NIFA CAP for Innovation in Genomic Technology to Accelerate Breeding

# Leveraging high-throughput genotyping and phenotyping technologies to accelerate wheat improvement and mitigate the impacts of climate change

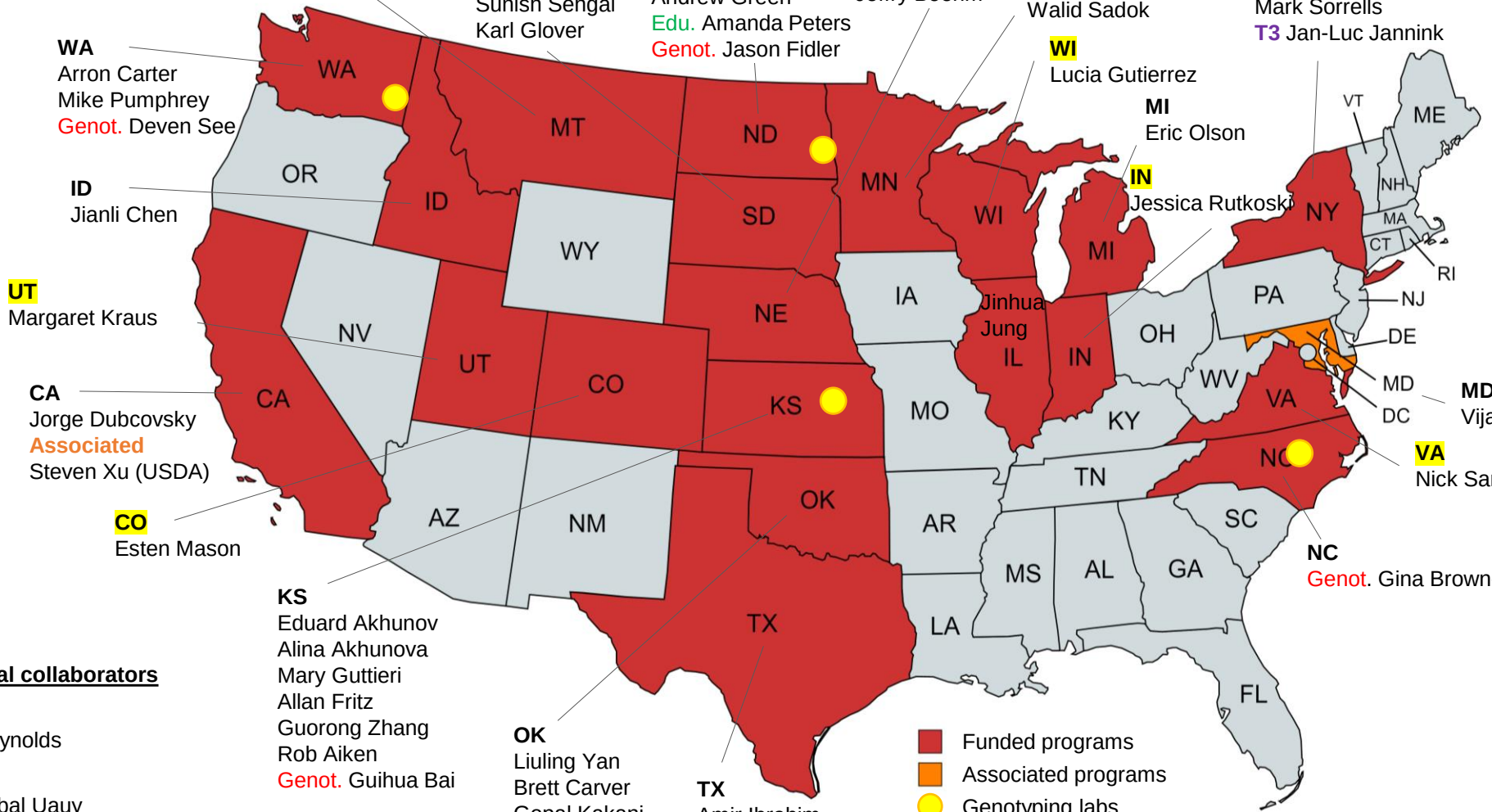
WHEAT CAP
Coordinated Agricultural Project

- 5 years (1/22 to 12/26)
- $15 M
- 41 collaborators
- 22 institutions
- 20 states

IWYP International Wheat Yield Partnership
Research to Deliver Wheat for the Future

USDA NIFA
United States Department of Agriculture
National Institute of Food and Agriculture

# WheatCAP 22-26




**MT**
Jason Cook

**SD**
Sunish Sehgal
Karl Glover

**ND**
Justin Faris
Andrew Green
Edu. Amanda Peters
Genot. Jason Fidler

**NE**
Katherine Frels
Jeffry Boehm

**MN**
Jim Anderson
Walid Sadok

**WI**
Lucia Gutierrez

**MI**
Eric Olson

**IN**
Jessica Rutkoski

**NY**
Mark Sorrells
T3 Jan-Luc Jannink

**WA**
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Mike Pumphrey
Genot. Deven See

**ID**
Jianli Chen

**UT**
Margaret Kraus

**CA**
Jorge Dubcovsky
Associated
Steven Xu (USDA)

**CO**
Esten Mason

**KS**
Eduard Akhunov
Alina Akhunova
Mary Guttieri
Allan Fritz
Guorong Zhang
Rob Aiken
Genot. Guihua Bai

**OK**
Liuling Yan
Brett Carver
Gopal Kakani
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Xuefeng Ma

**TX**
Amir Ibrahim
Shuyu Liu
Jackie Rudd
Juan Landivar
Anjin Chang

**IN**
Jinhua, Jung

**MD** Associated
Vijay Tiwari

**VA**
Nick Santantonio

**NC**
Genot. Gina Brown-Guedira

Funded programs
Associated programs
Genotyping labs

The WheatCAP participating states represent
**88.2 %** of the wheat acreage in the USA in 2020

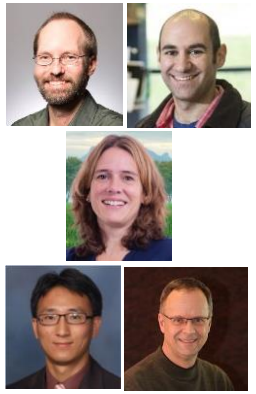
**International collaborators**

**CIMMYT**
Matthew Reynolds

**UK**
DFW Cristobal Uauy

**CANADA**
Curtis Pozniak

# Economic impact of previous WheatCAP



**Scientific Advisory Board**
Coordinator: E. Akhunov

* Ed Buckler (USA)
* Cristobal Uauy (UK)
* Susanne Dreisigacker (CIMMYT)
* Yufeng Ge (NE, UAS-HTP)
* Dave Bubeck (Corteva, NAPB)

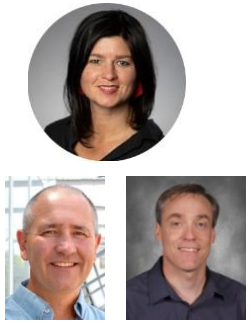
**Industry Liaison committee**
Coordinator: M. Sorrells

Rotating representatives from:

* NAWG
* US Wheat Assoc.
* Syngenta
* Bayer
* NAMA
* ABA
* LimaGrain
* Corteva

**Education Advisory Board**
Coordinator: Amanda Peters

* Sarah Davidson Evenga (Cornell)
* Allen. Van Deynze (UCD)
* Jason Rauscher (CORTEVA)



**Project Director**
Jorge Dubcovsky

**Project Co-Director**
Eduard Akhunov

**Executive Committee**
Gina Brown-Guedira
Jean-Luc Jannink
Amir Ibrahim
Amanda Peters
Rotating breeder

**Objective 1**
**Team Leaders**
G. Brown-Guedira
D. See
G. Bai
J. Fielder
J.-L. Jannink

**Objective 2**
**Team Leader**
Amir Ibrahim
Margaret Krause

**Objective 3**
**Team Leaders**
J.-L. Jannink
J. Rutkoski
L. Gutierrez
N. Santantonio

**Objective 4**
**Team Leader**
E. Akhunov

**Objective 5**
**Team Leaders**
Justin Faris
Amanda Peters

# WheatCAP 22-26 Objectives

1. Develop cost-effective medium-density SNP assays for effective genome-wide imputation using practical haplotype graphs and link these assays to a **centralized automated platform for GS** in public breeding programs.

2. Implement a **centralized pipeline for UAS-HTP** data processing, analysis and management aimed at accelerating the adoption of this technology in public wheat breeding programs and the deposit of UAS data in T3.

3. Develop **improved tools for T3/BreedBase** to accelerate the automatic deposit of genotypic and agronomic data from public breeding programs into T3, and actively promote the exchange of data and analyses tools with equivalent public wheat databases in CIMMYT and the UK.

4. Develop a public **genomic resource** including the characterized natural and induced genetic variants that regulate gene expression in wheat and integrate this information into GS and the T3/BreedBase database.

5. **Train a new cohort of 20 plant breeders** within an active Community of Practice in plant breeding, by integrating them into active wheat breeding programs developing improved wheat varieties.

# WheatCAP “big picture”

1. During the previous WheatCAP we identified multiple gene affecting different grain yield components and determined the value of different alleles. We realized that the effect of these genes is modulated by epistatic interactions with other genes and with the environment.

2. We also realized that the number of gene x genotype x environment interactions is too large to be tested experimentally by any single laboratory. "What is the effect of different allelic combinations among genes A x B X C x D in environments X and Y?”

3. A possible way to tackle these questions  is by using the extensive phenotypic / genotypic data generated by the breeding programs, which each year test thousands of lines in multiple environments across the US. We can generate a powerful tool to answer the questions *in silico* if:
   - The phenotyped lines are genotyped.
   - The genotypic and phenotypic data is deposited in T3/BreedBase.
   - Alleles for large number of genes are inferred with PHG

4. This extensive phenotypic/genotypic database can also increase predictive values in our GS programs…

# WheatCAP metrics to evaluate progress

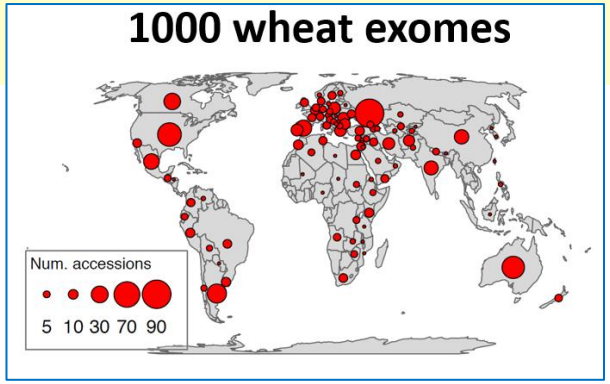
1. **Information deposited in T3/BreedBase**
   - Number of lines genotyped and submitted to T3/Breedbase (500/program/y).
   - Number of lines phenotyped (agronomic and UAS-HTP) deposited in T3/Breedbase.
   - Adoption of BreedBase in the public breeding programs.

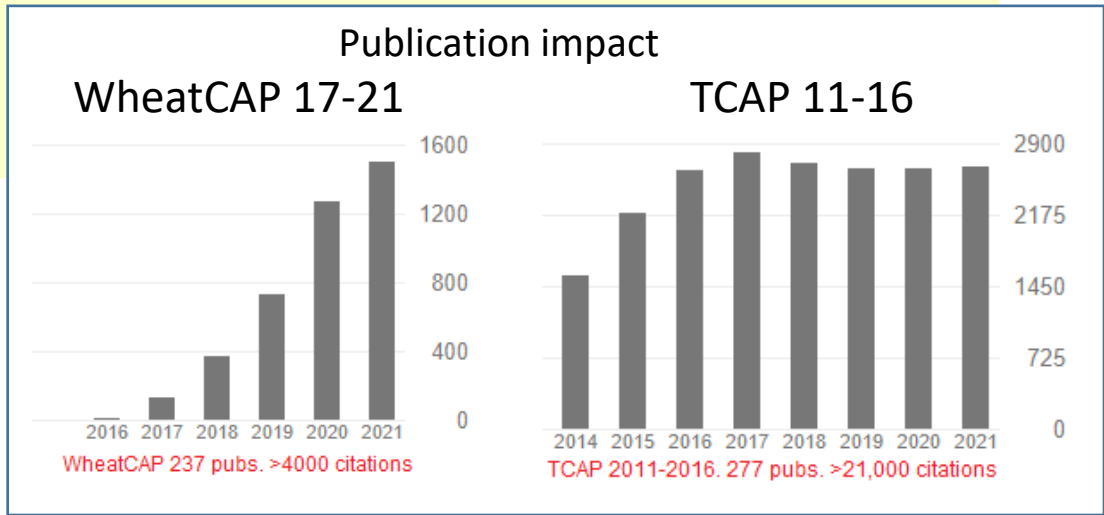
2. **Released varieties** and their economic impact. This is the central metric that USDA uses to ask for support for our program. Please report released varieties in the annual report. We need PVP application number and day of application for REEport. Keep track of the acreage of public wheat varieties in your state.

3. **Publications** explicitly acknowledging this grant: "This project was supported by the Agriculture and Food Research Initiative Competitive Grant 2022-68013-36439 (WheatCAP) from the USDA National Institute of Food and Agriculture"

4. **Trained students**. Number, quality of the training and jobs they get.

5. **Genomic resources** generated.



# WheatCAP projects. 20 years of progress from traditional breeding to genomics-based breeding

| | Years | Collab. | Pubs. | Var.+G. | Students | Highlights |
|---|---|---|---|---|---|---|
| **IFAFS Wheat** | 2001-04 | 12 | **38**<br>Cit: 4493<br>Avg: 118 | **93** | **12 G**<br>39 UG | • 1st molecular markers and MAS backcrossing.<br>• Markers 47 traits incorporated into 93 Var. & Germ. MASwheat site created<br>• Cloned: Vernalization genes *Vrn1* and *Vrn2.* |
| **1st WheatCAP** | 2005-10 | 17 | **102**<br>Cit: 9898<br>Avg: 97 | **90** | **86 G**<br>125 UG<br><br>Mapping and QTL courses<br><br>Coordinated training | • 23 mapping populations all market classes in 7 env.<br>• 1.5 M data-points. Mainly SSR first SNP exploration<br>• Markers 45 genes and 360 QTL (today in T3 and GG)<br>• Forward breeding MAS with Genotyping labs (930,000)<br>• Extension (21,000 stakeholders contacted)<br>• Changed perception of marker technologies<br>• Cloned: *Yr36, GPC-B1* (protein), *Vrn3, Fr2* (frost), *PSY1* (yellow pigment) |
| **TriticeaeCAP**<br><br>(wheat & barley) | 2011-16 | 56 | **277**<br>Cit: 21,000<br>Avg: 76 | **182** | **65 G**<br>115 UG<br><br>PBTN implemented<br>Educational trips and workshops + online resources | • SNP platforms developed (9K and 90K)<br>• Genotyped core wheat & barley germplasm NSGC and breeding lines<br>• Association panels and NAM populations developed<br>• Multiple GWAS in multiple locations.<br>• T3 database implemented and expanded<br>• Canopy spectral reflectance technologies implemented<br>• Cloned: *Sr35* (stem rust), *Vrn4* (vernalization) |
| **2nd WheatCAP** | 2017-21 | 21 | **237**<br><br>Cit:4070<br>Avg: 17.2 | **122** | **43 G**<br><br>Workshops<br>• Positional cloning<br>• RNAseq<br>• T3<br>• PHG<br>• Science com. | • Exome capture platforms implemented and 1000 wheat exomes sequenced<br>• 10,000,000 mutations sequenced in all coding regions<br>• Recombination map of wheat<br>• Open chromatin regions identified. Capture design in progress.<br>• Practical Haplotypes Graphs (PHG) being developed<br>• High density map and QTL cloning for yield components<br>• Wheat transformation methods improved<br>• Started implementation of genomic selection in public wheat breeding programs<br>• Cloned *WAPO1, TaCKX2*, *GW7, GS3*, *LFY, FT2, FUL3, AWNS1, Sr13, Sr21, Sr60*. |
| | 20! | | 654 (40K citations) | **487** | **206** graduates | • Most current genomics and marker assisted selections tools for wheat |

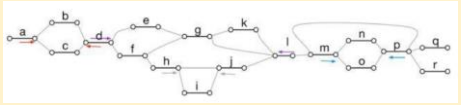
https://www.triticeaecap.org/publications-and-germplasm/

# Agenda

8:00 – 8:15. **J Dubcovsky**. Opening remarks.
- Introductions wheat Cap participants and organization
- Objectives and metrics by which the project will be evaluated
- The big picture

8:15 – 8:30. **Gina Brown-Guedira**.
- Medium throughput genotyping platforms.
- Lessons from the implementation of GS in the Eastern public wheat breeding programs.

8:30 – 8:45. **Eduard Akhunov** and PHG development group.
- PHG as a platform for the adequate representation of genomic diversity in wheat.
- Current PHG v1 design, value, utilization in the project and pending tasks to an improved PHG v2.
- Natural variation on wheat expression.



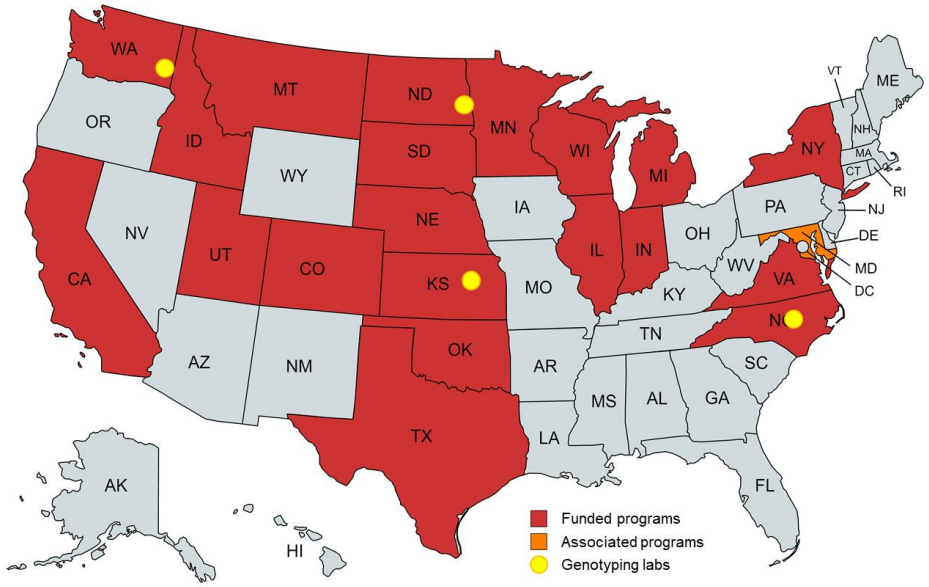
8:45 – 9:00. **Amir Ibrahim and TX-IN group**.
- Overview of the UAS-HTP pipeline.
- Technical characteristics of the images to be submitted and frequency during the growing season.
- Information expected to go back to breeders .

9:00 – 9:15. **Amanda Peters** Education coordinator.
- Transition students previous WheatCAP grant and plans for new students
- Expected activities for year 1

9:15 – 9:30. **Jean-Luc Jannink** T3/Breedbase
- Current tools provided by BreedBase to breeders' daily activities
- Role of T3 in the coordination of the data generated by the GS pipelines
- Planned BreedBase tools for this project

T3/Wheat

9:30 – 9:45. **Jessica Rutkoski** 9:30 – 10:10.
- Learned experiences from implementing BreedBase in a breeding program
- Advice for programs starting the transition: what are the first steps to focus

9:45 – 10:00. Open discussion

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