

Cover page

a. Award #: 2022-68013-36439

b. Project Title: “Leveraging high-throughput genotyping and phenotyping technologies to accelerate wheat improvement and mitigate the impacts of climate change”

c. Project Director: Jorge Dubcovsky

d. Project website: <https://www.triticeacap.org/>

- **Appendix 1.** Germplasm releases
- **Appendix 2.** Publications
- **Appendix 3.** Community resources
- **Appendix 4.** Graduate students

e. Institution name: University of California, Davis

f. Requested amount: \$3,000,000

WheatCAP Year 1 report

1. SUMMARY WheatCAP overall productivity: During the first year of the project, WheatCAP breeders have released 33 commercial varieties and 7 improved germplasm. The WheatCAP team published 47 peer-reviewed papers (not reported before). Data was collected from 173 UAS flights over 23.8 acres and a total of 25,400 samples were sent for genotyping (mostly with medium throughput genotyping platforms). Approximately 55,000 plots from 175 trials were entered by Breeders into T3, with data already incorporated for 167 trials, based on currently available information. This information was used to advance the implementation of genomic selection in public wheat breeding programs. In addition, the combined genotypic and phenotypic datasets represent an invaluable resource to investigate the effects of different alleles and their epistatic interactions across environments and germplasm. This year, 7 students completed their PhD and 42 participated in multiple educational activities organized by the project. Students' personal profiles and projects as well as links to project meetings and educational resources are available at the WheatCAP web site (<https://www.triticeacap.org/>). The complete lists of released varieties and publications are available in Appendices 1 and 2, respectively. Community resources are in Appendix 3 and students trained in Appendix 4.

2. Education

A central objective of the WheatCAP project is to train PhD students in molecular plant breeding. By leveraging funds from participating universities and inviting students from universities not funded by the project (e.g. Purdue University, University of Maryland-College Park) to participate in educational activities, the WheatCAP participants have exceeded the proposed target of 20 students. During the first year of this grant, we trained 49 graduate students, including 7 that started in the previous WheatCAP and graduated this year and 42 current (Appendix 4). Of these students, 47% are female, indicating a good balance, in a profession that was historically male-dominated.

In September 2022, all students were surveyed to determine their education level in the fields related to plant breeding and their WheatCAP projects. The 2022 annual survey results are posted on the WheatCAP website (<https://www.triticeacap.org/2022-graduate-student-survey/>). Annual surveys are being used to track WheatCAP student education progress, assess their preparedness for careers in plant breeding and help the educational team design workshops and meetings to meet the needs of the students.

A “Slack” work page was created for WheatCAP students to discuss their research projects and to connect with one another. Monthly meetings over Zoom occurred in the spring and fall of 2022, with a break during the summer for the field season. Monthly meeting topics included an introduction to the objectives of the WheatCAP grant and how to use T3 and BreedBase. This fall, we held a workshop on Equity in Plant Breeding and hosted a panel discussion with three breeders from private companies. Bi-weekly writing groups discussing student writing (manuscripts and dissertations) were formed with 14 students currently participating. A full-day workshop is planned for this January at the Plant and Animal Genome (PAG) conference dedicated to student presentations and discussion of their projects (in addition to the main annual meeting).

Educational activities have also included updating the online education delivery platform Plant Breeding Training Network (PBTN) (<https://passel2.unl.edu/view/community/b6721f4789d7>).

Leah Sandall has been working on identifying and fixing broken links and Amanda Peters Haugrud has been identifying and correcting out-of-date information. Additionally, we plan on adding lectures on topics that were identified as areas in which students feel less confident in, such as: genomics, selection theory and techniques, methods for breeding in selfing and outcrossing systems, plant breeding strategies, genomic selection, and UAS-HTP.

3. T3 database

3.1. Personnel: David Waring continues to support upload of and curate all incoming data. He also writes code to add and improve features on T3. Clay Birkett (full time USDA-ARS employee) works on integrating the PHG and uploads all genotypic data. A new postdoc should be able to start in early 2023 to work with WheatCAP breeders to develop genomic prediction models.

3.2. New wheat datasets made Findable, Accessible, Interoperable, and Reusable

Data Category	Current Total	Added since last Report *
Accessions with phenotypes	34,059	11,729
Accessions with genotypes	16,656	281
Total Accessions	57,407	20,146
Phenotyping Trials	3,283	239
Plots with phenotypes	286,000	(36,000) **
Phenotype Observations	1,138,372	239,423
Genotyping Projects	43	3

*The last report was the final report for the previous WheatCAP.

**This metric was not tracked in the last report. Estimated from breeders' reports.

There may be some discrepancies between the sum of numbers of plots and accessions reported by breeders and the T3 content status report. These discrepancies originate from two different sources. First, some breeders entered historical data in T3, which are not included in the above T3 tally for 2021-2022 results. Also, breeders reported trials that are still in the process of being uploaded to T3 and are therefore not yet included in the above T3 tally.

Among the 153 new field phenotyping trials uploaded since the last report, 136 were uploaded since the start of WheatCAP3 (Jan. 1st, 2022), 123 have documented field layouts that are important for communication with the UAS-Hub, and 102 already have some standard phenotype data. The number of accessions with genotypic data is expected to increase sharply once the low-cost medium density genotyping platform is completed.

3.3. Improvements to T3 usability for breeders: Given the emphasis in the current WheatCAP on collecting data from unoccupied aerial systems (UAS), we are focusing on improving features to upload, display, and operate on field layout. Among improvements to T3 in this area are:

- During upload, warn user if no field layout was included in the upload

- Enable multiple trials to occupy the same field. This feature includes not requiring trials to start on row 1, column 1.
- Ability to download plots in different orders as a function of serpentine or zigzag planting, phenotyping, or harvesting.

T3 has also improved breeder functionality and developed genotyping plate sample tracking.

- It is now possible to create trials with a p-rep experimental design in addition to other existing augmented designs.
- T3 has expanded functionality to manage seedlots, including tracking seed origin, storage location, and transactions that change the amount of seed in the lot. Seedlot records can be created directly from plots harvested in a trial.
- T3 now supports entry numbers in addition to accession and plot names.
- Genotyping plate sample tracking: T3 is developing features to enable barcode printing and management to accompany genotyping plates to the facilities and receive scored genotypes directly from those facilities.
- Robust user interface and guardrails to improve T3 content validity.
- T3 has implemented automated synonym searching to prevent the duplication of accessions with slightly different names. We continue to improve tutorial videos for training T3 users.

3.4. Communication with the UAS-Hub: T3 is working on establishing a server-to-server communication between the Texas A&M UAS-Hub and T3. Currently, the UAS-Hub is able to download field layouts from T3 so that it can tie images submitted by users to specific plots. T3 has created within its trait ontology all of the traits that are estimated by UAS-Hub so that these are available for UAS-Hub to transmit phenotypic values for them.

3.5. Practical Haplotype Graph integration: Wheat breeding lines have historically been genotyped with many different marker platforms, from Illumina chips, to genotyping by sequencing, to various amplicon sequencing methods. In order to unlock the power of aggregating data across time and breeding programs, different genotyping projects need to be imputed up to a high-density common set of markers. Along with collaborators K. Jordan and E. Akhunov, T3 is working to integrate the Practical Haplotype Graph (PHG) into T3 for this purpose. Version 1 PHG contained 65 wheat lines with exome capture sequence data, and now we are working with version 2 that has 472 wheat lines.

3.6. Outreach: T3 held two data upload practice sessions with WheatCAP graduate students on April and November, 2022. At that time, not all WheatCAP students had been recruited. YouTube tutorial videos for specific steps were provided to the students. They created accounts on the T3 sandbox and on the WheatCAP instance and uploaded scratch datasets. A publication is now available describing Breedbase (Publication 21 Appendix 1).

4. Genomics resources

4.1. Sequenced TILLING populations: WheatCAP has provided access to the sequenced mutant populations of tetraploid and hexaploid wheat including more than 10,000,000 mutations in the coding regions of the wheat genome. Recently, the UC Davis group performed promoter captures on 1,534 tetraploid wheat TILLING lines and identified 4.3 million sequenced

mutations in the promoters of all the high-confidence annotated genes. Results are available in GrainGenes and in the UC Davis website.

4.2. New regulatory capture for wheat: The previous promoter capture was discontinued by NimbleGen so we collaborated with Arbor BioSciences to develop a new regulatory capture for wheat, which is now commercially available. The core target space includes sequences from two Kbp upstream of each gene predicted in the Chinese Spring wheat genome and regions of open chromatin identified with ATAC-seq from wheat leaf and root samples. Repetitive sequences were aggressively filtered. The final design consists of 16.5 Mbp of predicted hybridization space in hexaploid wheat and showed increased specificity and coverage of targeted sequences relative to previous protocols. Test captures on hexaploid and tetraploid wheat and other diploid cereals show that the assay has broad potential utility for cost-effective promoter and open chromatin resequencing and general-purpose genotyping of various Triticeae species.

4.3. Gene expression variation: We have completed the first study on the natural variation in gene expression in wheat based on RNA-seq data from 2-week-old seedlings of 198 diverse accessions (He et al. 2022, Appendix 2). We used diverse allohexaploid wheat accessions to map expression quantitative trait loci (eQTL) and evaluated their effects on the population-scale variation in the homoeologs' expression levels. Both selection and polyploidization affected the relative contribution of wheat genomes to regulatory diversity, with the relative expression dosage of homoeologs influenced by cis-acting variants associated with the expression dysregulation of individual homoeologs. Joint modeling of eQTL and GWAS summary-level data and gene co-expression network analyses revealed association between common cis-acting variants affecting the homoeolog dysregulation and variation in productivity traits. Our study demonstrates the importance of genomic diversity affecting homoeolog expression dosage variation in shaping agronomic phenotypes and opens opportunities for improving polyploid crops by the targeted optimization of the relative expression of multiple homoeologs in trait-associated pathways. Currently, we are assembling and validating a larger panel of wheat, wild relative and synthetic lines for sampling multiple tissues for a more comprehensive eQTL analysis.

4.4. Developing multi-OMICs data for characterizing functional variation in the wheat genome: To assess the role of methylation in gene regulation, we used whole-genome methylation profiling of 96 hard red winter wheat lines from the US Great Plains. This panel was characterized for major agronomic traits in multi-year field trials. The Bismarck software was used to identify methylated cytosines in the CHH, CHG or CpG motifs. Genic regions showing high levels of variation in the levels of methylation among wheat lines have been identified. The methylation levels in the CHH, CHG or CpG contexts showed bi-modal distribution, where genomic regions occupied by transposons showed low coefficients of variation ($CV < 0.2$). The high-CV regions ($>95^{\text{th}}$ percentile of genome-wide CV) were mostly associated with genes. Currently, we are working on the integrated analyses of gene expression and methylation data to better understand the role of methylation in controlling the levels of gene expression in wheat. The methylation data will be deposited to T3 by the end of 2022 after quality checks aimed at assessing the accuracy of methylated cytosine calls.

4.5. Second generation PHG: The first-generation Practical Haplotype Graph (PHG) was based on the exome capture sequencing of 65 diverse wheat lines. This PHG showed high accuracy of imputation ranging from 93% to 96.9% in low-coverage sequencing data (0.01-0.5x) (Jordan et al., 2021). In 2022, we generated a second generation PHG including additional lines genotyped

using exome capture. The new PHG now has 472 lines, including 90 hard winter wheat from Southern Plains, 94 spring and winter wheat lines from Northern Great Plains, 95 soft winter wheat lines from Southern Regions, and 193 lines from the Pacific Northwest region. The updated second-generation PHG has more than 5 million SNP variants and has been transferred to T3 database to develop improved imputation tools.

4.6. Expanding the Wheat PanGenome to improve the PHG tool: To improve detection of genetic variants and the accuracy of imputation, we expanded the set of reference genomes for updating the PHG. We sequenced a set of six diverse wheat lines selected from world-wide sample of lines to capture maximum level of genetic diversity using the PacBio platform. The HiFi reads providing 10-12x genome coverage were assembled using Hifiasm software. The average N50 of assembled genomes was 7.98 Mb and the total average size of the assemblies was 14.5 Gb. The data is currently combined with the Wheat Pangenome data to use as references for variant calling in the exome capture and whole-genome re-sequencing datasets generated for the US wheat cultivars. We plan to use this newly generated data for developing the next generation of the wheat PHG.

4.7. Wild relative introgression improves adaptive potential of wheat: The KSU team characterized the introgression populations developed by crossing wheat with wild emmer and *Aegilops tauschii*. We performed deep sequencing (10x coverage) of parental lines and low-pass (0.01x coverage) sequencing of introgression lines, and we developed a pipeline that identifies parent-specific alleles and assigns chromosome segments to one of the parental lines. Using this approach, introgression segments were mapped in populations of ~350 *Ae. tauschii* introgression lines and 400 wild emmer introgression lines. The *Ae. tauschii* introgression population was grown in 2019-2022 field trials under irrigated and non-irrigated conditions and characterized for yield, yield components, development, and UAS-based spectral and thermal reflectance traits. The manuscript describing these results has been submitted for publication.

5. Genotyping Laboratories

Large numbers of samples were genotyped using non-targeted sequence-based approaches (GBS, MRASeq) as part of ongoing genomic selection and gene mapping efforts. This includes 9,856 samples processed in the regional genotyping labs, in addition to 8,779 samples processed by the breeding programs at University of Minnesota, Michigan State University and Colorado State University (**Table 1**).

Regional genotyping labs supported breeding programs by genotyping submitted samples using known informative markers (KIMs) based on the KASP and STS assays or amplicon sequencing approaches (GBMAS). The GBMAS approach targeting approximately 2,000 markers was used for 480 samples. A total of 14,976 samples were submitted to the genotyping labs by WheatCAP breeding programs that were evaluated with 1 to 102 KASP assays. An additional 1,152 wheat lines were evaluated with a PlexSeq primer pool developed in collaboration with Agriplex Genomics. Data for 81 agronomically important alleles were determined to be reliable and reported to breeders. While efforts continue to further develop and validate this platform, this current multi-plex amplicon sequencing primer pool is available from Agriplex as a targeted genotyping service.

Research was conducted by the regional genotyping labs on development of mid-density genotyping platforms that provide uniform genome coverage, have a high information content,

and include validated informative markers previously used in selection. The genotyping lab at Fargo has worked to develop a new genotyping platform based on the Illumina Infinium II array technology that targets approximately 3,000 SNPs in each wheat, oat and barley. Validation of this platform with ~12,000 previously genotyped lines showed good technical performance and high concordance with other platforms. As expected, at least 2,000 markers were informative within a given breeding program and are sufficient for the development of highly accurate genome prediction models. The platform is robust, requires only 200 ng of DNA, and has a fast turnaround time of three days for delivering usable data. The small grains content was added to a new 3,000 Soy array and has been released as the USDA-SoyWheOatBar-3K that is currently available for \$14 per sample. This multi-species format enables dual hybridization to decrease the per-sample cost. Concordance between dual and single mode is ~95% for all SNPs and increases to ~99% on a high-performing subset of SNPs.

Table 1. Overview of WheatCAP Genotyping samples for 2022

Genotyping Lab	Program	No. of samples	Genotyping platform	Genotyping Lab	Program	No. of samples	Genotyping platform
Western	WSU	2688	GBS	Northern	Regional	96	Illumina 3K
	UI	384	GBMAS		MSU	384	Illumina 3K
	UCD	96	GBMAS		MSU	1536	GBS
	UCD	192	SPET, Agriplex		USDA-Fargo	1104	Illumina 90K
Central	KSU	96	KASP, STS	Eastern	NDSU	192	Illumina 90K
	KS/ARS	1056	KASP, STS		MSU	288	AVR, 25K
	MSU	192	KASP, STS		NDSU/USDA	7968	KASP
	UNL	288	KASP, STS		UMN	1623	GBS
	UNL/ARS	192	KASP, STS		U. Idaho	384	Illumina 90K
	OSU	384	KASP, STS		MSU	2784	GBS
	TX A&M	960	KASP, STS		U IL	1344	GBS
	NDSU	96	KASP, STS		Cornell	384	GBS
	SDSU	288	KASP, STS		VA Tech	1056	GBS
	Regional	480	102 KASP, STS		ARS-NC	288	GBS
	KSU/ARS	1056	MRASeq		Regional	256	GBS
	TX	384	GBS		ARS-NC	1344	11 KASP
	SDSU	750	GBS		Regional	960	28 KASP
	KSU	480	GBS		Regional	960	Agriplex
	Regional	480	MRASeq		Regional	2112	SPET
	CSU	6372	GBS				

The Allegro platform that utilizes the single primer extension technology as a targeted sequencing approach was tested by the genotyping lab at Raleigh. Evaluation of 1,536 samples using a probe pool targeting 3,680 genome-wide loci recovered data for 2,845 loci, leading to an 84% conversion rate. Samples were sequenced using two lanes of Illumina NovaSeq S1, each having 768 pooled libraries at a total cost of \$8.95 per sample. A SNP calling pipeline was developed using Bowtie2 and BCF tools. Mean missing data levels were less than 4% and mean read depth was 250, indicated that higher levels of sample pooling are possible to further reduce costs. Using a subset of 1,000 markers, genomic prediction accuracies for FHB resistance traits were similar to predictions based on 6,000 GBS markers.

Together, the four regional genotyping labs are investigating development of an AmpliSeq highly multiplexed PCR platform targeting 5000 loci. Sequences flanking 1,500 exome capture

SNPs with high information content in each wheat market class and even distribution throughout the genome were selected for submission to ThermoFisher in early October, 2022 for an initial design phase. A total of 194 sequences targeting KIMs were also included. ThermoFisher will synthesize the primer pool and validate the pool on 384 samples selected to represent US germplasm. This validated platform will be available to the US wheat community for \$10 per sample as a genotyping service for three years.

6. UAS-Hub (Texas A&M University and Purdue University)

6.1. UAV data collection and processing: In the WheatCAP proposal, year 1 was set for the evaluation of the UAS-HTP centralized data pipeline, with full implementation planned for year 2. Still, significant progress was achieved in year 1, with 19 wheat breeding programs submitting data to the UAS-Hub. Four breeding programs with advanced UAS internal projects, submitted their data directly to the T3 database. A survey conducted by the UAS-Hub revealed different levels of expertise and access to UAS resources among WheatCAP breeding programs. The Texas A&M/Purdue team dedicated more time to programs new to UAS technology to help them identify the best platforms for their needs.

6.2. A centralized online platform was developed by the TAMU/Purdue UAS-HTP group (<https://wheatcap.uashubs.com/>) for data receiving, processing, and importation. The UAS-Hub completed UAS data processing for 9 fall planted wheat programs as shown in the table below. The team is currently is waiting on boundary correction from 3 programs. The UAS-Hub has begun working with two spring wheat programs that submitted raw UAS data later this year, and with the University of Wisconsin-Madison on identifying equipment for their platform. This program is now well set for flying in year 2. The UAS-Hub has not received a response from Michigan State University.

Table 2. Summary of UAS-Hub received and processed data

No.	Location	Flights	UAS-Hub Project created	Processing & Data Delivery
1	TX-College Station / McGregor	25	2022 College Station Wheat/ 2022 McGregor Wheat	CC, CH, CV, ExG, NDVI, NDRE.
2	TX-Amarillo Irrigated	23	2022 Amarillo Irrigated	CC, CH, CV, ExG, NDVI, NDRE.
3	Kansas-Colby (KS)	12	2022 Colby Wheat	CC, CH, CV, ExG, NDVI, NDRE.
4	Kansas-Hays (KS)	7	2022 Hays Wheat	CC, CH, CV, ExG, NDVI, NDRE.
5	UC Davis (CA)	9	2022 Davis Irrigated	CC, CH, CV, ExG, NDVI, NDRE.
6	Virginia Tech (VA)	16	2022 Virginia Tech	Will process their own data.
7	OSU (OK)	- ¹	2022 Oklahoma State U.	Will process their own data.
8	CSU (CO)	12	2022 Colorado State U.	Will process their own data.
9	WSU (WA)	29	2022 Washington Wheat	Will process their own data.
10	Cornell (NY)	2	2022 Cornell Wheat	CC, CH, CV, ExG, NDVI, NDRE.
11	UIUC	8	2022 UIUC Wheat – St. Peter	Waiting for boundaries.
12	UNL Lincoln/Sidney	4	2022 UNL Wheat – Lincoln	No GCP's. Uploaded orthomosaics.
13	USU (UT)	6	2022 Utah Wheat	CC, CH, CV, ExG, NDVI, NDRE
14	Idaho (ID)	11	2022 Idaho Wheat	Waiting for boundary correction
15	SDSU (SD)	6	2022 SDSU Wheat	Working on plot boundaries.
16	UMN (MN)	-	2022 UMN Wheat	Will start in year 2.
17	UW-Madison (WI)	-	2022 UW-Madison Wheat	Will start in year 2.
18	NDSU (ND)	-	2022 NDSU Wheat	Will start in year 2.
19	MSU (MT)	10	2022 Montana Wheat	No GCP's. Uploaded orthomosaics

¹ Change of personnel. See OK report.

6.3. List of spectral vegetation indices and canopy features developed by the UAS-Hub team: Canopy cover (CC), Canopy Height (CH), Canopy Volume (CV), Average Excess Green Index (ExG), Average Normalized Difference Vegetation Index (NDVI), and Average Normalized Difference Red Edge Index (NDRE).

6.4. Bottlenecks for efficient data processing & delivery: We have identified several areas that can be improved for more efficient data processing and delivery: a) Different breeding programs are using different sensors to collect data, which requires time to learn and validate results. We will elaborate a list of suggested platforms to standardize UAV data collection and ameliorate this problem as programs update their equipment. b) Programs are still learning and sometimes do not follow data collection and transfer protocols, provide insufficient information for the field layout, or fail to collect GCP survey results. c) Boundary creation and matching with field layout is very time-consuming. We are starting to enforce data collection before plant emergence, to ensure accurate assessment of canopy height and canopy volume. All these issues were communicated to breeders and will be discussed during the annual meeting.

6.5. Connection between T3 Breedbase Database and UAS-Hub Database: We made significant progress in accessing the quality of data uploaded by the plant breeders into the T3 Breedbase Database. We will use this information to create a common identifier connecting the phenotypic and genotypic information with the UAS data.

6.5.1. Program Design and Integration: We used the existing breeding application programming interface (BrAPI) calls within the python environment to get the plot-level data uploaded by each breeder program into T3 DB. One of our immediate goals is to explore the plot map information since it provides direct link to the UAS-Hub data.

6.5.2. Workflow: We established a process that connects two database systems. After pulling information from the T3 database, the processed information and plot-level indexes will be pushed back into the T3 database, where they will be available to users. The UAS-Hub is currently working on implementing this part of the data processing pipeline.

6.5.3. Updates and plans: We have implemented a pipeline in the production website, where users input the trial ID of each field trial, and obtain the plot map information and data visualization. We are working on adding the canopy cover, height, volume, and vegetation indices to the outputs of the pipeline.

6.5.4. Limitations: While most programs adhere to the agreed data and plot layout upload formats for T3, some users fail to follow approved guidelines. To improve standardization, we are implementing several educational activities.

6.5.5. Training video: The UAS-Hub team made a video on how to draw plot boundaries and posted it on the UAS-Hub website under the support tab (How to create Plot Boundaries). Additionally, there is a Fields EPSG file that contains information needed to create the boundaries. We will upload this video on the WheatCAP site. We plan to train the WheatCAP students so they can help the breeding programs with drawing plot boundaries in year 2 to expedite data processing.

7. Spring and winter Hubs

7.1. Winter Wheat Breeding Innovation (WWBI) Hub at KSU

WheatCAP collaborates with the WWBI Hub at KSU on introgression of alleles of genes controlling yield component traits. The donor germplasm of 8 genes identified in the WheatCAP projects have been provided to the WWBI Hub for introgression into 11 winter wheat cultivars.

The *Elf3* allele, increasing spikelet number per spike and *Tagw2*, increasing grain size, weight and grain protein content have been provided in the background of cv. Kingbird-Elf3-gw2. For all 11 winter-wheat recurrent parents, BC₂ generation populations have been already developed. The 1AL QTL allele, which has a positive effect on grain yield, was provided in the background of AGS 2000. To-date, the BC₂F₁ or BC₃F₁ crosses have been made between AGS 2000 and recurrent parents KS090387K-20, Hilliard, TAM 114, and Tekoa. The CRISPR-Cas9-edited alleles of *TaGW7*, *TaGW2*, *TaCKX2-1*, *TaCKX2-2* and *TaARF4* developed in collaboration with WheatCAP were used to generate BC₁ or F₁ crosses with the WWBI Hub parents OK16D101089, Bob Dole, OK13625, KS090387K-20, SF Fortify, Tekoa, and IDO676.

7.2. Spring Wheat Hub at CIMMYT

Five WheatCAP experiments were performed at the CIMMYT Spring-Hub, which are listed in Table 3. QTLs mapped and genes cloned in the previous WheatCAP by programs in CA, CO, MT, and WA were introgressed into high-yield and high-biomass breeding lines and were evaluated in the spring wheat Hub in Obregon, CIMMYT.

Table 3. List of the WheatCAP experiments in the CIMMYT-Hub Obregon cycle Y21-22.

	Trial	lines	blocks	plots	Scientist	Sowing details
Y2	CA Y21	4	12	48	J. Dubcovsky	hill plots Y20-21 (8reps), small plots Y21-22 (12reps)
Y2	MT Y21	10	8	80	Jason Cook	hill plots Y20-21 (5 reps), small plots Y21-22 (8 reps)
Y2	CO Y21	40	3	120	Andrew Katz, Esten Mason	hill plots Y20-21 (3reps), small plots Y21-22 (3reps but discard Bonus)
Y1	WA Y22	24	4	96	Arron Carter	small plots late sowing in Y21-22
Y1	MT Y21	4			Jason Cook	hill plots late sowing in Y21-22

7.2.1. CA: The *WAP0-A1* allele for high number of spikelets was introgressed into the two high biomass lines GID4314513 and GID4577963 by five backcrosses and the BC5F4 seed was evaluated at Obregon in an RCBD with 12 reps. Both genotypes showed significant increases in SNS (6.5% increase across the two genotypes). The effects in grain number and grain yield were not significant at CIMMYT but were significant in replicated experiments at UC Davis, suggesting interactions between genotype and environment. The results were published in PLOS Genetics (App. 2).

7.2.2. CO: CSU introgressed the high-value *Qsn.csu-6Bb* and *WAP0-A1b* alleles for greater spikelet number into three CIMMYT high biomass parents; ‘Bonus’, ‘Nadi’, and ‘GID:4314513’. Field trials were conducted at CIMMYT with the three BC1F2 populations in 2021 and two of the BC1F2 populations in 2022 (‘Nadi’ and ‘GID:4314513’). Across all five trials, variation in spikelet number was never significantly associated with *Qsn.csu-6B*. However, in both 2021 and 2022 *Qsn.csu-6B* was significantly associated with thousand kernel weight effect size between 3.3 and 3.7 grams (*P*-value <0.01) in the population with ‘Nadi’ as the recurrent parent. A BC3F2 population has been developed with ‘Nadi’ as the recurrent parent to further understand the effect of *Qsn.csu-6B*. *Qsn.csu-6B* was mapped to a 108.0 Mbp region between markers KS0617_761651 (Chr6B: 545.3Mbp) and KS0617_768340 (653.3Mbp).

7.2.3. MT: A 6BQTL for number of fertile tillers from Vida was introgressed into the CIMMYT lines BAJ and KINGBIRD to generate isogenic lines. The experiment, performed as an RCBD with 5 blocks showed a significant 10.2% increase in total number of grains per m². No significant differences were

detected for the number of spikelets per spike, suggesting that the increase in grain number per m² reflects an increase in the number of pikes per m², which is the expected result. The high tillering alleles of the 6BQTL showed a positive effect on grain yield of ~4.4%, but the differences were not significant.

7.2.4. WA: The WSU team is focused on a strong QTL for kernel weight (LOD=6.5) and kernel number (LOD=6.6) identified in the cross between elite spring cultivars Kelse and Scarlett. They sent near-isogenic hard red spring wheat lines to CIMMYT for evaluation in 2022. They were planted in January 2022 and harvested summer 2022. Lines were BC3 lines of QTL for increased seed number and size from the WSU cultivars Scarlet and Kelse crossed into five high-biomass CIMMYT lines. CIMMYT collaborators collected data on phenological, morphological, and agronomic traits. Data summarized indicates a large distribution of trait values. While most traits had significant differences between some of the isogenic lines, the traits thousand kernel weight, grain number, grain filling period, and days to heading were some of the most significant across all backgrounds. The trial in collaboration with CIMMYT will be replicated for another growing season to understand the interaction of these QTL with different high-biomass lines.

8. Progress by individual breeding programs

8.1. CA. University of California, Davis. Jorge Dubcovsky

Education: PhD student Priscilla Glenn graduated in 2022 and a new PhD student candidate Maria Rottersman is currently doing a rotation in our lab and will likely join the lab in 2023.

Germplasm & publications: 4 germplasm releases (App. 1) and 7 publications (App. 2).

UAS: Submitted 9 flights covering ~2 acres and received data back including canopy cover, height, ExG, and NDVI/NDRE values. Initial analyses showed strong (~0.9) correlation between height measured by the UAS and directly.

Genotyping: 408 samples from the field were submitted for genotyping to WA and we received information back (~1,255 SNPs). We observed inconsistency in some controls so the data has been resubmitted before depositing in T3. We also sent 192 lines to NC and received approximately 3,095 SNPs. Data was received and deposited in T3. Markers for *Yr5*, *Yr15* and *GPC-B1* were run internally for ~300 lines.

Breedbase: We submitted 19 trials including 3,117 plots, and have already deposited the yield and agronomic data for 18 trials including 3,027 plots. Uploading trials and data was simple, but uploading data directly from the Fieldbook app was not working well.

Genomic selection: We are at the beginning of the project and currently genotyping our training populations.

8.2. CO. Colorado State University. Esten Mason

Education: Andrew Katz (PhD) completed all course and prelim exam requirements for graduation in Fall 2022. Mik Hammers completed her MS in summer 2022 and started a PhD in fall 2022 and Selena Lopez (PhD) in spring 2022. Zachary Winn (former WheatCAP student at Univ. of Arkansas) started a postdoc at CSU in September 2022. Both Selena and Mik have been participating in regular project update meetings and small writing groups.

Germplasm & publications: 4 varieties (App. 2) and 3 publications (App. 1).

UAS: CO processes all flight images/data in-house. 12 flights totaling 25.15 acres across two locations were completed and data was collected for NDRE, NDVI, canopy temperature, and plant height.

Genotyping: 36 lines submitted to the Manhattan, KS genotyping center as part of the SRPN and RGON cooperative nurseries. In house genotyping of 6,372 by sequencing and 3,130 by KASP.

Breedbase: CSU has uploaded 11 trials to T3 containing 5,200 plots with agronomic data.

Genomic selection: CSU GEBVs at the preliminary yield nursery (PYN) stage for conventional crosses and the head-row stage for doubled haploids. In 2022, GEBVs were generated for 6,372 total lines. Predicted traits included grain yield, test weight, heading, height, lodging, loaf volume, flour yield, bake mix time, protein, stripe rust severity, and wheat streak mosaic virus severity. Prediction accuracy using a univariate G-BLUP model ranged from $r = 0.32$ to 0.69 . The program is currently working to implement a multivariate approach pipeline for 2023. In addition, sequencing data was used to conduct GWAS and identify haplotypes to postulate the presence of the *Sst1* locus for stem solidness, a wheat curl might resistance gene (WCM6D), and the wheat streak mosaic virus resistance gene *WSM2* on all 6,372 lines.

8.3 ID. University of Idaho. Jianli Chen

Education: Meng Su graduated in May 2022 and is now a postdoc at UI. Yaotian Gao (PhD) started in fall 2021, and Pabitra Joshi (PhD) in spring 2021. They participated in the monthly meetings, writing groups, and trainings in and T3 database.

Germplasm & publications: 3 varieties + 1 germplasm, and 1 publication (Appendices 1 and 2).

UAS: 11 flights submitted to the UAS-Hub for 1.2 acres. Orthomosaic images received and plot boundary correction in progress.

Genotyping: 384 winter wheat lines were genotyped with 90K SNP at Fargo USDA and with 3K GMS at Pullman. 85 spring wheat lines were genotyped with 90K SNP at Fargo. In-house genotyping of ~5,000 lines by KASP for multiple traits. The average number of SNPs per line is ~ 6k from the 90k SNP data. Upload to T3 pending.

Breedbase: 251 lines for one spring wheat diversity panel was evaluated in two replications and the data were submitted to T3 (grain yield, test weight, protein content, kernel weight, spikelet number per spike).

Genomic selection: Preliminary analysis was completed for three traits: test weight, protein, and yield. The prediction accuracy was 0.44, 0.64, and 0.44, respectively. We are selecting lines with specific genotypes and keep adding genotypes to update our training population.

8.4 IL. University of Illinois. Jessica Rutkoski

Education: Lucas Berger Munaro (new PhD) regularly attended the WheatCAP monthly graduate student meetings and the writing group.

Germplasm & publications: 8 varieties were licensed to different seed companies.

UAS: 8 flights over 2.2 acres were submitted to the UAS hub and NDVI data were received. Data from flights over additional field experiments are being processed in-house.

Genotyping: 885 samples were submitted in 2022, on average 12,505 SNPs were identified by GBS.

Breedbase: 821 trials (168,807 plots) were entered in a local instance of T3, 796 with submitted agronomic data. 57 trials (18,554 plots) from 2021 and 2022 were uploaded to the WheatCAP

instance of T3. The IL program is leading the way on the implementation of Breedbase and suggested multiple improvements

Genomic selection: At the University of Illinois, all the lines being phenotyped are also genotyped, and all selection decisions are made based on Genomic Estimated Breeding Values (GEBVs) that are estimated using all phenotypic and genotypic data available.

8.5. KS. USDA-ARS Manhattan & KSU. M. Guttieri, G. Zhang, G. Bai, E. Akhunov

Education: Previous WheatCAP student Wardah Mustahsan graduated in 2022 and Yuzhou (Bruce) Xu will be graduating soon. New KSU PhD students Dwight Davidson, Adriano Abreu Moreira, and Lawrence Tidakbi attended student meetings, participated in the UAS data collection and T3/Breedbase workshop, and actively participated in a writing group.

Germplasm & publications: PVPs issued in last 12 months for three varieties reported on previous WheatCAP, and three new released varieties pending PVP (App. 1). 17 publications.

UAS: 20 flights over 3.65 acres. In addition, 1.65 acres were flown five times at each of two other locations and processed internally. Part of the data entered into T3. Three acres were flown 5 times at primary KSU trial site, with processing pending (total will be 8 acres).

Genotyping: 935 lines genotyped by MRASeq (~15,000 SNPs) & 480 by GBS (~14,000 SNPs).

Breedbase: 13 trials with 15,000 plots. Agronomic data has been already submitted for 11 of the 13 trials (6 also have UAS data uploaded).

Genomic selection: at initial stages.

8.6. MI. Michigan State University. Eric Olson.

Education: Previous WheatCAP student Jonathan Turkus completed his MS degree and is doing a postdoc in NE. Jonathan Concepcion is a new PhD student working on the WheatCAP objectives. He attended the educational online meetings but had reduced participation.

Germplasm & publications: soft winter wheat ‘MI16R0720’. 1 publication (Lopez et al. 2022).

UAS: not reported

Genotyping: 500 samples submitted to the Raleigh genotyping lab for specific markers (*Rht-B1*, *Rht-D1* and *Fhb1*). SNP genotyping using GBS was performed in-house for 3,040 samples. Submission to T3 pending.

Breedbase: MSU has nine trials and ~6,000 FHB nursery plots and data from ~4,900 grain yield testing plots to enter, but no trials have been entered into T3 so far.

Genomic selection: Prediction models were built using 362 individuals tested in two replicates at four locations in 2021 and three locations in 2022. Bayes A, B and C, Bayesian LASSO, Bayesian Ridge Regression, Random Forest and Support Vector Regression models were developed. Traits included grain yield from seven individual site years, grain yield across all years and locations with and without genotype by environment interaction terms and DON mycotoxin. Multi-year, multi-location genomic predictions were made for 3,040 F4 selection candidates. A set of 500 individuals were advanced based truncation selection on predicted breeding values for grain yield across years and locations as well as truncation selection for DON mycotoxin. The set of 500 selection candidates were planted along with four commercial checks in an augmented design.

8.7. MN. University of Minnesota. Jim Anderson.

Education: Previous WheatCAP PhD student Max Fraser is expected to graduate by the end of 2022. MS student Nanthicha Krueger started in June 2022. She has participated in monthly WheatCAP meetings and multiple activities in the MN breeding program.

Germplasm & publications: 1 variety (MN-Rothsay). WheatCAP MN variety MN-Torgy, released in 2020, was the no. 1 wheat variety in Minnesota in 2022.

UAS: 10 flights for a 1.25 ac field (St. Paul) were submitted to UAS-Hub.

Genotyping: 6,770 samples submitted to the ND Genotyping Center: 3,072 for GBS and 3,698 for MAS with 14 markers. 55 genotypes used in crossing blocks were genotyped in-house with more than 50 KASP markers.

Breedbase: Trials for 2022 not submitted to T3 yet.

Genomic selection: Genomic selection, utilizing 3,306 lines (3,251 F₆ lines and 55 parents), was used to predict FHB reaction prior to sending lines for our winter nursery. Further training data on FHB parameters and gluten strength will also be added to the GS model prior to final winter nursery selections are made in Feb. 2023.

8.8. MT. Montana State University. Jason Cook

Education: Two PhD students were recruited for the WheatCAP project: Jared Lile and Mei Ling Wong. Both participated in the monthly online meetings. Mei Ling is currently in a writing group and Jared is interested in getting involved with one.

Germplasm & publications: MT Sydney PVP 202200291. 2 publications: Glenn et al 2022, He et al. 2022.

UAS: 10 UAS flights including 468 plots. Data submitted to the UAS-Hub.

Genotyping: 702 breeding lines were sent to the ND Genotyping Lab.

Breedbase: 1 trial submitted. Harvest finished 9/2022 so additional trials will be submitted later.

Genomic selection: MT is in the early stages of implementing GS. They have genotyped all breeding lines produced by their breeding program since 2010, and are using the genotypic data and historical yield trial data from these lines to develop genomic selection models.

8.9. NC. USDA-ARS Raleigh. Gina Brown-Guedira

Education: Previous WheatCAP student Noah DeWitt graduated in spring 2022 and is now an Assistant Professor at Louisiana State University. PhD student Nico Lara has started on the project, and participated in writing group sessions, group meetings, and attended training modules. PhD student Daniela Miller continued from the previous WheatCAP and participated in student meetings. She was selected for the IWGSC Early Career Award and will present her research at the main IWGSC workshop at PAG.

Germplasm & publications: 1 (ARS16W1067), 4 publications (App. 2). The Genetics paper investigates a novel approach to understanding grain yield variation across environments.

UAS: UAS trials will start in 2023.

Genotyping: The NC-ARS program submitted 1,344 samples to the genotyping lab in Raleigh that were evaluated with 11 KASP assays for disease resistance and quality traits. Imputed data for approximately 14,000 GBS SNP were obtained for an additional 287 samples. Data were used in decisions about line advancement and for developing a training population for genomic selection. Data have not been deposited into T3

Breedbase: Transfer of NC-ARS hard wheat breeding program data to BreedBase is ongoing with formatting mostly completed.

Genomic selection: In 2022, work was done to incorporate genome-wide markers for prediction of yield and quality traits. Yield and quality data from historic breeding program trials were organized and processed alongside deep pedigree data and used to predict phenotypes based on kinship. Moderate to high mean predictive abilities obtained from five-fold cross validation through pedigree BLUP supported a genomic prediction approach, and 287 historic breeding lines from this training population were genotyped with high-density markers. Minor improvements in predictive ability were observed after incorporating marker data. Multivariate analyses of quality data from historic breeding program trials along with KASP markers for major quality genes validated the importance of those major genes. Based on these results, a two-step marker-based selection scheme was adopted for the 2022 field season. Leaf tissue was collected from a set of 1,344 late-stage head rows selected on the basis of disease resistance, phenology and family-based pedigree BLUPs, and markers for major disease resistance and quality genes run by the ERSGL were used for within-family selection of 582 individuals for both high-density genotyping and advancement to a single-rep observation nursery.

8.10 ND. USDA-ARS and North Dakota State University, Fargo. Justin Faris and Andrew Green

Education: Previous WheatCAP PhD student Katherine Running graduated in August 2022 and is currently a postdoc at NDSU. PhD student Pooja Kumari joined as a WheatCAP student in August 2022. She has participated in the WheatCAP monthly meetings.

Germplasm & publications: ND Heron (PVP 202200266). Publication 1 in G3 (App. 2).

UAS: UAS trials will start in 2023.

Genotyping: A population of 192 RLs was genotyped with the 90K Illumina array (1939 SNPs). The NDSU HRSW breeding program submitted 190 lines for 90K Illumina genotyping and 96 lines for MAS with 26 markers for disease and grain quality traits.

Breedbase: No trials or data submitted.

Genomic selection: Not reported.

The ND group has made significant progress towards the cloning and validation of the gene underlying a QTL on chromosome 2B associated with number of grains per spike identified in a RI population derived from Ben (*T. durum*) crossed with PI 41025 (*T. dicoccon*).

8.11. NE. University of Nebraska. Katherine Frels

Education: PhD student Sydney Graham participated in the August and October monthly student meetings. She also is a member of a weekly writing group.

Germplasm & publications: 1 publication in the Journal of Plant Registration.

UAS: 8 flights covering 2.5 ac submitted to TX. Orthomosaic files for the RGB flights have been received.

Genotyping: Samples will be submitted in late 2022.

Breedbase: 9 trials and 1,950 plots submitted to T3. 6 trials have agronomic data and 2 were not harvested due to hail and freeze damage.

Genomic selection: Genomic selection is regularly applied for yield at the F₄ preliminary observation stage and F₅ preliminary yield trial stage in the UNL program. Through the

WheatCAP program, we will begin evaluating genomic selection for wheat stem sawfly resistance including solid stem, yield, and non-preference traits.

8.12. NY. Cornell University. Mark Sorrells

Education: Previous WheatCAP PhD student Ellie Taagen graduated in 2022 and is now employed with Bayer Crop Sciences. PhD student Timothy Mulderrig joined the program in August and attended monthly WheatCAP meetings and the coPIs virtual meeting. Miranda Penney, is not directly supported by WheatCAP but will participate in WheatCAP activities

Germplasm & publications: 7 new publications

UAS: 9 flights were flown over our Winter Wheat Master (PYT) trial of 0.5 acres. The images have been submitted to the UAS-Hub and data has been received back.

Genotyping: 260 samples submitted for GBS to the Raleigh Genotyping lab. Using available phenotypic data, they generated BLUP values. Data was requested for upload in T3.

Breedbase: 1 trial consisting of 260 plots was submitted to T3 but the agronomic data have not yet been submitted.

Genomic selection: The Cornell Wheat Breeding program was one of the first ones to implement Genomic Selection and trained many of the WheatCAP breeders in this area. In 2021 GS predictions were used for 318 entries.

8.13. OK. Oklahoma State University. Liuling Yan and Brett Carver

Education: Two graduate students are currently working on the WheatCAP project: M.S. student Jennifer Tapia and PhD student Wenxuan Zhai.

Germplasm & publications: 3 publications with one in Science reporting the cloning of the *TaCol-B5* regulating grain number and yield. The OSU team developed a molecular marker to accelerate the introgression of this trait <https://maswheat.ucdavis.edu/protocols/TaColB5>.

UAS: Dr. Gopal Kakani, who was in charge of the UAS part left the University and the data he collected was incompatible with the UAS-Hub. Professor Phil Alderman (OSU) replaced Dr. Kakani and has a different multi-spectral drone that is compatible with the WheatCAP framework, and that will be used in 2023.

Genotyping: No data reported.

Breedbase: No trials reported.

Genomic selection: No data reported.

8.14. SD. South Dakota State University. Sunish K. Sehgal.

Education: Previous WheatCAP PhD student Jyotirmoy Halder graduated in Fall of 2021 and is now a post-doctoral fellow at SDSU. Another Ph.D. student Harsimardeep Gill is expected to graduate in spring 2023. One new PhD student Swas Kaushal has initiated his research and participated in UAS and T3 training and the student meetings. Dante Koupal and Mackenzie Henning are two undergraduates that are also getting experience in UAS data collection.

Graduate students attended the UAS-WheatCAP and T3 Workshops.

Germplasm & publications: 2 varieties (SD Midland and Ascend SD) and 5 publications.

UAS: Six flights were submitted to the UAS-Hub for ~2 acres, some of the RGB ortho mosaic images have been received and we are waiting for multispectral images. The UAS-Hub is processing the rest of the data.

Genotyping: 750 HWW lines were genotyped at UDSA HWW genotyping lab. The samples were genotyped using two enzyme GBS and the data was received. The average number of SNPs per line are > 8,000 with 25% missing data after filtering. The data is being processed and verified and will be uploaded to T3 this winter.

Breedbase: 6 trials with 1,080 plots were uploaded into T3 and the agronomic data (GY, TW, Protein%) has been also uploaded to T3.

Genomic selection: We have evaluated genomic selection (GS) in the SD winter wheat breeding program for agronomic traits including grain yield, test weight, grain protein content, fusarium head blight resistance (see publications), and end-use quality traits. The data collected in 2022 will be used to improve GS prediction in 2023.

8.15. TX. Texas A&M. Shuyu Liu, Amir Ibrahim, Jackie Rudd

Education: Two PhD students (Kyle Parker and Zhen Wang) and one MS student (Kylie Scott) participated in the educational meetings and the USAS-HTP, T3 and equity in Plant Breeding workshops. The TX group organized the UAS educational workshop.

Germplasm & publications: 4 new varieties (TAM 116, TX14V70214, TX14M8024, TX16M9216), and two previously reported varieties that obtained PVP in 2022 (TAM 115 and TAM 205) and two publications. An interesting discovery was that the wheat curl mite resistance gene in ‘TAM 112’ is the same gene as *Cmc4*.

UAS: 48 flights covering in total 6.3 acres distributed in three locations. Images were submitted to the UAS-Hub and processed data was sent back to the breeding programs that found it useful.

Genotyping: 935 lines screened by GBS and gene linked KASP markers at the genotyping center at Manhattan, KS.

Breedbase: Texas elite yield trials were submitted to T3 and other trials were in preparation for submission.

Genomic selection: A training set of 935 Texas A&M AgriLife Research breeding lines were evaluated for grain yield in 11 environments across two years and six locations. In 2021 and 2022, 559 and 534 lines were evaluated, with 158 lines shared in both years. Lines were genotyped with a set of 87,000 SNPs. Grain yield was predicted by utilizing single environment data and different methods, but gBLUP showed higher prediction accuracy. After excluding a subset of damaged lines from the 2021 testing environments, predictions using a multi-environment model had accuracies ranging from 0.43 to 0.85. The next step will be the integration of major gene linked markers into the prediction model.

8.16. UT. Utah State University. Margaret Krause

Education: MS student Dalton Jones attended the virtual student meetings for WheatCAP. Dalton and other students from the UT program participated in the workshop on equity in plant breeding.

Germplasm & publications: None to report

UAS: 6 flights covering 2.2 acres were submitted to TX and data was received back.

Genotyping: 256 lines were submitted to the genotyping lab in WA, with an average of 940 SNPs per line

Breedbase: 17 trials including 2,424 plots were submitted to T3. Agronomic data will be submitted before the end of the year.

Genomic selection: The UT program used the genotyping data generated by WA in their GS program and prediction accuracies for yield were decent at around 0.4. GEBVs of F₆-F₈ lines were calculated and used inform selection of parents for crossing for the dryland wheat breeding pipeline. A priority for the UT program is to amass more phenotypic and genotypic data to develop a better training population.

8.17. VA. Virginia Tech. Nick Santantonio

Education: WheatCAP supports PhD student Sunilda Frias and partially MS student Francis Reith. Sunilda Frias has taken part in all the monthly WheatCAP meetings and she has reported her research to the group, and participated in discussions to increase inclusion for graduate students in wheat breeding. She also participates in the writing groups.

Germplasm & publications: Three soft wheat varieties and one hard wheat variety were released during 2022, all of which were privately licensed to seed companies.

UAS: 16 flights were conducted across two locations including 1,988 SWW and 317 HWW and covering 11.5 acres. Orthomosaics were constructed in-house. The VA program is currently working on modeling growth and development through time using random regression models to fit genotype specific growth curves and relate these to end-use phenotypes, such as grain yield.

Genotyping: A total of 1,045 wheat lines were submitted for genotyping by sequencing (GBS) in 2022 at the USDA-ARS Wheat Genotyping Lab in Raleigh, and was combined with 4,524 lines genotyped in 2021. We expect to submit to T3 once data have been fully vetted and verified to not contain errors or other problems. In addition, 97 inbreds were genotyped with markers to 53 known loci.

Breedbase: 27 trials including 6,256 yield plots across two VA locations were submitted to T3. Agronomic data for grain yield, test weight, heading date, and plant height for all these trials were submitted to T3.

Genomic selection: The soft wheat breeding program currently uses genomic prediction for both mate pair decisions and advancement decisions. Genomic prediction is primarily used for first year advancement decisions, where lines are unreplicated within environment and planted in a sparse design. Genomic information is used to produce a genomic estimated breeding value (gEBV) within each location for each line using a multi-environment model that estimates the genetic correlation of environments. Selections are then based on performance both within specific environments and across environments using a selection index to select lines with both generalist and specialist behavior. Genomic information is also used to assign a GEBV for parent selection in the fall, allowing lines with limited information to be considered as parents alongside lines with multiple years of phenotypic data. Then genomic information is used to predict performance of mate pairs between those selected parents. The genotypes of the F₁s were constructed using the parent genotypes from the previous year. GEBVs of family means for multiple agronomic, quality and disease traits, as well as expected segregation of single loci for all possible mate pairs were constructed in silico to determine the best potential crosses to be made in the spring of 2022 using a selection index. The VA program has developed software for field design *fieldMapR* and made it available to the group.

8.18. WA. Washington State University. Arron Carter and Mike Pumphrey

Education: PhD student Morgan Hasler, is fully funded by WheatCAP (start 5/22), and Peter Schmuker and Andrew Herr are partially funded. Graduate students participated in the UAS training put on by TX. In addition, 2 underrepresented undergraduate researchers were interns in the program during the summer of 2022.

Germplasm & publications: 3 new varieties (Inspire, Jameson and Roger) were released in 2022. Five not previously reported papers were published by the WA group.

UAS: All UAS-HTP in WA is done through in-house processing to remain consistent with previous years data. All flights were submitted to TX to be part of the data set, but they did not process the data. Nine winter wheat locations were flown for a total of 29 flights, with over 2000 plots and 626 unique genotypes. Nine spring wheat locations were flown weekly, for a total of 80 flights, with over 5000 plots and 1500 unique genotypes. Data is being incorporated into genomic selection models to support future grain yield predictions

Genotyping: A total of 768 winter and 1200 spring wheat lines were sent for genotyping-by-sequencing to the Eastern Regional Small Grains Genotyping Laboratory. Data has not been submitted to T3 yet as we are still processing it. There is an average of 150,000 SNP per line. Other marker-assisted selection data is generated within the spring and winter wheat breeding programs for use in selection.

Breedbase: Both the spring and winter wheat breeding programs are submitting their largest breeding locations along with all agronomic and HTP data. We have not used BreedBase yet as both of our programs are fully incorporated into the Genovix database (a private database we have used for the past 20 years), and thus are still evaluating the best use of BreedBase in our programs.

Genomic selection: The spring wheat program is gearing up for genomic selection in their program to be used in 2023. The winter program used seven years of past breeding program data to perform genomic selection on 2022 breeding lines for various disease, end-use quality, and grain yield traits.

8.19. WI. University of Wisconsin. Lucia Gutierrez

Education: Graduate student Rishap Dhakal started the PhD program in June 2022. Rishap is taking courses and got his UAV flying license in July 2022. He is also attending the monthly meeting, journal clubs and writing group of the WheatCAP student group.

Germplasm & publications: Breeder seed from the 2 promissory cultivars have been harvested in the season 2021-2022 and was planted to produce foundation seed during the 2022-2023 season by UW-foundation seed. One publication on high-quality value-added cereals for organic systems (Sandro et al. 2022).

UAS: The University of Wisconsin team has completed the setup for the UAS system and the first flight was completed successfully in October and will continue throughout the season. UAS data will be uploaded to the UAS-Hub before the end of the year.

Genotyping: Not reported

Breedbase: After final check and confirmation, wheat organic field trials from 2017 to 2022, will be uploaded to T3 (transformation of the data to T3 template, traits id, and quality standard is in the process).

Genomic selection: WI team focuses on developing new strategies and data analysis tools for incorporating various yield relating source and sink components and environmental covariates accounting GEI into the genomic prediction models. To develop the training model population, a compilation of the dataset from T3/wheat for hard red winter wheat (HRWW) was done. This included the lines from 2012-2019 consisting of around 450 lines. This year (2022-2023), two trials representing the populations from the different geographical areas of the US (Wisconsin, South Dakota, Montana, Virginia, and Cornell) have been planted in two locations in Wisconsin.

9. Priorities for Year 2

9.1. Education: The educational priorities for 2023 include training in the utilization of T3/Breedbase database resources, on the standardization of data entry into the UAS-Hub, and on genomic selection. Online and in-person workshops focused on these topics will be held during spring, summer, and fall 2023. Monthly student meetings and writing groups will continue as during the first year. Topics for monthly meetings will include presentations and discussion with early career public plant breeders and meetings with the directors of the different genotyping labs to discuss the specialized services offered by each lab. Additionally, one monthly meeting will include a Strengths-Based leadership training where students identify their leadership strengths and potential strategies to best use those strengths to be successful graduate students, researchers, and collaborators.

9.2. Genomic Resources: The panel of diverse lines including bread wheat, wild relatives and synthetic wheat will be assembled for sampling multiple tissues across different developmental stages. The genotyping of these lines will be performed using the whole-genome low-pass sequencing to create a dense diversity map for downstream eQTL and trait mapping analyses. RNA-seq analysis of these samples will be performed to develop a more comprehensive tissue-specific eQTL map of wheat. This resource will be combined with the diversity datasets hosted by the T3 Breedbase. By combining eQTL maps with the phenotyping and genotyping data generated in the WheatCAP projects, we will improve our ability to interpret the functional significance of trait-associated SNPs and prioritize them for developing new functional markers for MAS and genomic selection.

The PanGenome-based wheat PHG will be created by combining variant calling data generated by mapping the existing wheat NGS datasets to the expanded panel of wheat reference lines developed by WheatCAP and the wheat community. The new PHG will be integrated into the T3 Breedbase to improve the accuracy and coverage of genotype imputation.

During the second year of the project we will complete the publications for the promoter sequencing of the Kronos EMS mutations (4.3 M mutations), the description of the new regulatory capture in collaboration with Arbor-Biosciences (submitted to The Plant Genome), and the INTACT-ATAC results for wheat roots. We will continue the distribution of seeds of the sequenced EMS mutant lines and of the vectors for the GRF4-GIF1-CRISPR-Cas9 improved transformation in wheat.

9.3. T3/Breedbase

During the second year, we will hire a postdoc to work with individual WheatCAP programs to develop genomic prediction models. We will continue to work with WheatCAP PIs to ensure that their data is uploaded and curated. The pace of data upload is increasing. Some non-breeding

trial data, such as the methylation sequences from the Akhunov lab and ATAC-Seq data from the Dubcovsky's lab, will also be uploaded.

T3 has a good user interface for uploading trials and associated metadata, with functionality to improve data validity (e.g., avoiding breeding line name duplications in the system, ensuring valid plot coordinates, etc.). Breeders will upload their trial metadata to T3 and their images to the UAS-Hub. The UAS-Hub will pull the trial field layout from T3, analyze the images, associate Level 2 phenotypic data with plots, and push those phenotypes back to T3. Most components of this server-to-server connectivity are in place. In Year 2 of WheatCAP, we will ensure full circle functionality.

In the steps of the process of submitting samples to a genotyping lab there are small probabilities of mislabeling or switch errors. The large number of steps, however, means that some errors overall are common. Industry reduces errors by extensive use of barcodes. In collaboration with the genotyping labs, we will continue developing processes whereby WheatCAP breeders design genotyping plates on T3, T3 creates the templates needed by the labs, templates are sent with the samples to the labs accompanied with barcodes, the labs generate the data and upload it, tagged by the barcodes back to T3. All samples then are accompanied point to point by digital identifiers, reducing mislabeling or switch errors.

In Year 2 we will complete integration of the version 2 Practical Haplotype Graph. There are two components to this integration: First, we will complete the software integration of the PHG into T3. The PHG generates marker score calls in a different way and at much higher density than standard genotyping platforms. Integrating the PHG so that its outputs are easily available through the same interface presents a challenge that we will overcome in Year 2. Second, we will work on improving imputation accuracy validation. Different wheat market classes (subpopulations) need to be validated for imputation accuracy independently. We will identify the per-market class validation sets to test the PHG. These sets will allow us to swap in new PHG builds as they become available.

We will also build out the spatial analysis capabilities of T3. Because of the use of UAS-Hub, trials now systematically have field layout data associated with them. This information can also be used for spatial analysis of the trials. Finally, we plan to provide a two to three-day workshop covering data upload and trial aggregation features of T3 in early spring 2023.

9.4. UAS-Hub

To accelerate communication between the UAS-Hub and T3/Breedbase, we have already developed a feature to pull data from the T3 database using BrAPI and integrated this feature into the UAS-Hub. During the second year, we will focus on developing a feature to push extracted phenotypic features from the UAS-Hub back to T3/Breedbase. We will test this feature on a sandbox instance before streamlining it for automated data push from the UAS-Hub to T3.

With the UAS-Hub platform equipped for full implementation, our team will continue its focus on the timely processing and delivery of processed data products and their upload into T3. During the second year we will work on adding canopy cover, height, volume, and vegetation indices to the outputs of the pipeline.

Finally, we will develop new training modules and train graduate students on plot boundary delineation for feature extraction

9.5. Genotyping labs

During the second year of the WheatCAP, the four Regional Genotyping Labs will continue working in the development and testing an AmpliSeq highly multiplexed PCR platform targeting 5,000 loci. Sequences flanking 1,500 exome capture SNPs from each wheat market class and even distribution throughout the genome submitted to ThermoFisher in October, 2022 and the first design will be tested. ThermoFisher will synthesize the primer pool and validate the pool on 384 samples selected to represent US germplasm. The objective is to have a unified medium throughput genotyping platform available to the US wheat community for \$10 per sample.

10. Budget and Project changes

There have been no changes in the budgets or original objectives. The budget of USDA-ARS Ithaca will continue to be transferred to Cornell University to provide T3 more flexibility and to simplify administration as approved last year for the complete duration of this grant. The only change in personnel is a change in the Educational Coordinator. Amanda Peters Haugrud was selected for a Research Geneticist position at the USDA-ARS in Fargo in the Cereals Crops Research Unit. She will be replaced by Katherine Running, who is also from ND and participated in previous WheatCAP projects. She is already overlapping with Amanda to facilitate the transition. This change will not alter any of the educational objectives and activities and there are no changes in the overall ND WheatCAP budget. However, to accommodate the different sources of funding for the Educational Coordinator, an internal redistribution of \$37,698 from ORISE to ARS was implemented for the second year of the WheatCAP project. Besides this change, there are no other changes in the budget, objectives or proposed activities in the WheatCAP proposal for the second year of the project.

11. Deliverables & Other Outputs:

- **Appendix 1.** Germplasm releases
- **Appendix 2.** Publications
- **Appendix 3.** Community resources
- **Appendix 4.** Graduate students. <https://www.triticeacap.org/educational-activities/>

12. Concluding remarks

The first year of the WheatCAP has been very productive with new knowledge presented in 47 new publications including high profile publications in Science, Nature Communications, Genetics and PLOS Genetics. Data was collected from 173 UAS flights over 23.8 acres, 25,400 samples were sent for genotyping, and 55,000 plots from 175 trials were uploaded in T3. WheatCAP breeders released 40 new varieties and 7 improved germplasm that benefitted from high-throughput genotyping and phenotyping platforms. Presentations of these varieties in field days across the country showcased the value of these new technologies and of the USDA-NIFA support to the growers and to the wheat industry. The improved disease resistance of the new varieties to pathogens will reduce the applications of fungicides, reducing costs, benefiting the population, and the environment. The increased productivity of these new varieties will provide

high-quality products for consumers while boosting the competitiveness of USA wheat growers and industry.

The genomic tools and databases generated by the WheatCAP continue to accelerate the pace of discoveries in wheat improvement which is essential to anticipate solutions to the accelerating changes caused by climate change. One of the most important contributions of the WheatCAP is the coordination among all the major wheat breeding and research programs in the country, which eliminates unnecessary duplications and generates positive and synergistic collaborations. Finally, the training of the next generation of plant breeders guarantees the continuity of the US agricultural enterprise into the future.

None of these would have been possible without this integrated Collaborative Agricultural Projects and the wheat community and wheat industry is grateful for this support.

APPENDIX 1. Varieties and Germplasm releases 2022 (40).

Variety releases with PVP (3)

1. **‘ND Heron’** (PVP 202200266, submitted 2/15/22) is an early maturing wheat variety best adapted to central and western North Dakota. It has high grain protein, very high-water absorption, and is moderately resistant to FHB, leaf rust and stem rust. It was genotyped at the USDA-ARS genotyping lab in Fargo during its development.
2. **‘Ascend SD’** (PVP 202200513, submitted 8/01/22) is a South Dakota HRS wheat variety released in the Fall of 2021. Ascend SD has excellent yield potential and has above-average to good end-use quality. It has good resistance to BLS and FHB.
3. **‘MT Sidney’** (PVP 202200291 submitted 03/04/2022) is a hollow-stem, high yielding semi-dwarf hard red spring wheat variety released by Montana State University in 2021. MT Sidney is moderately resistant to FHB (Scab), has 0.5% higher grain protein content than Vida, above average TWT and average end-use quality.

Variety releases with pending PVP (30)

1. **‘Windom SF’** = CO18SF009W = Warhorse/Breck//CO12D1028 (PVP pending) ‘Windom SF’ is a Hard-White Winter wheat, released by Colorado State University in summer 2022. It has the semi-solid-stemmed trait for partial resistance to wheat stem sawfly.
2. **‘UI GOLD’** (PVP pending) is a Hard-White Spring wheat cultivar released in October 2022 by the University of Idaho. It has very high grain yield and excellent bread-baking quality and good resistance to stripe rust.
3. **‘IDO2002S’** is a Hard-White Spring wheat line developed by the University of Idaho using combination of DH technology and characterized via molecular marker for bread-baking quality. It will be submitted to NSGC in spring 2023.
4. **‘IDO2202 CL2’** is a Hard-White Spring wheat line developed by the University of Idaho via MAS for herbicide resistance to Beyond.

5. **'IL19-14856'** is a breeding line licensed by the University of Illinois to a private seed company, and is ultra-early, high-yielding, and Fusarium Head Blight (FHB) resistant.
6. **'IL17-8930'** is a breeding line licensed by the University of Illinois to a private seed company, and is ultra-early, high-yielding, and Fusarium Head Blight (FHB) resistant.
7. **'US16-IL-063-063'** is a breeding line licensed by the University of Illinois to a private seed company, and is ultra-early, high-yielding, and Fusarium Head Blight (FHB) resistant.
8. **'IL19-5466'** is a breeding line licensed by the University of Illinois to a private seed company, and is ultra-early, high-yielding, and Fusarium Head Blight (FHB) resistant.
9. **'IL18MSFRS-18'** is a breeding line licensed by the University of Illinois to a private seed company, and is a high-yielding, and Fusarium Head Blight (FHB) resistant line with medium maturity.
10. **'IL18-17905'** is a breeding line licensed by the University of Illinois to a private seed company, and is a high-yielding, and Fusarium Head Blight (FHB) resistant line with medium maturity.
11. **'IL18-14534'** is a breeding line licensed by the University of Illinois to a private seed company, and is a high-yielding, and Fusarium Head Blight (FHB) resistant line with medium maturity.
12. **'US17-IL-108-039'** is a breeding line licensed by the University of Illinois to a private seed company, and is a high-yielding, and Fusarium Head Blight (FHB) resistant line with medium maturity.
13. **'KS Providence'** (PVP pending) is a Kansas Hard-Red Winter with excellent yield potential and yield stability. It has demonstrated good drought tolerance and is expected to be well adapted to the Central Corridor of Kansas. It carries *Lr34*, *Lr46* and *Lr68*, giving it very good resistance to leaf rust but is intermediate to stripe rust. Benefitted from genotyping lab analysis of regional nursery germplasm.
14. **'KS Big Bow'** (PVP pending) is a Kansas Hard-White wheat with excellent yield potential. Viewed as a Joe replacement having better yield, sprout tolerance and coleoptile length than Joe. Carries the *Wsm2* gene for WSMV. Benefitted from genotyping lab analysis of elite/regional nursery germplasm.
15. **'KS Territory'** (PVP pending) is a Kansas Hard-Red Winter wheat with good resistance to WSMV based on *Wsm2*. Benefitted from genotyping lab support of elite/regional nursery germplasm.
16. **'MN-Rothsay'** (PVP pending) is a Hard-Red Spring wheat that was released in January 2022 by the University of Minnesota. It has high grain yield and strong straw. The Fargo USDA-ARS Genotyping Center contributed DNA marker data used in the selection and development of MN-Rothsay.
17. **'TAM 116'** (TX14A001035= Billings/TX03A0563, PVP pending) TAM 116 is resistant to leaf rust, stripe rust, and stem rust. Good bread-making quality and adapted to intense management systems in the Texas High Plains and Texas Rolling Plains.

18. **'TX14V70214'** (PVP pending) Pedigree: Art/TAM 401. It is awnless with high biomass yield and resistance to leaf, stripe and stem rust. It has statewide adaptation and is suitable for dual purpose, silage, and graze-out management systems.
19. **'TX14M8024'** (PVP pending) Pedigree: TAM 203/Duster. It is resistant to Hessian fly, leaf rust, stripe rust, and stem rust. Good bread-making quality and is adapted to the Texas Rolling Plains, Texas Blacklands, and South Texas.
20. **'TX16M9216'** =TX07A001482/TAM 401//Duster (PVP pending). TX16M9216 is resistant to Hessian fly, leaf rust, stripe rust, and stem rust. It has very good bread-making quality and is adapted to all wheat growing areas in Texas.
21. **'MI16R0720'** was released as a soft red winter wheat from Michigan State University. This line was genotyped as part of the 5-State nursery.
22. **'VA17W-75' marketed as 'EPIX 1375'** (PVP pending) is a high yielding, high test weight, semi-dwarf, awnless soft red winter wheat with excellent resistance to foliar diseases, including leaf rust and powdery mildew, as well as expressing moderate resistance to fusarium head blight (FHB) in the mid-Atlantic and southern U.S. Molecular markers were used in the development.
23. **'15VDH-FHB-MAS38-01'** (PVP pending) is an exceptionally early, high yielding, short, semi-dwarf, awned soft red winter wheat with good leaf rust and powdery mildew resistance, and exceptional FHB resistance (contains the Fhb1 locus) developed with substantial resources from the USWBSI. Molecular markers were used in the development.
24. **'15VDH-FHB-MAS33-13'** (PVP pending) is a high yielding, high test weight, semi dwarf, awnless soft red winter wheat with excellent FHB (contains the Fhb1 locus), leaf rust and septoria leaf blotch resistance developed with substantial resources from the USWBSI. Molecular markers were used in the development.
25. **'14VDH-HRW-02-029' marketed as 'Phoenix 29'** (PVP pending) is a Hard-Red Winter wheat specifically adapted to Mid-Atlantic, and the first hard wheat developed with yield potential comparable to commercial soft red winter wheat varieties grown in the region with acceptable milling and baking qualities for use in flour blends to manufacture bread products. Molecular markers were used in the development.
26. **'Inspire'** (PVP pending) is a soft white winter wheat and was developed for the intermediate rainfall areas of Washington with excellent disease resistance, end-use quality, and high falling numbers. Developed with the assistance of molecular markers.
27. **'Jameson'** (PVP pending) is a soft white winter wheat developed for the low rainfall areas of Washington with excellent emergence from deep planting, snow mold tolerance, and good end-use quality. Developed with the assistance of molecular markers.
28. **'Roger'** (PVP pending) is a spring club wheat developed for production in Washington with high grain yield, excellent end-use quality, and the first spring club wheat developed with Hessian fly tolerance. Developed with the assistance of molecular markers.
29. **'AR09137UC-17-2'** is a common soft red winter wheat variety released by the Board of Trustees of the University of Arkansas in 2021 before Esten Mason moved to CO.

30. ‘**ARS16W1067**’ =ARS05-1044/Baldwin. ARS16W1067 is a HRW intended to replace NuEast in local milling and baking as a wheat with comparable quality but substantially higher yields. The release is supported by 4 y of testing in the USDA Uniform Bread Wheat Trial and genotyping for major disease resistance, bread-making quality, and phenology genes.

2022 PVP that were reported as pending in previous WheatCAP reports (7)

1. ‘**Amplify SF**’ (PVP 202300009 submitted 09/16/2022) Amplify SF (Bearpaw/Antero//Antero) is a Hard-Red Winter wheat, released by Colorado State University in 2021. It has the semi-solid-stemmed trait for partial resistance to wheat stem sawfly.
2. ‘**Kivari AX**’ = CO14A055-258 = AF28/Byrd/3/AF10 /2*Byrd. (PVP 202200001, submitted 10/04/2021). Kivari AX is a new high-yielding CoAXium wheat that was released by Colorado State University in summer 2020.
3. ‘**KS Hatchett**’ (PVP 202100488, application submitted 09/02/2021) is a Hard-Red Winter wheat cultivar developed by Kansas State University for central Kansas. It has excellent yield potential and good test weight. It has durable resistance to leaf rust.
4. ‘**AM Cartwright**’ (PVP 202100489, application submitted 09/03/2021) is a Hard-Red Winter wheat variety developed by Kansas State University. It has competitive yields, excellent disease resistance package, and good baking quality.
5. ‘**SD Midland**’ (PVP 202200516, application submitted 8/26/22) is a HRW semi-dwarf variety with medium-tall in height and late in maturity. It is high yielding with average protein and test weight and good to excellent milling and baking quality. SD Midland is moderately resistant to stripe rust and yields well in lower rainfall areas. SD Midland got Miller’s choice ‘Best-of-Show’ award at the 2022 for good end-use quality.
6. ‘**TAM 115**’ (PVP 202000429, application submitted 9/18/2020). TAM 115 (TX11A001295 = TAM 112/TX02U2508) is resistant to greenbug (*Gb3*), wheat curl mite (*Cmc4*), leaf rust, stripe rust, and stem rust. It has good bread-making quality and is adapted to the Texas High Plains and Texas Rolling Plains.
7. ‘**TAM 205**’ (PVP 202000430, application submitted 9/18/2020) TAM 205 (TX12V7415 = ND 801/TX02D5813]//RonL) is resistant to leaf rust, stripe rust, stem rust, Fusarium head blight (*Fhb1*) and wheat streak mosaic virus (*Wsm2*). It has excellent bread-making quality and is adapted to the Texas High Plains, Texas Rolling Plains, and Central Texas.

2022 Germplasm (6)

1. ‘**CdDH-266**’ is a Hard-White Spring wheat line developed by the University of Idaho using combination of DH technology and characterized via molecular marker for bread-baking quality. It will be submitted to NSGC in spring 2023.
2. **PI 698810**: *Wapo-A1b* allele (haplotype H2) for increased number of spikelets per spike introgressed into tetraploid Kronos. Developed by UC Davis.
3. **PI 699107**: *FT-A2 A10* allele for increased number of spikelets per spike introgression into tetraploid Kronos. Developed by UC Davis.

4. **PI 700734:** stem rust resistance gene *SrKN* (*Sr9e*) introgressed into Fielder. Developed by UC Davis.
5. **PI 700735:** stem rust resistance gene *Sr22b* introgressed into Fielder. Developed by UC Davis.
6. **Eight *Sst1* isogenic pairs** (CSU): Near isogenic lines with and without the solid-stem locus *Sst1* locus in eight different genetic backgrounds. These were distributed to Katherine Frels (UNL) and Jeffrey Boehm (USDA-Lincoln) for screening in 2023.

APPENDIX 2. Peer reviewed publications WheatCAP 2022 (Year 1, 47 publications)

Google Scholar Impact of previous WheatCAP publications (measured 11/29/2022)

WheatCAP (2017-2021): 5,762 cross-references (h index = 42).

TriticeaeCAP (2011-2016): 24,194 cross-references (h index = 75).

2022 publications

1. Alarcón-Reverte R, Xie Y, Stromberger J, Cotter JD, Mason RE, Pearce S (2022) Induced mutations in *ASPARAGINE SYNTHETASE-A2* reduce free asparagine concentration in the wheat grain. *Crop Science* 62:1484–1496. <https://doi.org/10.1002/csc2.20760>
2. Baenziger PS, Frels KA, Boehm J, Belamkar V, Rose DJ, Xu L, Wegulo SN, Regassa T, Easterly AC, Creech CF, Santra DK, Klein RN, Jin Y, Kolmer J, Chen MS, Guttieri MJ, Bai G, El-Basyoni Salah I, Masterson SD, Poland J (2022) Registration of ‘Epoch’ hard red winter wheat. *Journal of Plant Registrations* 16:613–621. <https://doi.org/10.1002/plr2.20247>
3. Chen H, Su Z, Tian B, Liu Y, Pang Y, Kavetskyi V, Trick HN, Bai G (2022) Development and optimization of a Barley stripe mosaic virus-mediated gene editing system to improve Fusarium head blight resistance in wheat. *Plant Biotechnology Journal* 20:1018–1020. <https://doi.org/10.1111/pbi.13819>
4. Chen H, Su Z, Tian B, Hao G, Trick HN, Bai G (2022) TaHRC suppresses the calcium-mediated immune response and triggers wheat Fusarium head blight susceptibility. *Plant Physiology* 190:1566–1569. <https://doi.org/10.1093/plphys/kiac352>
5. Chen Y, Liu Y, Zhang J, Torrance A, Watanabe N, Adamski NM, Uauy C (2022) The *Triticum ispahanicum* elongated glume locus P2 maps to chromosome 6A and is associated with the ectopic expression of SVP-A1. *Theor Appl Genet* 135:2313–2331. <https://doi.org/10.1007/s00122-022-04114-y>
6. Chu C, Wang S, Rudd JC, Ibrahim AMH, Xue Q, Devkota RN, Baker JA, Baker S, Simoneaux B, Opena G, Dong H, Liu X, Jessup KE, Chen MS, Hui K, Metz R, Johnson CD, Zhang ZS, Liu S (2022) A new strategy for using historical imbalanced yield data to conduct genome-wide association studies and develop genomic prediction models for wheat breeding. *Mol Breeding* 42:18. <https://doi.org/10.1007/s11032-022-01287-8>
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9. DeWitt N, Guedira M, Murphy JP, Marshall D, Mergoum M, Maltecca C, Brown-Guedira G (2022) A network modeling approach provides insights into the environment-specific yield architecture of wheat. *Genetics* 221(3) iyac076. <https://doi.org/10.1093/genetics/iyac076>
10. Fan M, Zhang X, Nagarajan R, Fan M, Zhang X, Nagarajan R, Zhai W, Rauf Y, Jia H, Ma Z, Yan LL (2022) Natural variants and editing events provide insights into routes for

- spike architecture modification in common wheat. *The Crop Journal*.
<https://doi.org/10.1016/j.cj.2022.04.009>
11. Gill HS, Halder J, Zhang J, Rana A, Kleinjan J, St. Amand P, Bernardo A, Bai G, Sehgal SK (2022) Whole-genome analysis of hard winter wheat germplasm identifies genomic regions associated with spike and kernel traits. *Theor Appl Genet* 135:2953–2967.
<https://doi.org/10.1007/s00122-022-04160-6>
 12. Glenn P, Zhang J, Brown-Guedira G, DeWitt N, Cook JP, Li K, Akhunov E, Dubcovsky J (2022) Identification and characterization of a natural polymorphism in *FT-A2* associated with increased number of grains per spike in wheat. *Theor Appl Genet* 135:679–692. <https://doi.org/10.1007/s00122-021-03992-y>
 13. He F, Wang W, Rutter WB, KW Jordan, Ren J, Taagen E, DeWitt N, Sehgal D, Sukumaran S, Dreisigacker S, Reynolds M, Liu S, Chen J, Fritz A, Cook J, Brown-Guedira G, Pumphrey M, Carter A, Sorrells M, Dubcovsky J, Hayden MJ, Akhunova A, Morrell PL, Szabo L, Rouse M, Akhunov E (2022) Genomic variants affecting homoeologous gene expression dosage contribute to agronomic trait variation in allopolyploid wheat. *Nat Commun* 13:826. <https://doi.org/10.1038/s41467-022-28453-y>
 14. Jiang D, Hua L, Zhang C, Li H, Wang Z, Li J, Wang G, Song R, Shen T, Li H, Bai S, Liu Y, Wanga J, Li H, Dubcovsky J, Chen S 2022. Mutations in the miRNA165/166 binding site of the HB2 gene result in pleiotropic effects on morphological traits in wheat. *The Crop Journal*. Online first. <https://doi.org/10.1016/j.cj.2022.05.002> .
 15. Kissing Kucek L, Dawson JC, Darby H, Mallory E, Davis M, Sorrells ME (2021) Breeding wheat for weed-competitive ability: II—measuring gains from selection and local adaptation. *Euphytica* 217:203. <https://doi.org/10.1007/s10681-021-02905-w>
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<https://doi.org/10.1007/s10681-021-02930-9>
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<https://doi.org/10.3389/fpls.2021.715314>
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36. Taagen E, Jordan K, Akhunov E, Sorrells ME, Jannink JL (2022) If It Ain't Broke, Don't Fix It: Evaluating the Effect of Increased Recombination on Response to Selection for Wheat Breeding. *G3 Genes|Genomes|Genetics* jkac291. <https://doi.org/10.1093/g3journal/jkac291>
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<https://doi.org/10.3389/fpls.2022.926621>

APPENDIX 3. Community resources generated

2022 Public databases

1. T3 database <https://triticeaetoolbox.org/wheat/>
2. Sequenced mutant populations https://dubcovskylab.ucdavis.edu/wheat_blast
3. Protocols for Marker Assisted Selection <https://maswheat.ucdavis.edu/>

2022 Mapping Population

1. PI173438xWA8137 winter wheat doubled haploid mapping population developed for snow mold tolerance and accepted for publication to the Journal of Plant Registrations and has the designation Reg. no. MP-16, NSL 543858 MAP.

2022 Tools for marker-assisted selection (MAS)

1. **Univ. of Idaho:** A KASP marker was designed and validated that is related to a novel FT-D1 variant for selecting higher SNS and grain yield in spring wheat.
2. **Univ. of Idaho:** Optimal glutenin subunits combination was identified to predict excellent bread-baking quality.
3. **KS USDA-ARS:** "Agronomic and Quality Impact of a Shortened Translocation for Wheat Streak Mosaic Virus Resistance" in production with *Crop Science* provides three codominant KASP assays for the shortened 'rec213' *Wsm1* translocation.
4. **OK:** A CAPS marker for gene *TaCol-B5* that can increase the spikelet number per spike.
5. **CA:** Molecular markers for new alleles for increased number of spikelets per spike in genes *WAPO-A1* (<https://maswheat.ucdavis.edu/protocols/WAPO1>) and *FT-A2* (<https://maswheat.ucdavis.edu/protocols/FTA2>).

APPENDIX 4. Graduate students (7 completed + 42 current = 49, 47% female)

Individual student projects and profiles at <https://www.triticeaecap.org/meet-our-students/>

Institution	1 st name	Last name	Deg.	Gender	Start Date	Graduated
Colorado State U.	Mikayla	Hammers	PhD	F	8/1/2020	
Colorado State U.	Selena	Lopez	MS	F	1/1/2022	
U. of California-Davis	Maria G.	Rottersman	PhD	F	9/1/2022	
U. of California-Davis	Priscilla	Glenn	PhD	F	9/1/2017	*
U. of Idaho	Pabitra	Joshi	PhD	F	1/1/2021	
U. of Idaho	Yaotian	Gao	PhD	M	1/1/2021	
U. of Idaho	Meng	Su	PhD	F	8/1/2018	*
U. of Illinois	Lucas	Munaro	PhD	M	1/1/2022	
Purdue University	Ismaila	Olaniyi	PhD	M	5/1/2022	
Kansas State U.	Dwight	Davidson	MS	M	8/1/2021	
USDA-Kansas State U.	Adriano	Moreira	PhD	M	9/1/2022	
USDA-Kansas State U.	Wardah	Mustahsan	PhD	F	6/1/2018	*
USDA-Kansas State U.	Xiaoting	Xu	PhD	F	8/1/2020	
USDA-Kansas State U.	Yuzhou	Xu	PhD	M	8/1/2017	
U. of Maryland	Adam	Schoen	PhD	M	8/1/2020	
U. of Maryland	Anmol	Kajila	PhD	F	8/1/2021	
Michigan State U.	Jonathan	Concepcion	PhD	M	9/1/2021	
U. of Minnesota	Max	Fraser	PhD	M	7/1/2017	
U. of Minnesota	Nanthonica	Krueger	MS	F	7/1/2022	
Montana St. U.-Bozeman	Mei Ling	Wong	PhD	F	8/1/2022	
Montana St. U.-Bozeman	Jared	Lile	PhD	M	5/1/2021	
USDA-N Caroline St. U.	Noah	DeWitt	PhD	M	1/8/2018	*
USDA-N Caroline St. U.	Nico	Lara	PhD	M	8/1/2020	
USDA-N Caroline St. U.	Daniela	Miller	PhD	F	1/1/2019	
USDA-N Dakota St. U.	Pooja	Kadian	PhD	F	8/1/2022	
North Dakota St. U.	Lucas	Batista	MS	M	1/1/2021	
USDA-North Dakota St. U.	Katherine	Running	PhD	F	1/1/2018	*
U. of Nebraska-Lincoln	Sydney	Graham	PhD	F	5/1/2022	
Cornell U.	Timothy	Mulderrig	PhD	M	8/1/2022	
Cornell U.	Miranda	Penney	PhD	F	8/1/2022	
Cornell U.	Ellie	Taagen	PhD	F	6/12/2017	*
Oklahoma State U.	Jennifer	Tapia	MS	F	8/1/2021	
Oklahoma State U.	Abby	Tucker	MS	F	8/1/2022	
South Dakota State U.	Harsimardeep	Gill	PhD	M	1/1/2021	
South Dakota State U.	Swas	Kaushal	PhD	M	5/1/2022	
South Dakota State U.	Jyotirmoy	Halder	PhD	M	8/22/2017	*
Texas A&M	Zhen	Wang	PhD	M	9/1/2019	
Texas A&M	Kyle	Parker	PhD	M	9/1/2020	
Texas A&M	Kylie	Scott	MS	F	9/1/2021	
Texas A&M	Russ	Garretson	PhD	M	9/1/2021	
Texas A&M	Jose	Landivar Scott	MS	M	9/1/2021	
Utah State U.	Dalton	Jones	MS	M	5/1/2022	
Virginia Tech	Sunilda	Frias	PhD	F	6/1/2022	
Washington State U.	Peter	Schmuker	PhD	M	8/1/2020	
Washington State U.	Andrew	Herr	PhD	M	8/1/2019	
Washington State U.	Morgan	Hasler	MS	F	1/1/2022	
U. of Wisconsin-Madison	Rishap	Dahakal	PhD	M	6/1/2022	
U. of Wisconsin-Madison	Pablo	Sandro	PhD	M	1/1/2021	
U. of Wisconsin-Madison	Gopika	Gopinathan	PhD	F	6/1/2022	