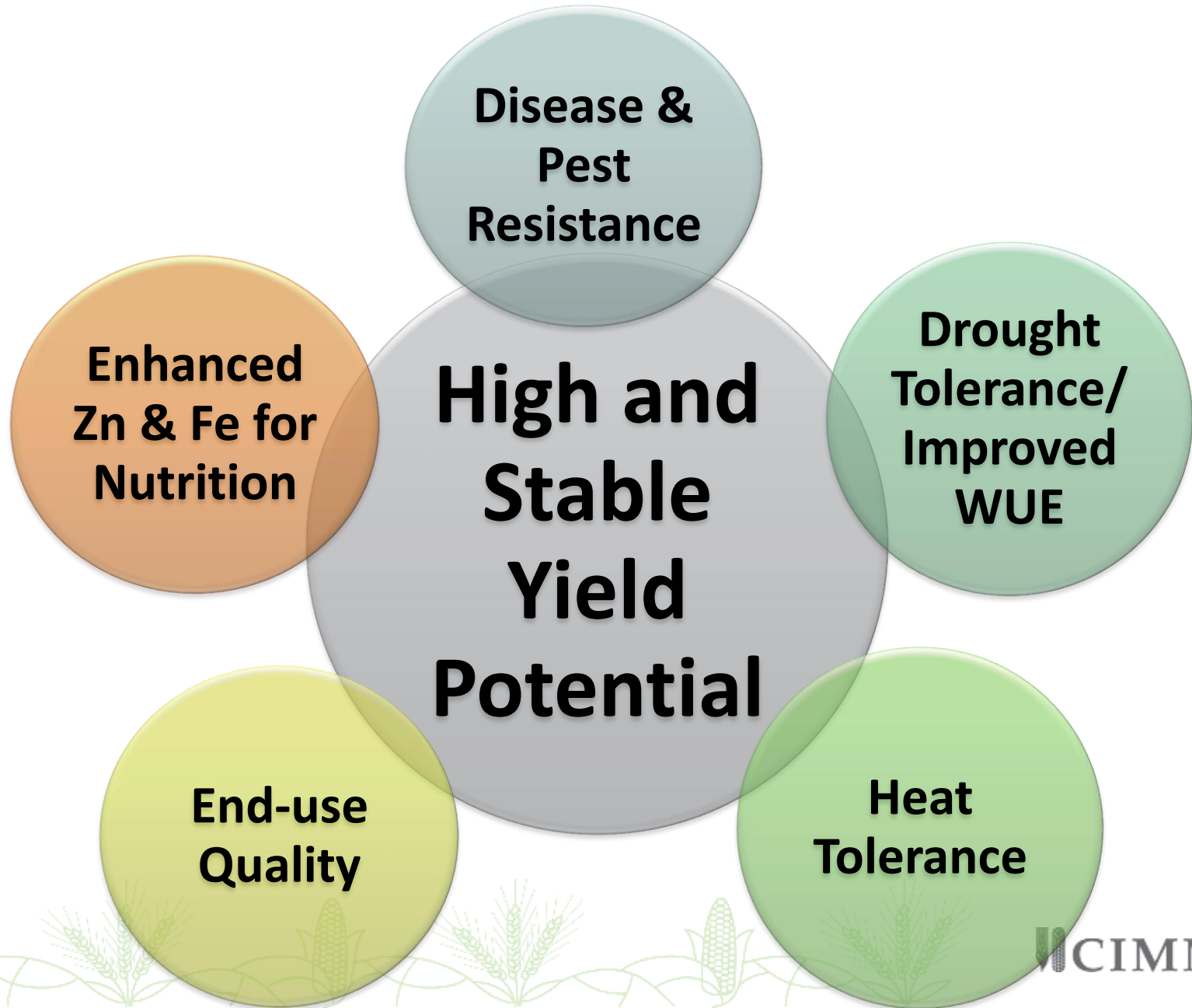


Bread Wheat Breeding Program at CIMMYT

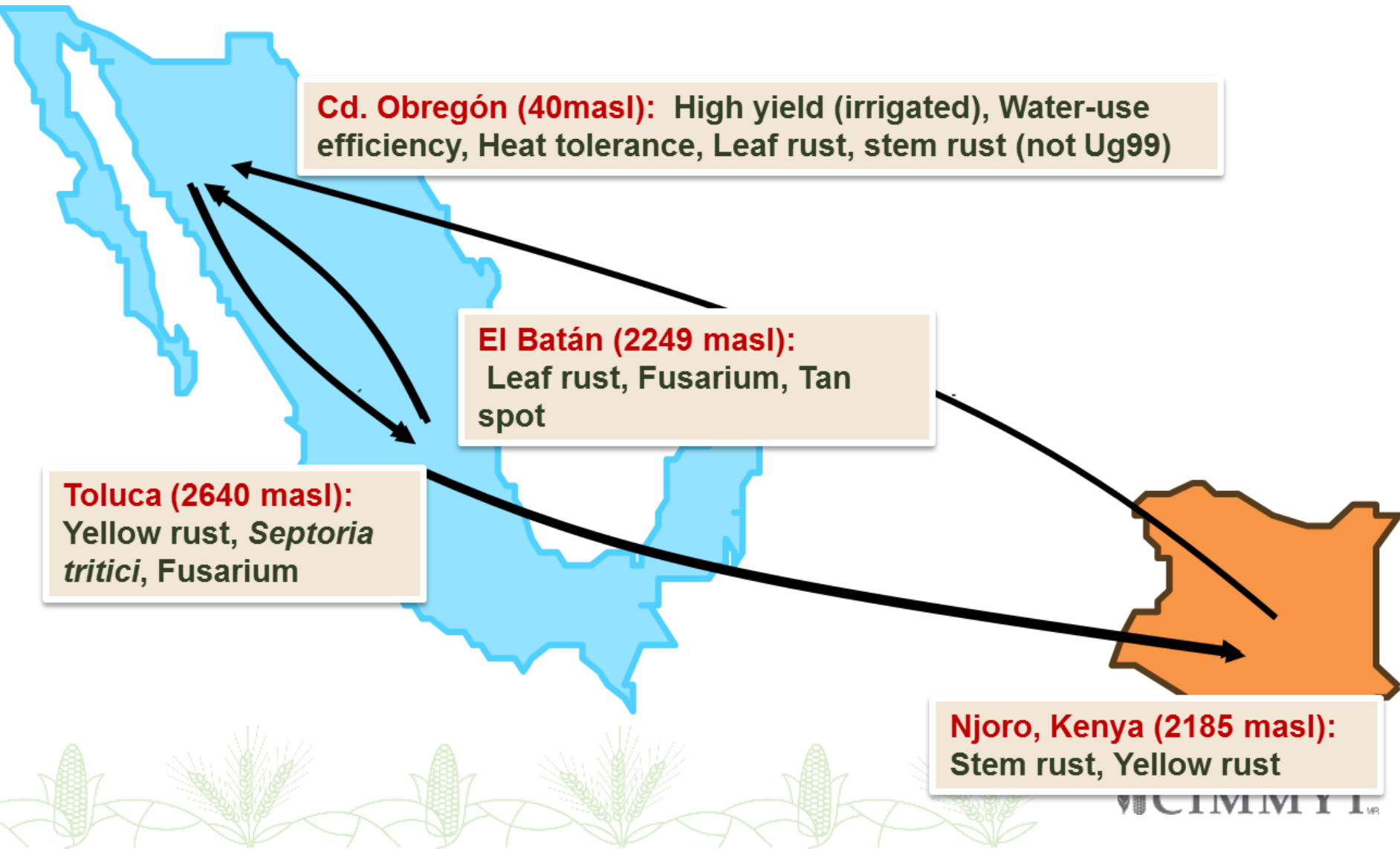
Suchismita Mondal

Wheat Breeder
International Maize and Wheat Improvement
Center, CIMMYT

Wheat breeding priorities

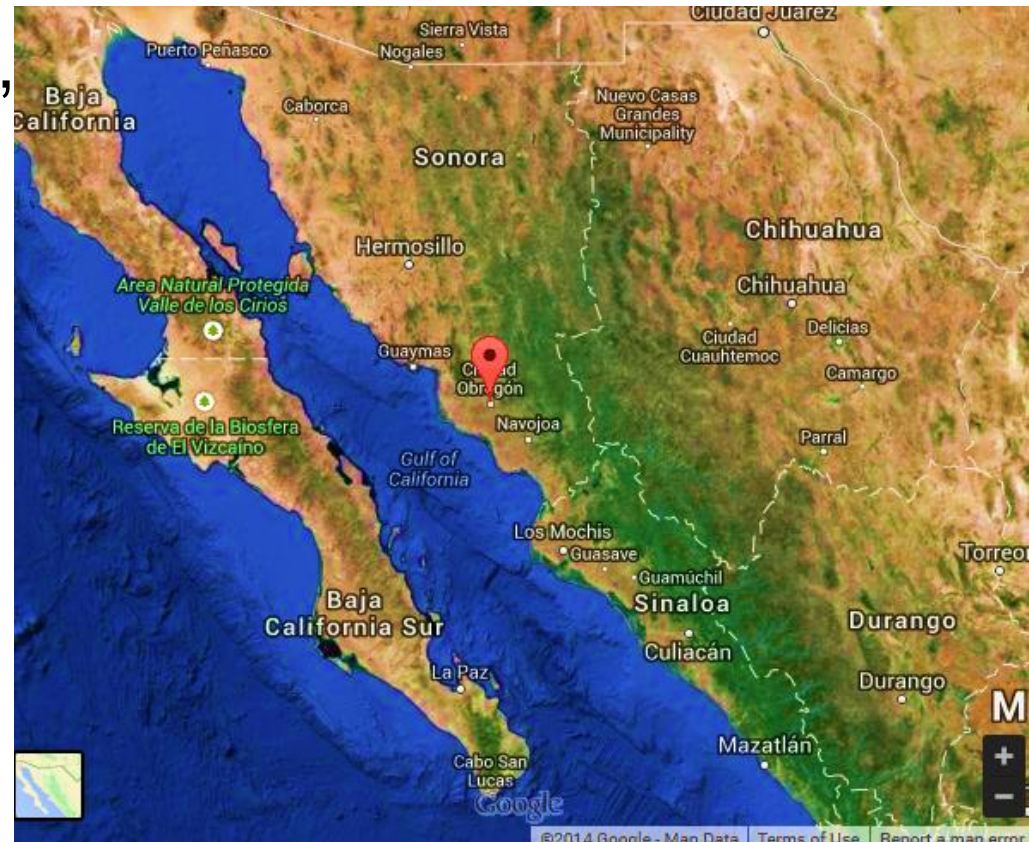


Up-scaled breeding and testing to deliver genetic gain (5 years breeding cycle)



Cd. Obregon Cycle

- Ciudad Obregon, Sonora, Mexico
 - Lat: 27°22' N, Long : 109°55' W
 - Elevation : 40m above sea level
 - Hot desert climate



Obregon Cycle

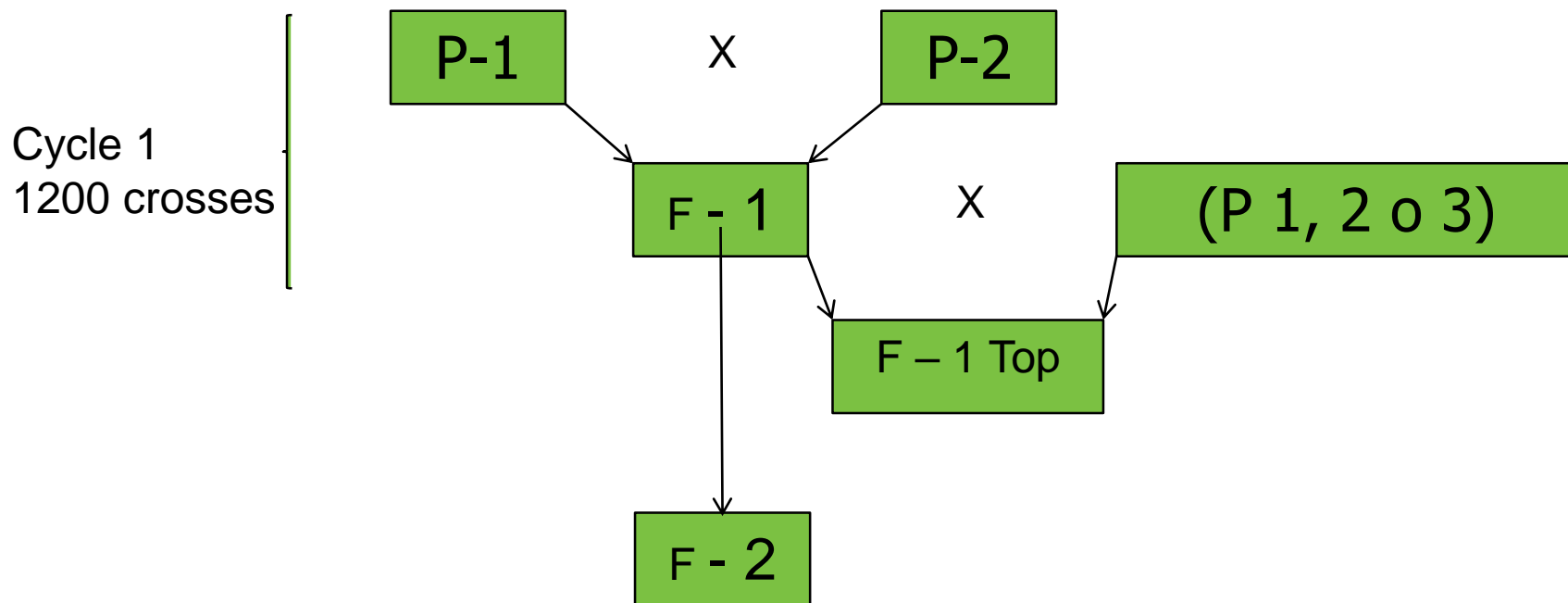
- Planting in November – 60 ha or 148 acre
- Field maps prepared in Fieldmap app.



Hand Planting (6 ha or ~ 70-80K lines)



Making crosses & generation advance



The crossing plan is prepared in Excel based on all available information about the parents

Eg. of data sheets

The screenshot displays a Microsoft Excel spreadsheet titled "CR RW 2018 All Data for printing (Read-Only) - Excel". The interface includes the standard Excel ribbon with tabs for File, Home, Insert, Page Layout, Formulas, Data, Review, View, Developer, and Power Point. The Home tab is active, showing options for Font, Paragraph, Styles, Cells, and Editing. The spreadsheet itself contains a large table of data with many columns and rows. The columns are color-coded in groups: yellow, green, blue, pink, orange, and grey. The rows are labeled with genotype IDs on the left. The bottom of the spreadsheet shows a status bar with the text "Ready" and a zoom level of 100%.

We can have 60-70 columns of data to make decisions regarding crosses



Crossing in field



Cycle 2

1500 populations

Each population

2000 plants

4-5 ha or 9-12 acre

F - 2

SB

SB : selected bulk approach for selection in segregating generation

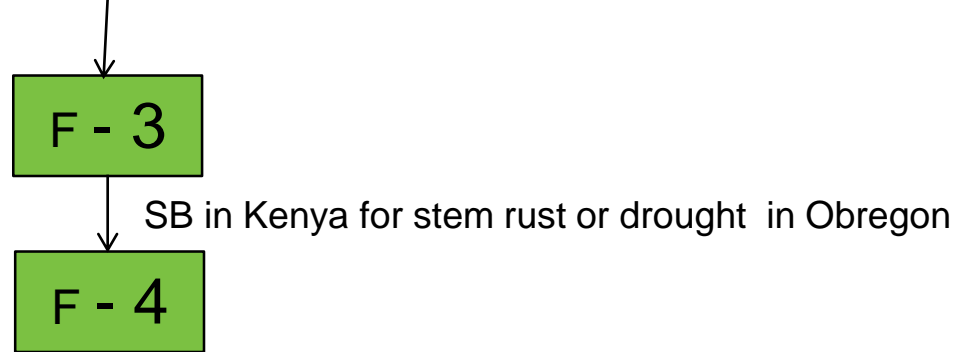


Selection: Resistance to rust, agronomic type, height



Cycle 3

2000 populations
evaluated both in
Cd. Obregon &
Njoro



Cd. Obregon, Mexico under drought



Selection: Yield, NDVI, CT

Njoro, Kenya Stem rust evaluations

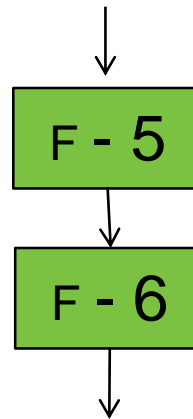


Selection: Resistance to stem rust

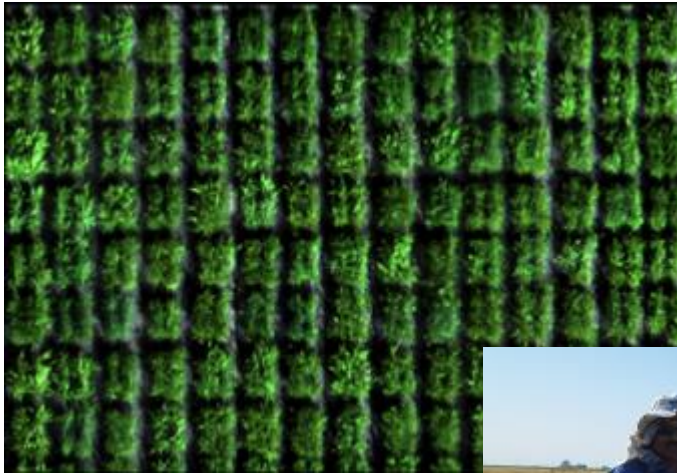
Cont. Breeding cycle

Cycle 4

~ 60,000 head
rows



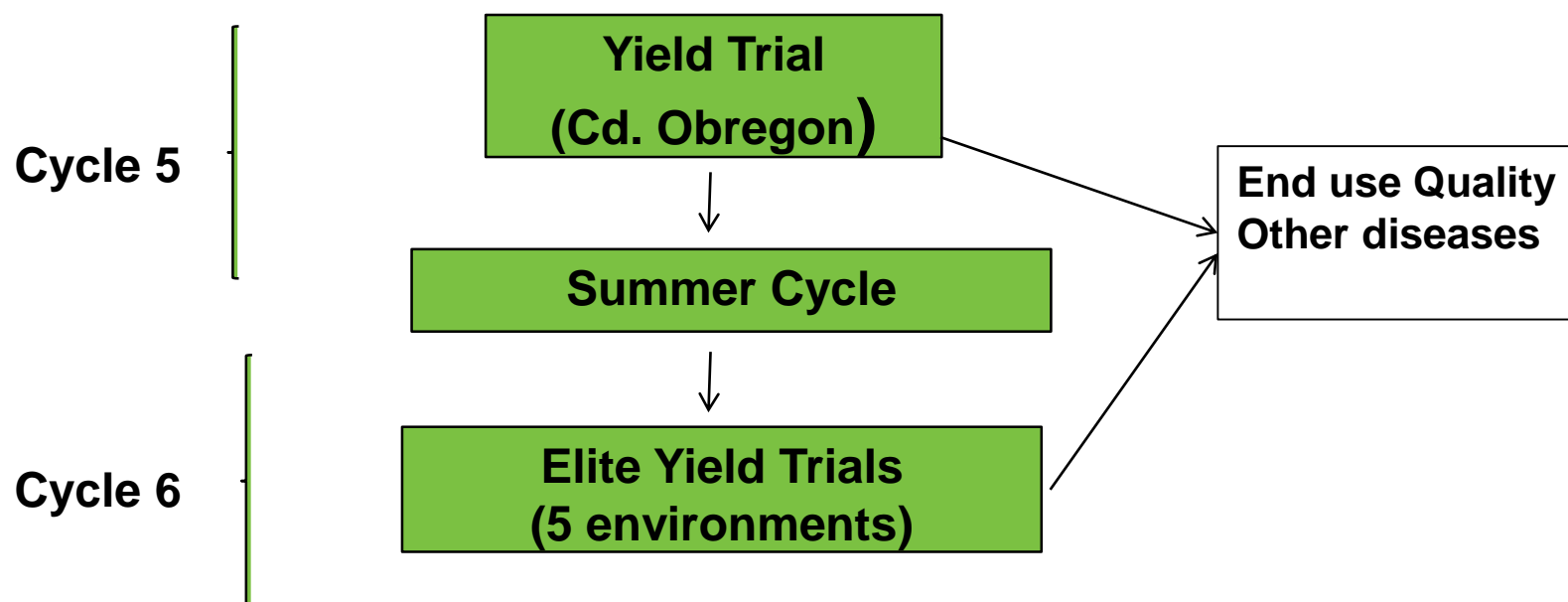
HR o IP HR – head to row or IP – individual
plant to row



Grain selection

~ 100,000 envelopes
2 week activity
Selection: Grain size,
grain diseases

Cont. breeding cycle



EYTs are tested across 6 environments: Melga (Flat), Bed, Early Heat, Drought, Heat



Grain yield evaluations advanced lines

Cd. Obregon, Mexico

**Bed sowing
normal irrigation**



**Late heat sowing
in beds**



**1st year Yield Trial,
9044 lines, 323
trials, 2 reps
20,000 plots**



Data collection

- Data collection using KSU – Fieldbook app
- Challenges –
 - CIMMYT database
 - Reformating current files



Harvest and Sowing



~40,000 yield bags are arranged and weighed

- Materials are threshed and prepared for sowing in El Batan and Toluca
- 2-3 weeks in between harvest threshing and sowing



Final Information from Cd. Obregon

The image displays two side-by-side screenshots of Microsoft Excel spreadsheets. The left spreadsheet, titled 'Final Subtotal 2013-2015', shows a grid of data with columns for 'Year', 'Location', and various yield measurements. The right spreadsheet, titled 'Final Subtotal 2016-2017', shows a similar grid of data. Both spreadsheets have a complex layout with multiple columns and rows, and some cells are highlighted in yellow or red.

Most advanced yield testing : Information columns range between 100-150 (across years and locations of evaluations)
Utilized for decision making of Internationally distributed germplasm

81 Countries receiving CIMMYT Spring Wheat nurseries 2016/17



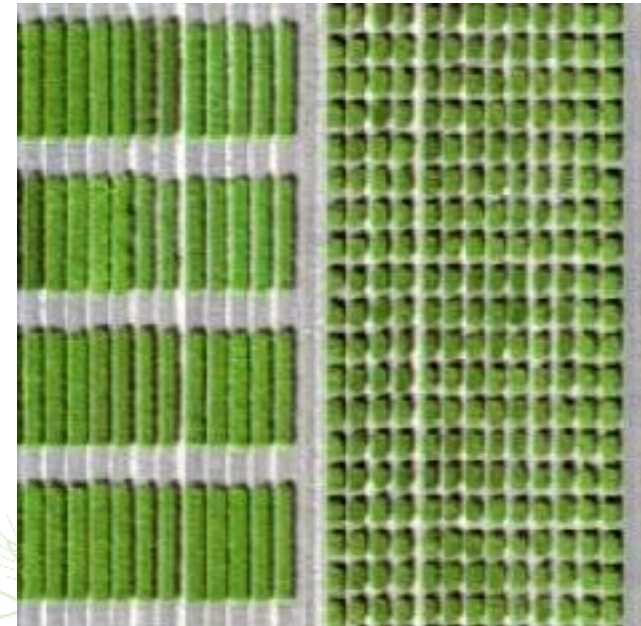
Possibilities with high throughput phenotyping in wheat breeding

- Aerial and UAV based HTP implemented
- CT and NDVI highly correlates with grain yield ($r = 0.5-0.7$)

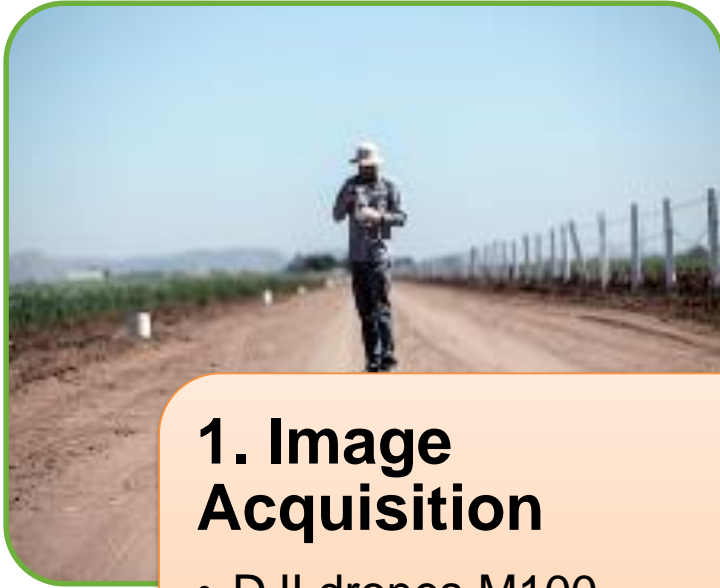


Looking forward:

- Complementing early generation selections with HTP
- Algorithms to estimate other agronomic traits, e.g. heading (days) and plant height
- Evaluating feasibility of assessing certain foliar disease

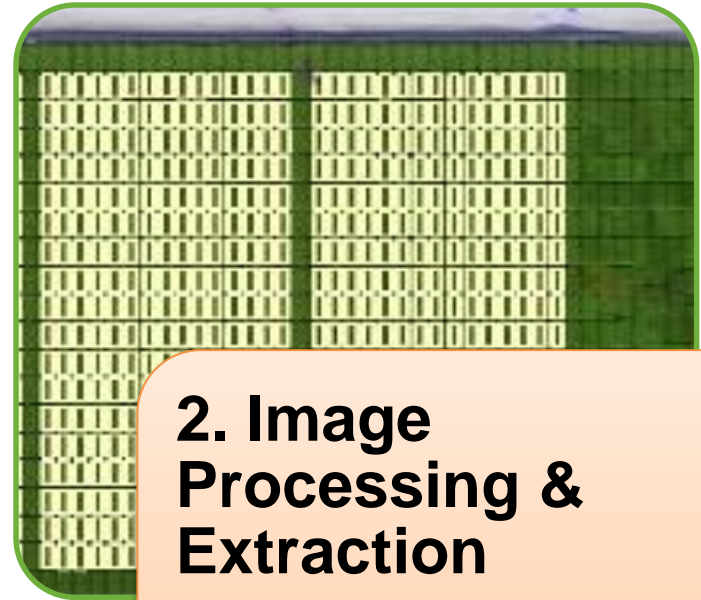


Phenomics in Breeding pipeline



1. Image Acquisition

- DJI drones M100
- Red edge camera
- Thermal camera
- Hyperspectral camera



2. Image Processing & Extraction

- Generation of ortho - mosaics
- Phenotypic trait extractions





1. Image Acquisition

- DJI drones M100
- Red edge camera
- Thermal camera
- Hyperspectral camera



1st Year Yield trials

2nd Year Yield trials

**Head rows/
plant to rows**

CIMMYT RESEARCH STATION, CIUDAD OBREGON

CIMMYT

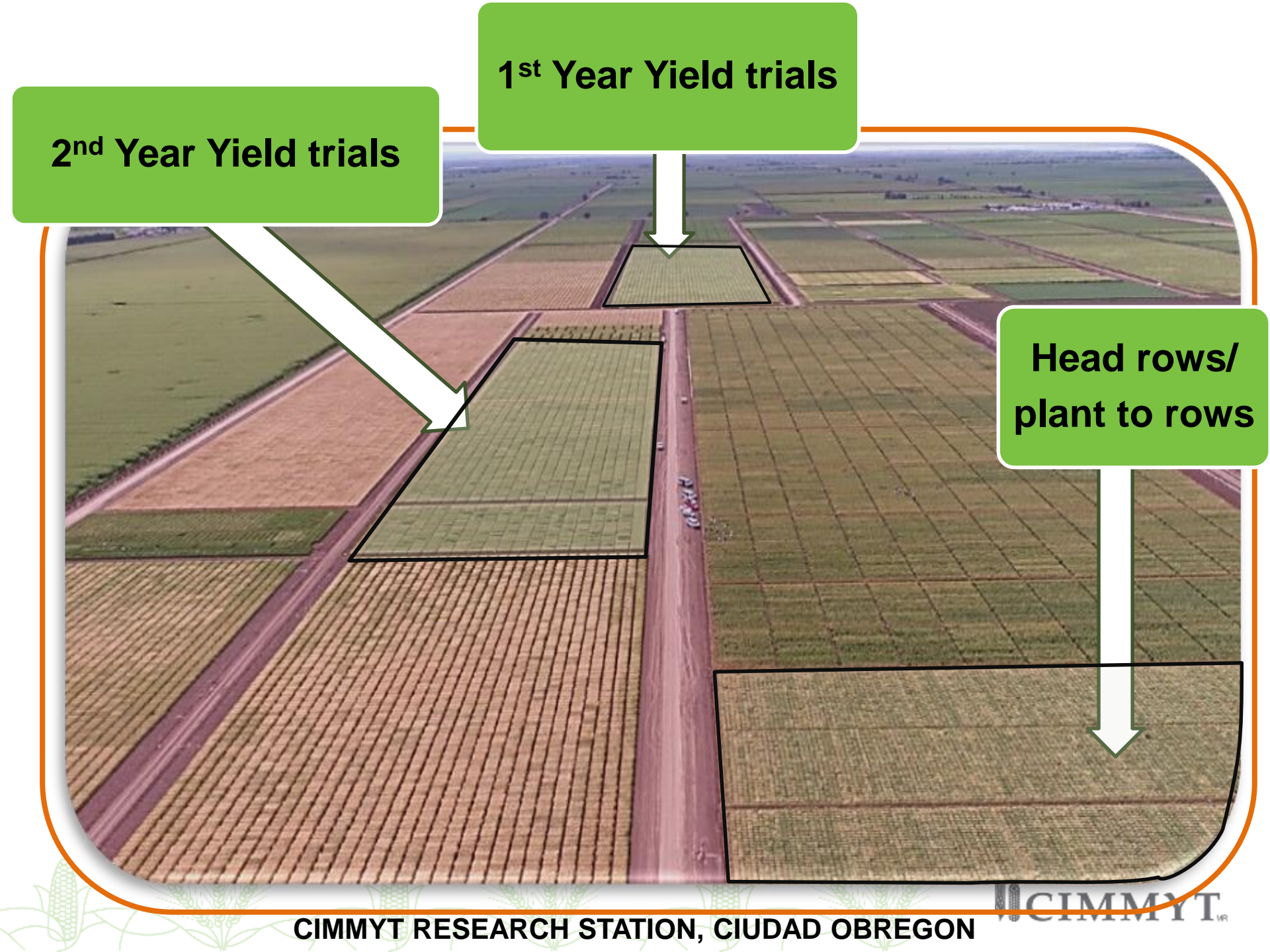


Image Acquisition

- Around 25 ha of land area
- Survey ground control points
- Mission Planner (free software) – flight plans
- 3 days – time between 10.30 am till 2.00 pm
- Heading till physiological maturity



NDVI and vegetation indices

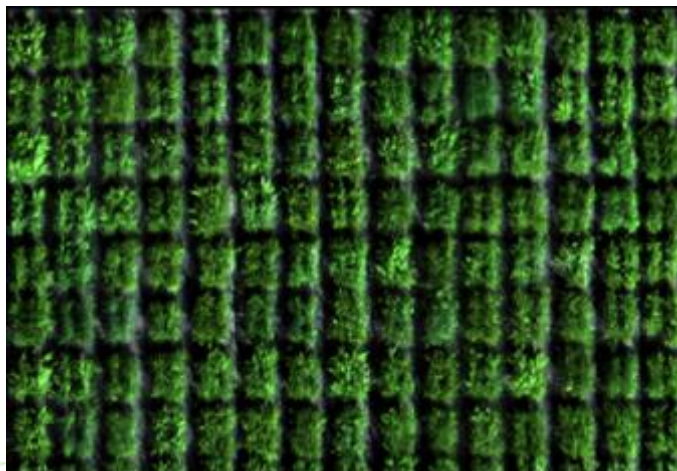


RedEdge, MicaSense
Bands: 475, 560, 668,
840, 717 nm
Measure: NDVI, SR
GSD at 30cm: 2cm/pixel

Thermography



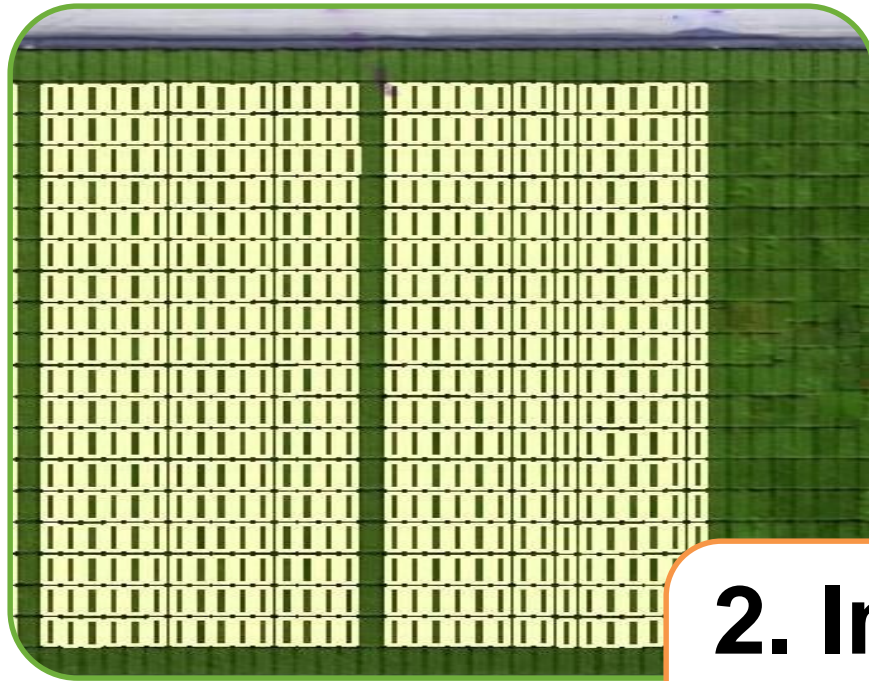
*Zenmuse XT,
DJI/FLIR*
Range: 8-14 μ m
GSD at 30m:
4 cm/pixel



Hyperspectral



*Micro-Hyperspec,
Headwall Photonics*
Range: 600 – 1700 nm
n. bands: 267
GSD at 30m: 1.8
cm/pixel



2. Image Processing & Extraction

- Generation of ortho -mosaics
- Phenotypic trait extractions



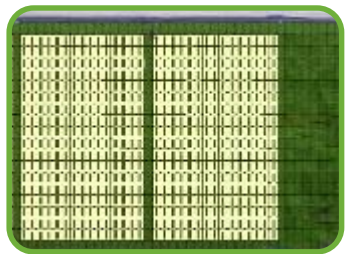


Image Processing & Extraction

- Pipeline in development and use (Red-edge camera)
 - Agisoft Photoscan: automated by python scripts (by Kevin Wang, KSU)
Code – github.com/xwangksu/uavBatch

xwangksu / uavBatch

Unwatch 1 Star 0 Fork 0

Code Issues 0 Pull requests 0 Projects 0 Wiki Insights Settings

Branch: master uavBatch / src /

xwangksu Marker file description changes

- micasense
- pyimagesearch
- uavBatchGcpAssignment.py
- uavBatchGroup.py
- uavBatchImAlignment.py
- uavBatchMarkerDetection.py
- uavBatchModelGeneration.py
- uavBatchPreProcess.py

uavBatch

The objective to develop the "uavBatch" Python scripts is to scientifically and automatically generate the ortho-photos from the aerial images captured by the MicaSense RedEdge(-M) camera.

This trial (beta) version of the Python scripts is for local use, meaning no network connection needed. However, that also means necessary meta-data should be provided through files, such as field boundary coordinates and ground control points (GCPs) within in the boundary. Also, this version is only applied to the images captured by the MicaSense RedEdge(-M) cameras with the firmware after v2.1.x. Python v3.5 is used for coding.

The radiometric calibration model is according to <https://support.micasense.com/hc/en-us/articles/115000351194-RedEdge-Camera-Radiometric-Calibration-Model>. The Python scripts to do the radiometric calibration is modified based on <https://github.com/micasense/imageprocessing>.

Python libraries used in the scripts need to be pre-installed to run the scripts successfully.

The Agisoft Photoscan Python API used in this version is v1.3.2. The trial version has been tested on a Windows machine.

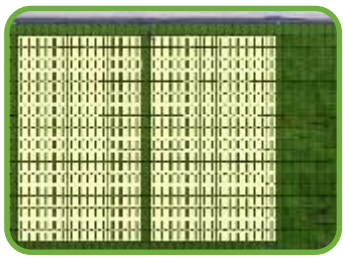
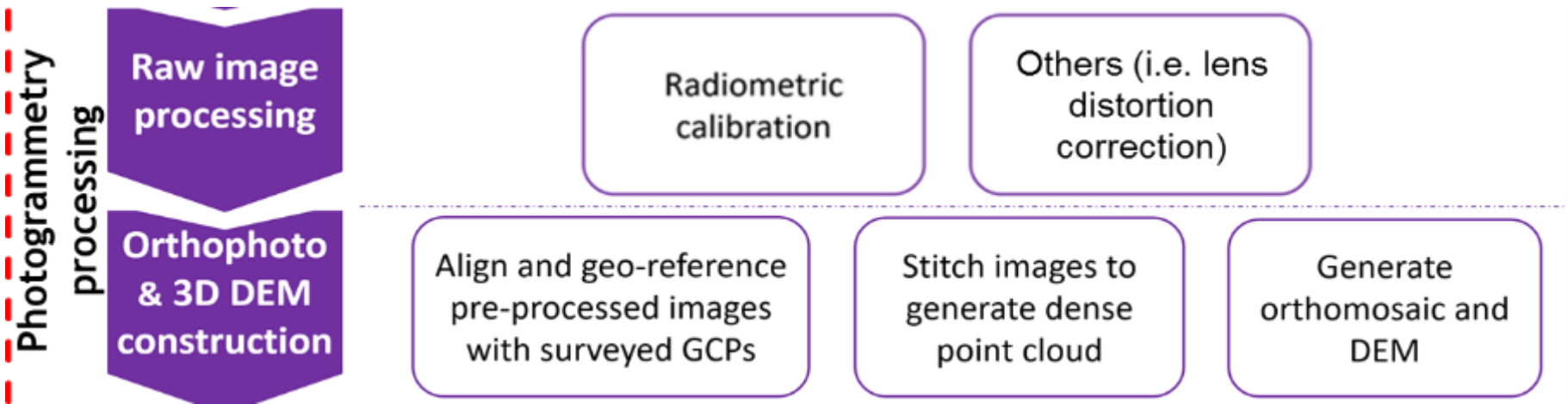


Image Processing & Extraction

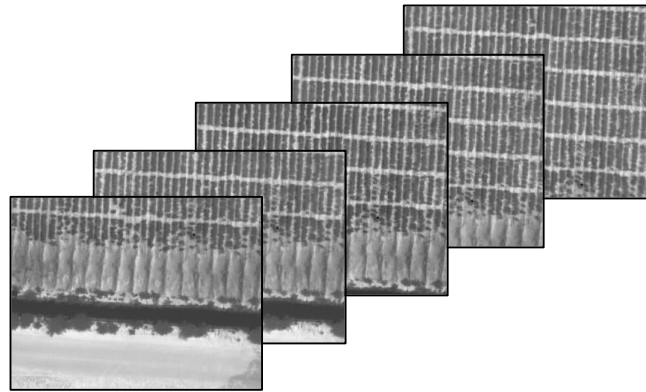


- Time reduction from months to weeks
- Extracted data available by the end of cycle

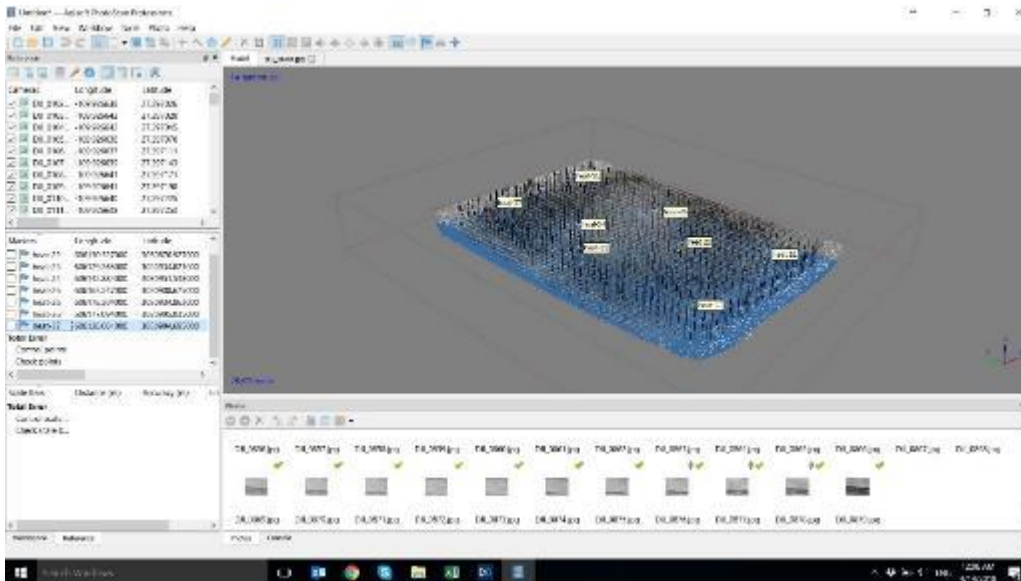
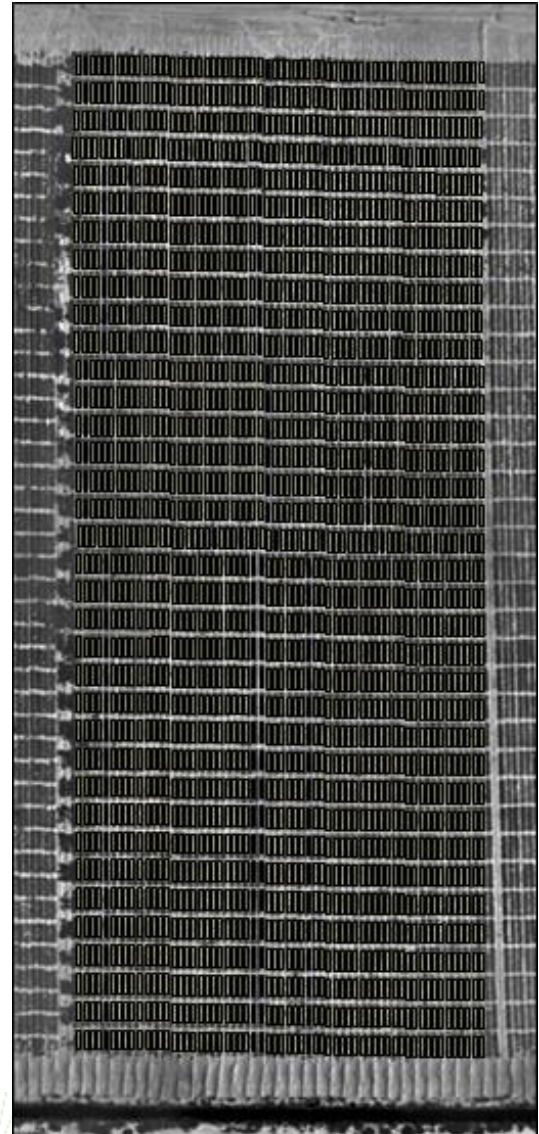


Thermal imaging

- Semi- automatic data processing:
 - Mosaics (Agisoft Photoscan)
 - Data Extraction (ArcMap + R)



80% image overlap

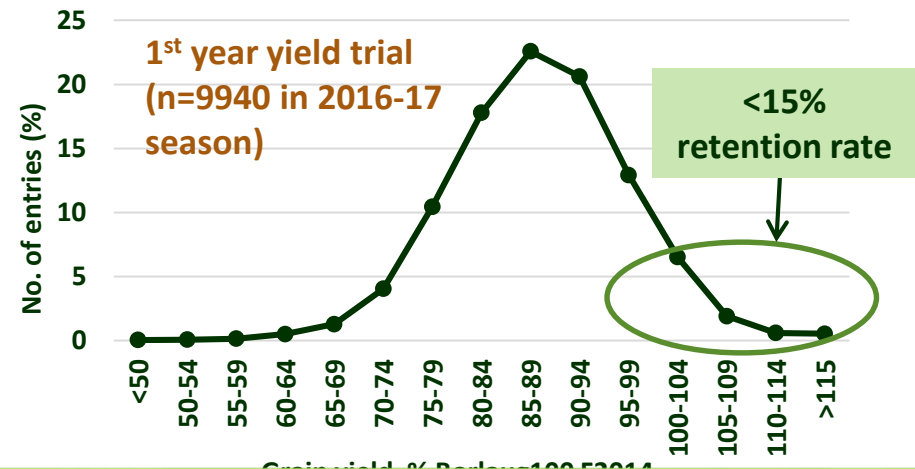


Mosaics using Agisoft Photoscan

Data extraction per plot
using polygons

Potentials of genomic selection

- USAID Feed the Future Innovation Lab at KSU and DGGW focus on implementing GS and HTP at different stages of breeding program
- GBS, phenotypic, yield data for about 46,000 lines (2013-14 to 2017-18) utilized



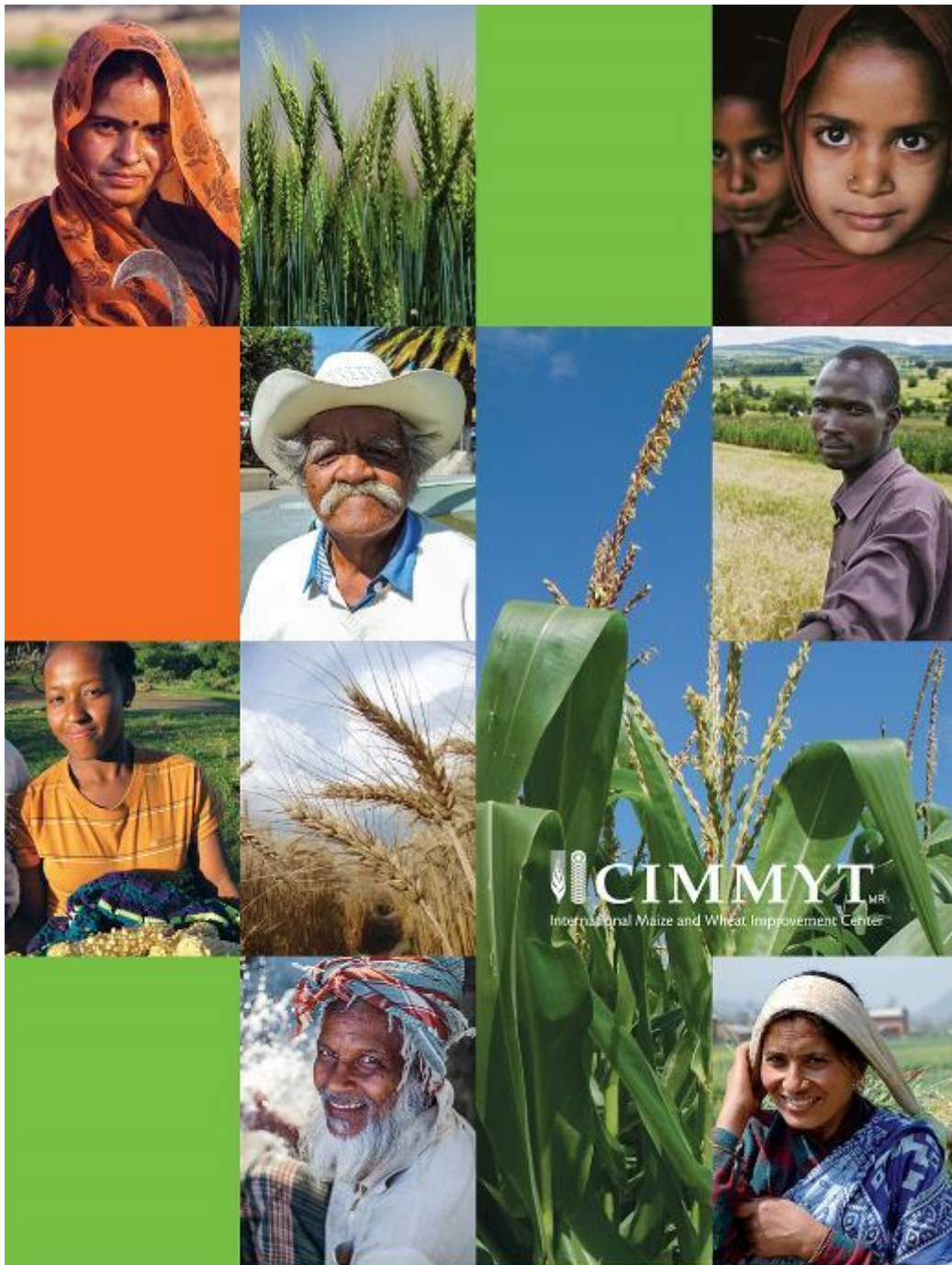
Genomic predictions are very promising for some diseases & quality traits.
Challenges: G x E and G x Y interactions need extensive research to improve predictions for grain yields

1st year yield trials

- Average within-nursery prediction accuracy Yield= 0.67, Stem rust=0.60
- Average across-nursery prediction accuracy Yield= 0.42, Stem rust=0.50

2nd year yield trials, prediction accuracy (r)

	Within	Across	Within	Across	Within	Across	Within	Across	Within	Across
Grain yield	Bed 5IR		Flat 5IR		Bed 2IR		Flat drip		Late heat	
	0.59	0.15	0.60	0.05	0.59	0.14	0.59	0.09	0.60	0.17
Disease	Stem rust		FHB		S. tritici blotch		Spot blotch			
	0.79	0.60	0.38	0.11	0.57	0.17	0.55	0.24		
Quality	Alveogram W		Flour protein		Flour yield		Loaf volume		Mixing time	
	0.72	0.52	0.73	0.5	0.61	0.43	0.72	0.5	0.76	0.48



**Thank you
for your
interest!**