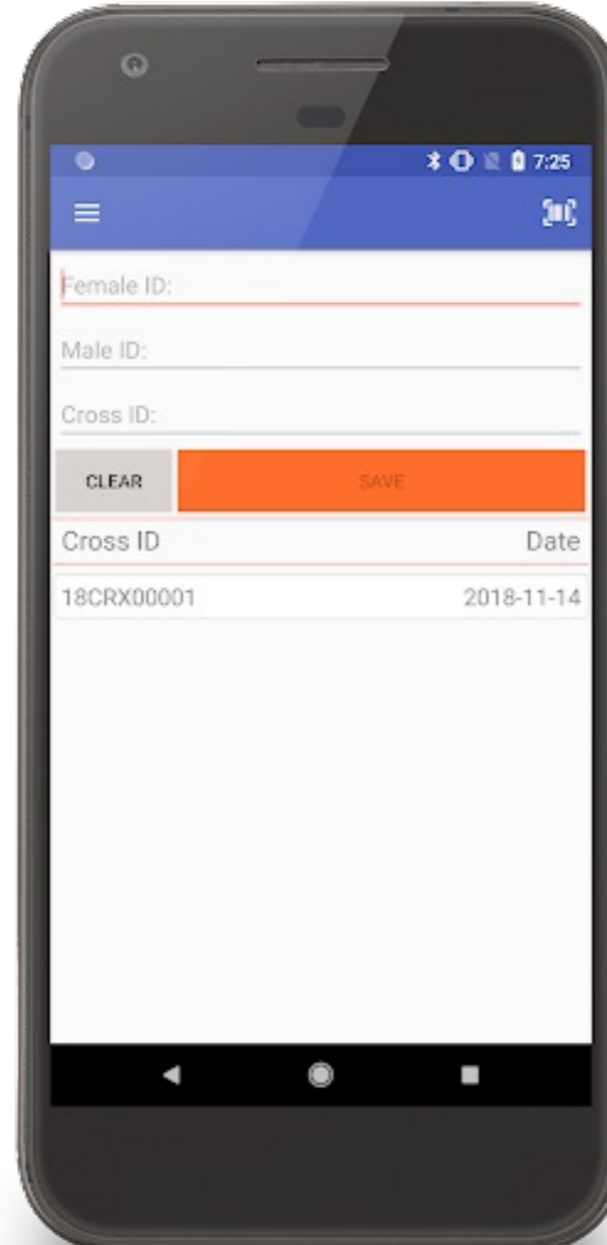
**analyses,
make selections
(genomic selection, etc.)
perform crosses**



PHENOAPPS



FieldBook



InterCross



Coordinate


Field Management

CassavaBase

CASSAVABASE Search Manage Analyze Maps About

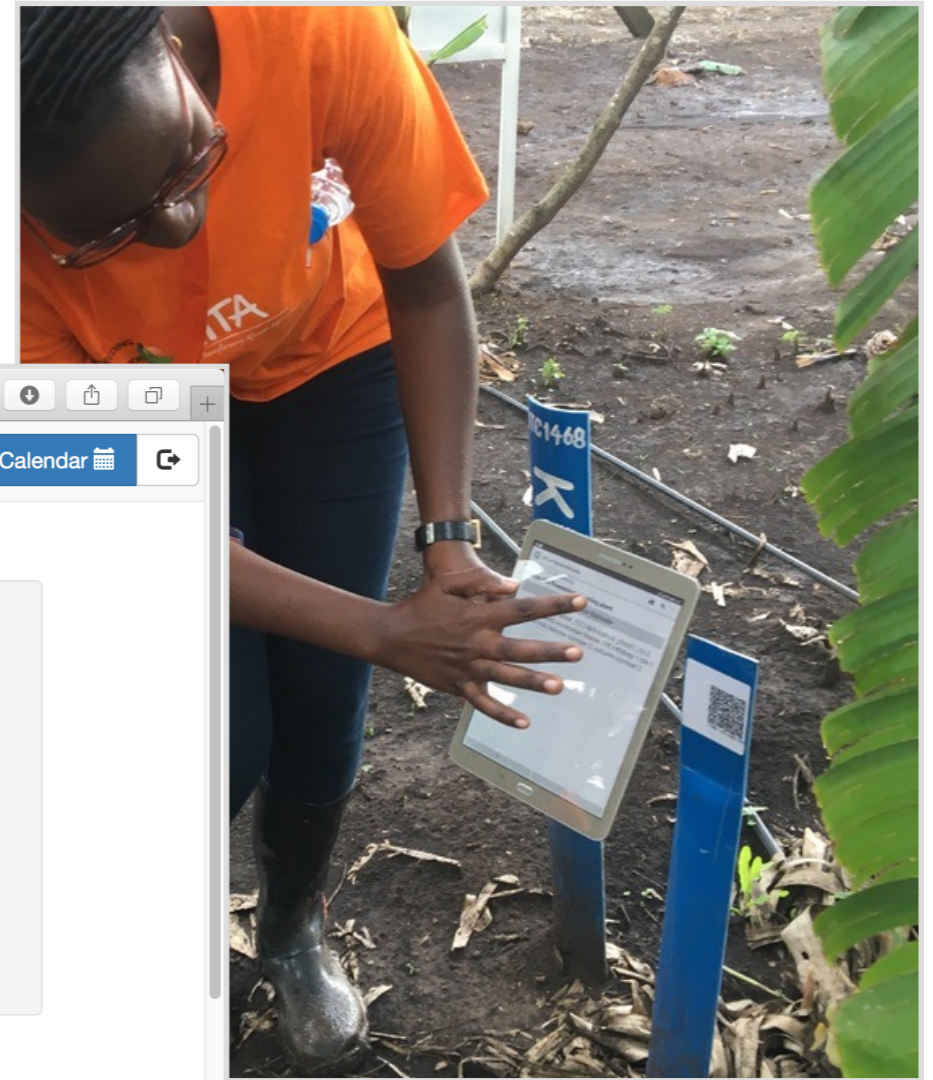
Q lam87@cornell.edu Lists Calendar

12	1201	1202	1203	1204	1205	1206	1207	1208
11	1101	1102	1103	1104	1105	1106	1107	1108
10	1001	1002	1003	1004	1005	1006	1007	1008
9	901	902	903	904	905	906	907	908
8	801	802	803	804	805	806	807	808
7	701	702	703	704	705	706	707	708
6	601	602	603	604	605	606	607	608
5	501	502	503	504	505	506	507	508
4	401	402	403	404	405	406	407	408



Alex Ogbonna

Barcoding



The screenshot shows the CassavaBase Label Designer web application. The browser address bar shows www.cassavabase.org/tools/label_designer. The navigation menu includes Search, Manage, Analyze, Maps, and About. The user is logged in as lam87@cornell.edu. The main interface is titled "Label Designer" and contains several configuration options:

- Data Source:** CBSD_GxE_Namulonge_2016B
- Optional:** TSC_label
- Page Format:** Custom
- Label Format:** Custom
- Label For Every:** Plot
- Labels to Print:** All
- Page Width:** 288 (72 pixels/inch)
- Page Height:** 576 (72 pixels/inch)
- Label Width:** 144 (72 pixels/inch)
- Label Height:** 72 (72 pixels/inch)

An "Apply" button is located at the bottom right of the configuration panel. Below the configuration panel, a preview of a label is shown on a grid background. The label contains the text "UG110016", a QR code, and the number "100".

A sample label with a QR code and text. The text on the label is:

IITA-TMS-IBA141095
313
15ayt16highTCIK



Bryan Ellerbrock

Inventory

- Track seed (planting materials) in the database
- Barcoded
- Storage location
- Track quantities

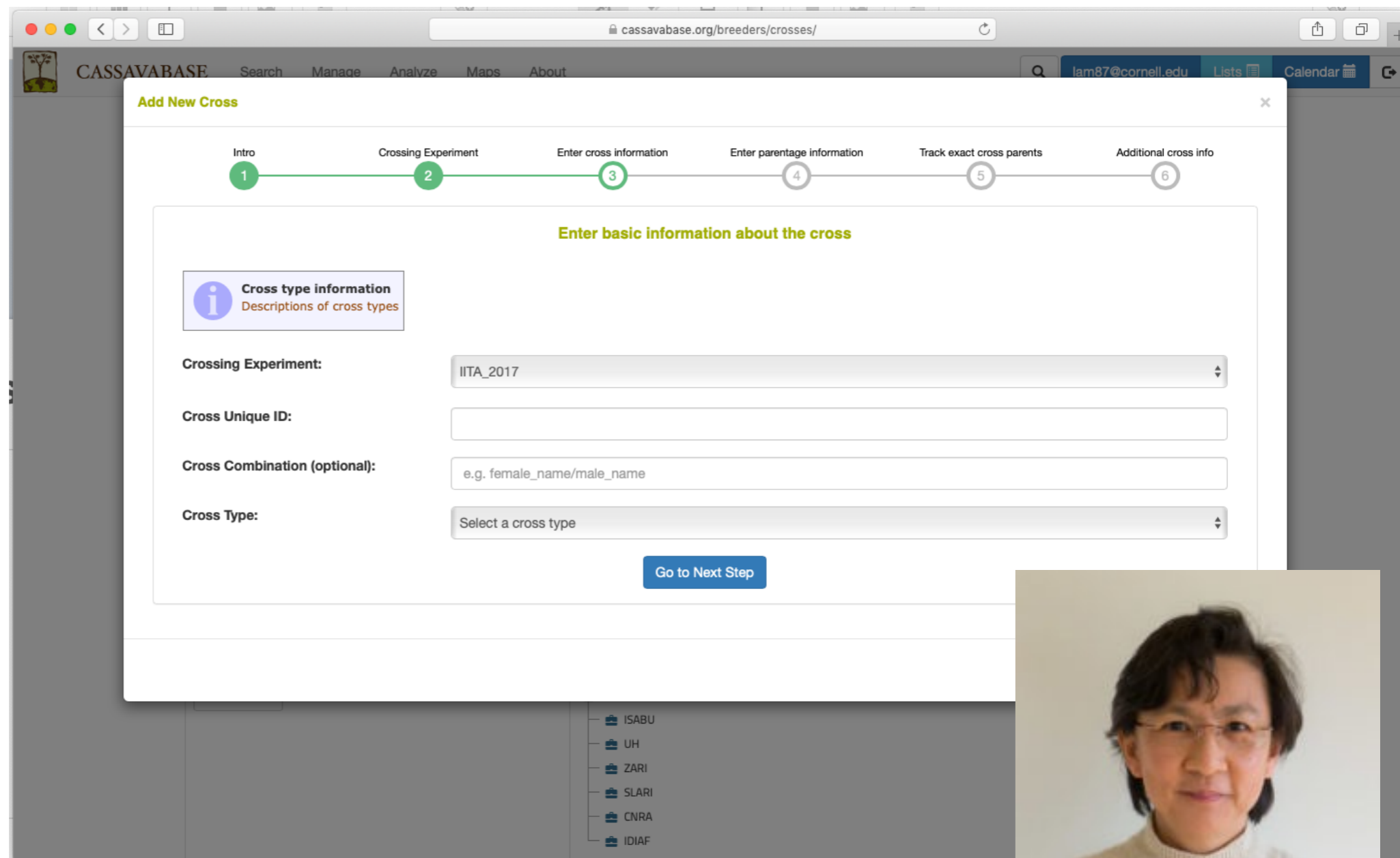
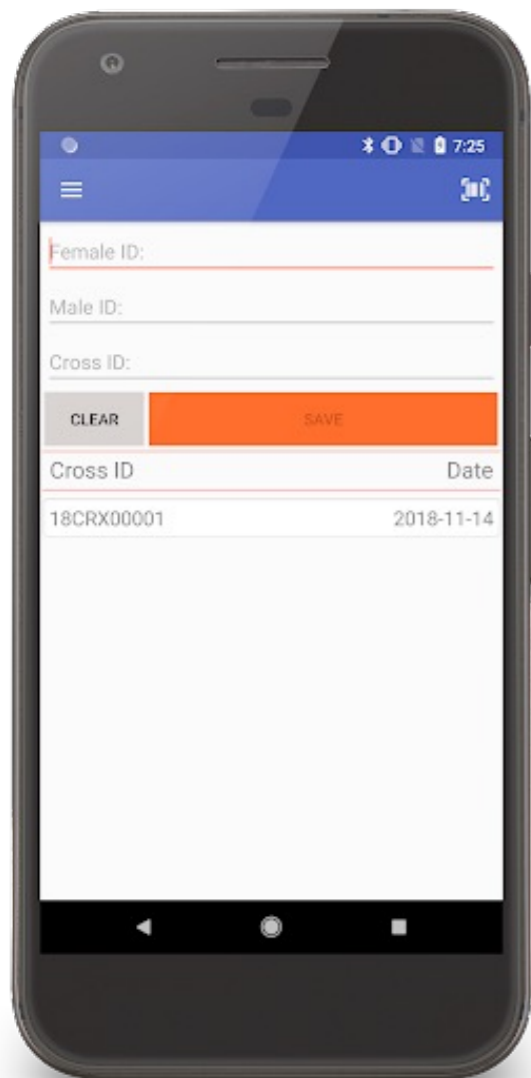


**Nick
Morales**

Crossing Manager



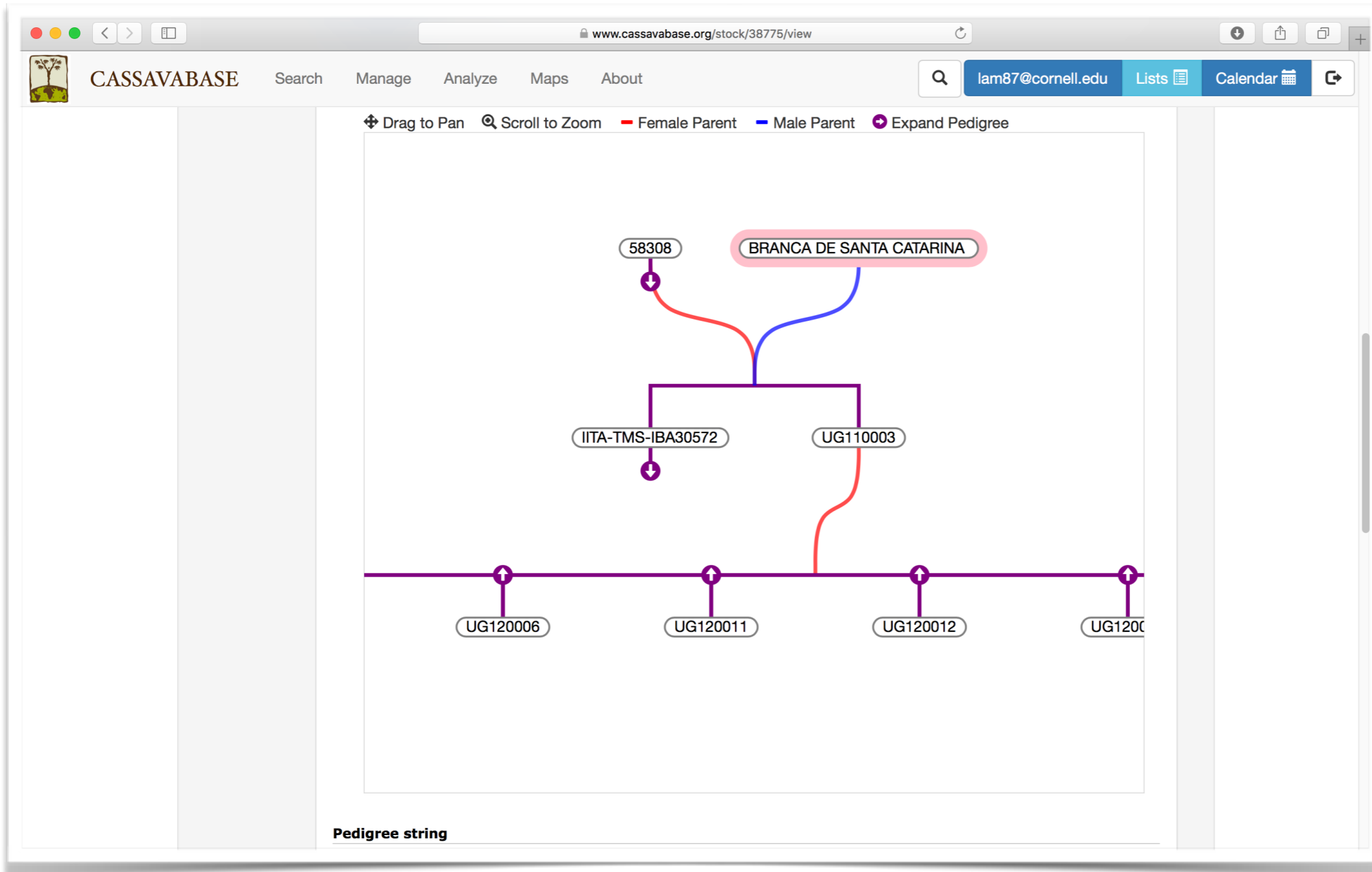
Intercross App



Titima Tantikanjana

Interfaces with InterCross App as well as Btract (Trushar Shah and Margaret Karanja)

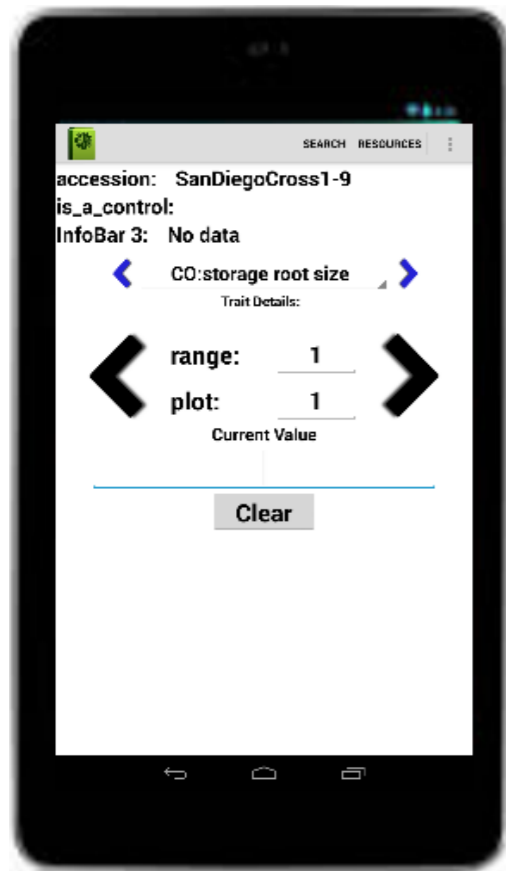
Pedigree Tracking



David Lyon

Data Collection

PHENOAPPS



Tablet-based



Drones

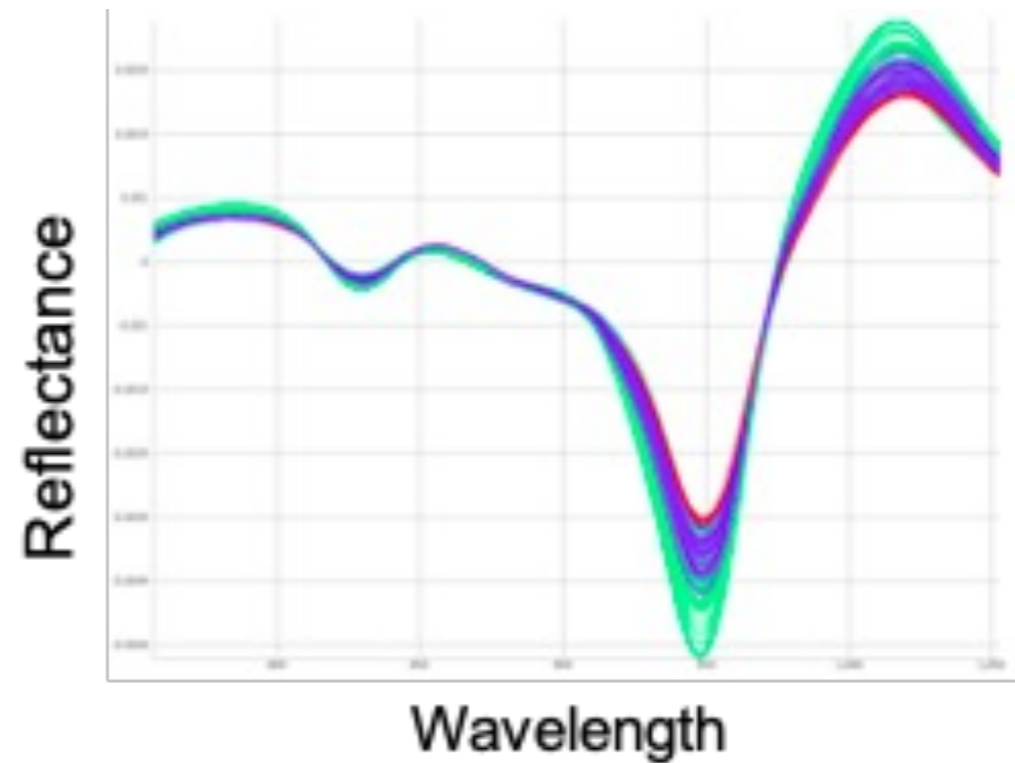
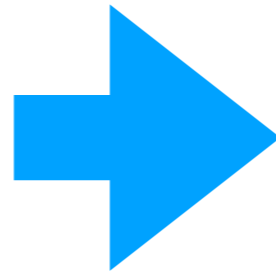


NIRS



Ground penetrating radar

NIRS Phenotyping



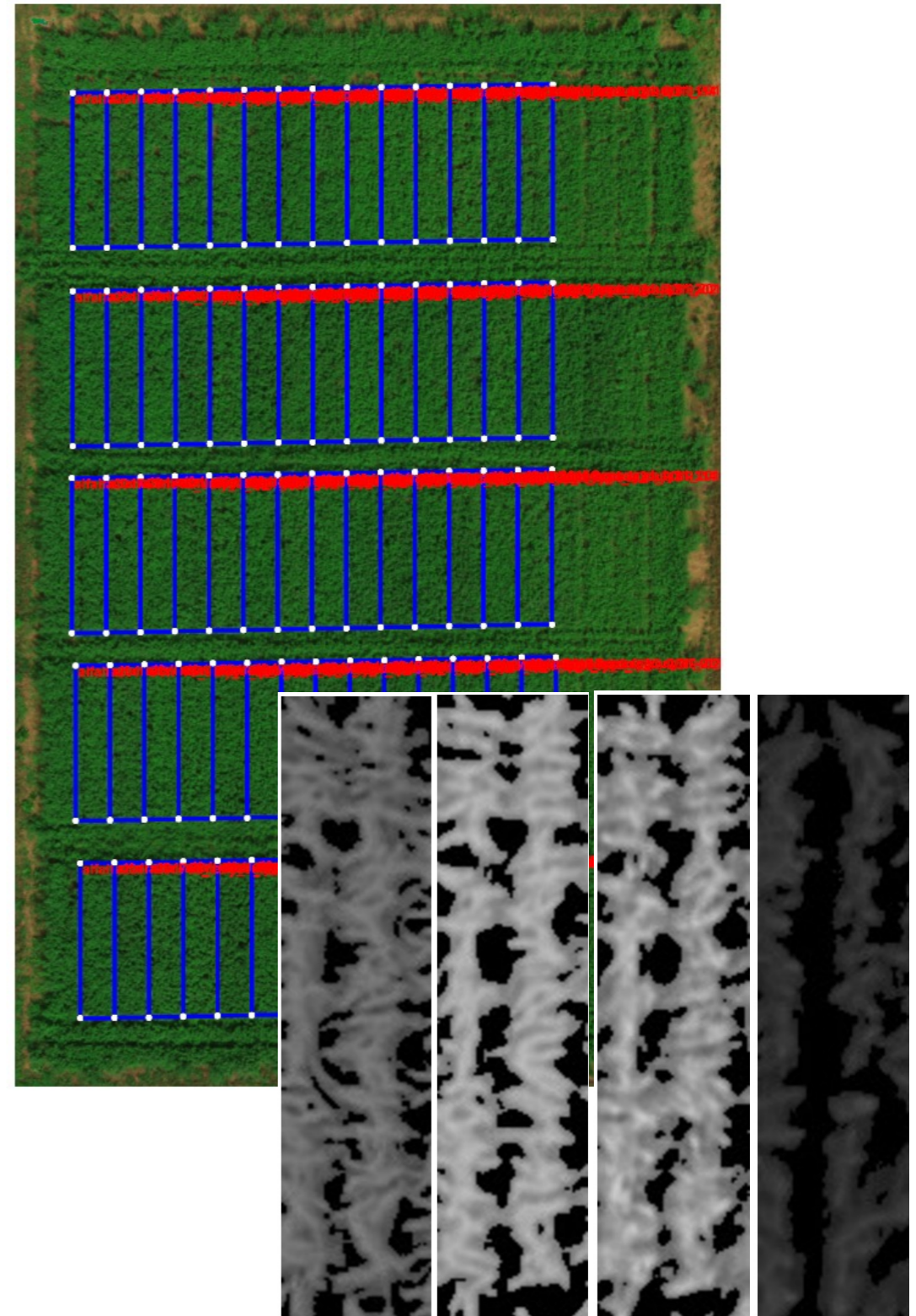
- Portable devices revolutionize phenotyping
- Spectra can be correlated with specific compounds / properties
- Calibration and prediction can be performed in Breedbase directly
- Jenna Hershberger, Clemson U, WAVE R-module

Drone Data Collection

- Assemble drones images
- Overlay plots
- Excise and store plot-level pictures
- Image analysis



Nick Morales



Genotyping Data

- Collect genotyping samples using **Coordinate App**
- Genotypic data are voluminous
- Raw data
 - many terabytes
- Processed data (snp calls)
 - billions of datapoints
- Breedbase manages all processed genotyping data



Analyze

Analyses & Models

Breeder Tools

Selection Index

Genomic Selection

Population Structure

Clustering

Kinship & Inbreeding

Stability AMMI/GGE

Heritability

Accession Usage

Mixed Models

Compare Trials

Graphical Filtering

BoxPlotter Tool

GWAS

Image Analysis

Sequence Analysis

BLAST

VIGS Tool

HapMap Jbrowse

Other

Ontology Browser

Compose a New Trait

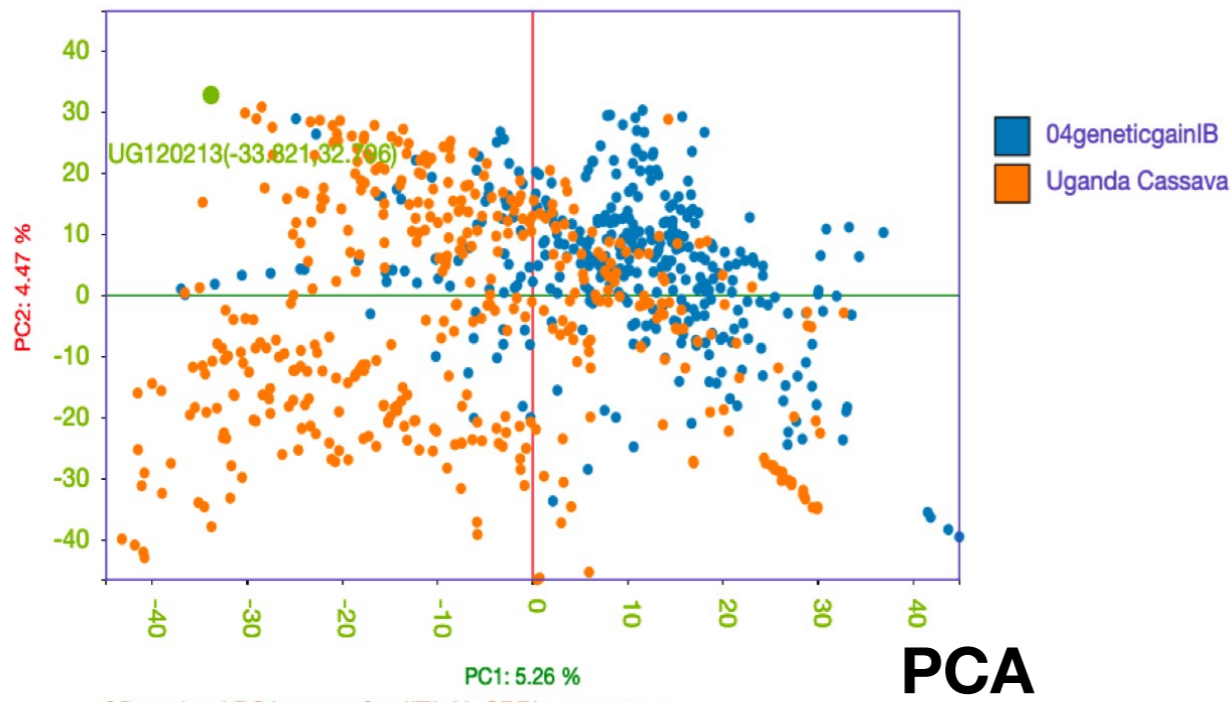
SolGS

- Tool for Genomic Selection in Breedbase
- Build prediction models from phenotypic and genotypic data in the database
- Predict breeding values from genotyping data
- Verify data (PCA, distribution)
- Build Selection Indices
- Advance breeding cycle



Isaak Tecele

Data Visualization

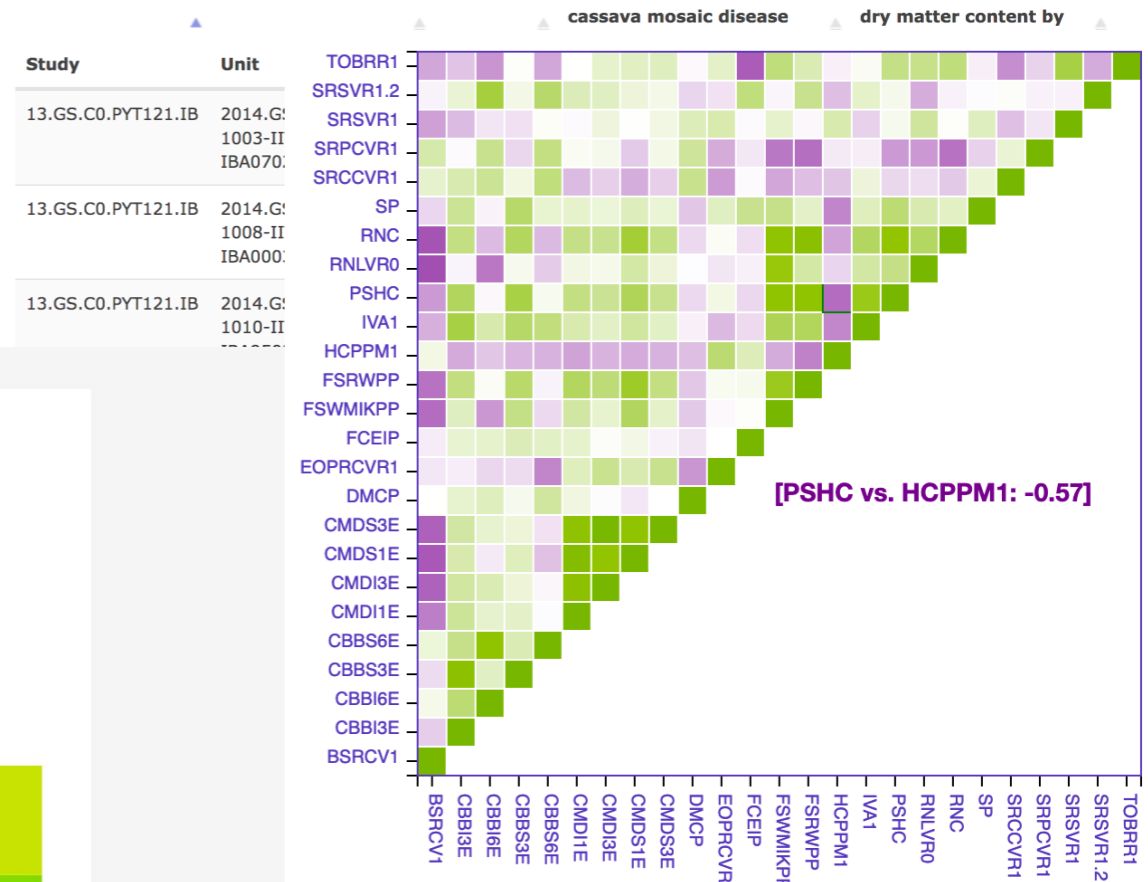
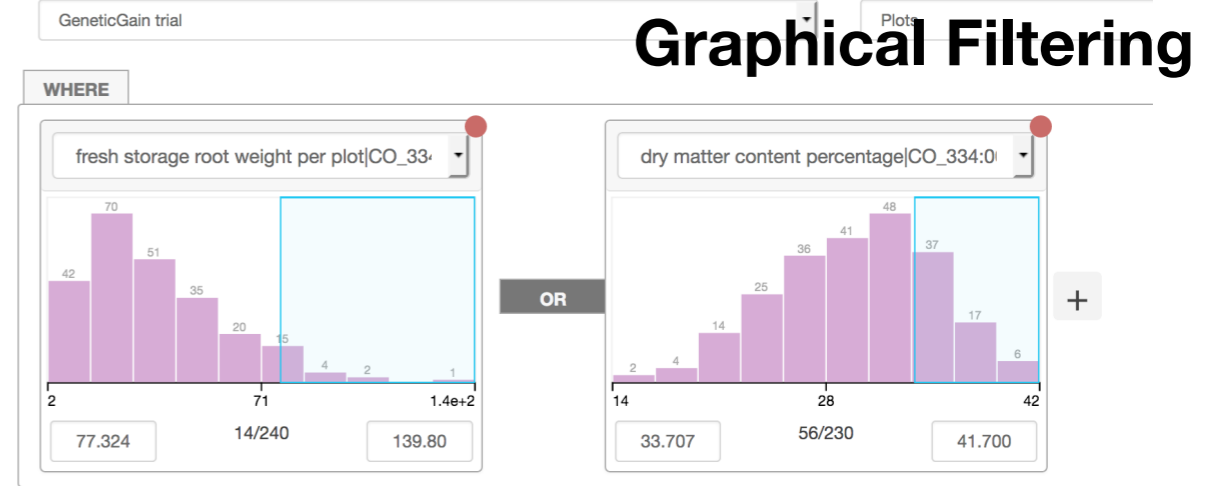


[Download PCA scores] -- IITA-NaCRRRI -- genotype

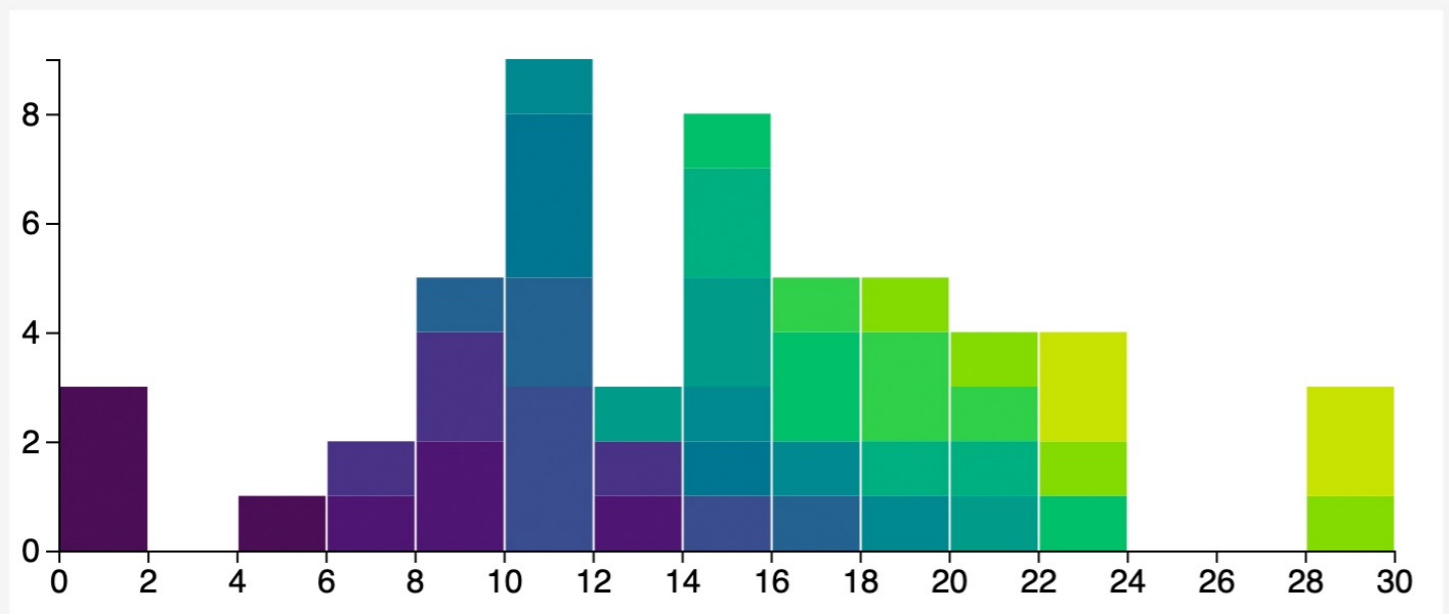
Select:

Display:

Definition
















































[Download correlation coefficients]



Correlations



Breedbase: a digital ecosystem for modern plant breeding

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¹⁸Present address: NRGene, Morristown, NC, USA.

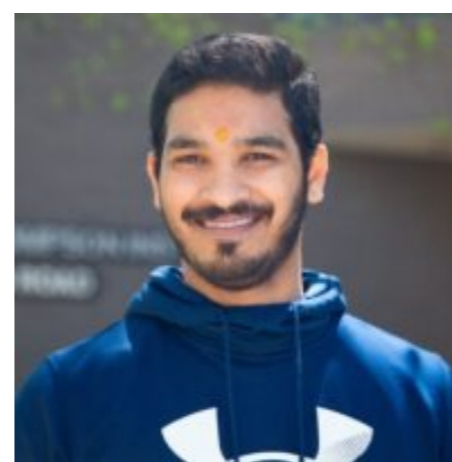
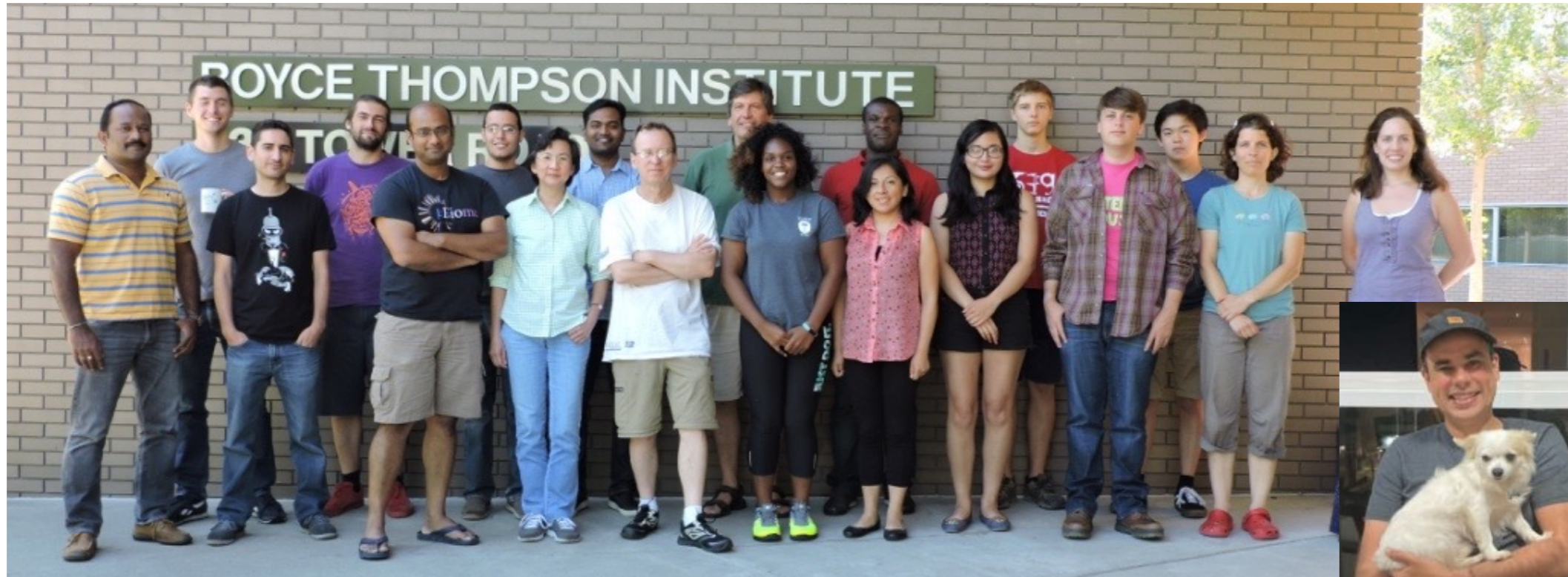
*Corresponding author: Boyce Thompson Institute, 533, Tower Road, Ithaca, NY 14853, USA. Email: LAM87@cornell.edu

†These authors contributed equally to this work.

Conclusions

- Breedbase is fully Open Source and FAIR
 - Can also be used to manage fully private data
- Manages fields, phenotypic and genotypic information
- With PhenoApps, implements a complete digital ecosystem for breeding

Acknowledgments



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