Cover page

a. Award #: 2017-67007-25939

b. Project Title: "Validation, characterization and deployment of QTL for grain yield components in wheat"

c. Project Director: Jorge Dubcovsky

d. Project website: https://www.triticeaecap.org/

- **Appendix 1.** Germplasm releases
- **Appendix 2**. Publications
- **Appendix 3**. Community resources
- **Appendix 4.** Graduate students.
- **Appendix 5.** Education survey.

e. Institution name: University of California, Davis

f. Requested amount: $2,500,000 (already available at UCD as a retention from year 1-4)

A. Review of WheatCAP 2020 accomplishments

A. 1. WheatCAP overall productivity

During the fourth year, the WheatCAP project published 35 peer-reviewed papers acknowledging the USDA-NIFA support and identified 9 candidate genes for grain yield components. WheatCAP breeders released 22 new improved commercial varieties in all wheat market classes, 4 improved germplasm, and 5 mapping populations. Seventeen additional varieties reported in 2019 received PVP in 2020. The complete lists of released varieties and publications are available in Appendices 1 and 2, respectively. Those lists are also available through the WheatCAP web site (http://www.triticeaecap.org/). Community resources are in Appendix 3 and students trained in Appendix 4. Students' personal profiles, workshops and links to the positional cloning projects are available at the WheatCAP web site. Appendix 5 presents the education survey.

A. 2. Education

Education: One of the main objectives of the WheatCAP project is to educate 15 PhD students in molecular plant breeding. By leveraging funds from participating universities, 26 PhD students and 9 MS students have been supported by the WheatCAP project (40% female). Seven PhD students and five MS students have graduated. Additionally, four new international graduate students are waiting for approval to enter the United States to join their respective WheatCAP research groups. As more students approach the completion of their graduate degree, a number of students have been recognized for their leadership, hard work and dedication towards the field of plant breeding and genetics. In 2020, WheatCAP graduate students Saarah Kuzay (UC Davis), Brittney Brewer-Jones (Montana State University) and Ella Taagen (Cornell University), received three out of 16 "NAPB 2020 Borlaug Graduate Scholars" awards. The Borlaug Graduate Scholars program was established by the National Association of Plant Breeders (NAPB) and funded through the Agronomic Science Foundation (ASF) to develop the plant breeding science profession by strengthening the next generation of leaders. Lastly, to date, student research progress has culminated in eight first author peer-reviewed manuscripts.

Every year the education team assesses student progress using an annual survey to monitor student progress in learning concepts that are essential for completing their WheatCAP research project and preparing for future employment. The survey also serves as a guide to help plan future education activities. This year's survey included a question about how the Covid-19 pandemic has impacted student education and research progress, and asked how the WheatCAP project could help the students cope with the negative impacts of Covid-19. Overall, most of the students indicated the pandemic has caused delays in their research progress, and a few of the students said they had to drop projects. Additionally, students indicated they are suffering from isolation, because they are not able to interact with their peers on a regular basis. Based on the survey results, the education team will adjust the education activities to help the students' better cope with the Covid-19 pandemic. A summary of the survey results are presented in Appendix 5.

Education activities in 2020, started off by hosting an in person soft skill workshop in San Diego, CA (January 10) in conjunction with the WheatCAP annual meeting and the PAG conference.

The soft skill workshop was hosted by Bonsai, and focused on developing the students' leadership skills by identifying and leveraging their strengths, how to manage a team, and develop interpersonal communication skills. The T3 group co-hosted a PAG workshop: "Connecting Crop Phenotype and Genotype Data" in January 11 2020. For the week of March 15-21, the education team had planned to send the students to CIMMYT research sites located in Obregon and El Batan, Mexico where the students would have had an opportunity to attend a CIMMYT field day, tour research facilities and interact with international research scientist. Unfortunately, the CIMMYT workshop was canceled due to the Covid-19 pandemic to protect the safety of the students. It is uncertain if the CIMMYT trip can be rescheduled before the end of the WheatCAP grant. A second workshop was planned for the week of July 5-11 at the University of Minnesota and North Dakota State University where the students were going to visit public and private breeding programs, meet with growers, and end-use stake holders. The workshop was cancelled due to Covid-19.

In lieu of our in person workshops, the students have been participating in online education activities. These activities include starting two writing groups where the students meet each week to discuss writing their manuscripts, provide edits and help each other overcome writers block. Students have also been acquiring video and photos from their summer field season for doing virtual field tours this fall. Other students are planning to augment the virtual field tours with webinars focused on topics of interest that include genomic selection and end-use quality.

A. 3. T3 database

Education: The T3 Breedbase website incorporated training videos recorded during a workshop in March 2020. These videos can be found on the website at About => Video Tutorials. As mentioned in the education section, the T3 group co-hosted the workshop: "Connecting Crop Phenotype and Genotype Data" at PAG.

T3 Database and Research project: The T3 team completed loading all data from T3 into the Breedbase platform developed by the Mueller lab. As of January 2020, datasets are no longer uploaded to "T3/Wheat Classic" but only to "T3/Wheat Breedbase". T3 Classic is still being maintained and is accessible at: https://triticeaetoolbox.org/wheat/

T3 Breedbase is accessible at: https://wheat.triticeaetoolbox.org/

The benefit of the transition is two-fold. First, BreedBase is in use by applied breeding programs such that it has implemented more functionality for applied breeding. It has experimental design pages, pages managing barcodes, communication with tablets used for data capture (through the Android Field Book), and tracking software for submission of samples for DNA marker analysis. Now that T3 datasets have transitioned to BreedBase, all of these functions are available to small grains breeders. More importantly, BreedBase has greater support for software development than did the previous code base for T3. First, the BreedBase team itself is supported by the Bill and Melinda Gates foundation, as it serves as breeding management software for a number of priority crops in sub-Saharan Africa. Second, BreedBase is the code currently being adopted by the Breeding Insight project. Breeding Insight is working for USDA-ARS to improve software for

the many small specialty crop breeding programs supported by ARS. While Breeding Insight is a new project, they have a half-dozen developers to work on this underlying software so that it facilitates the workflows of ARS breeding programs. T3 sees an opportunity both to leverage that investment and to contribute to it.

To date, T3/Wheat Breedbase contains 20,639 accessions with phenotype data and 11,473 with genotype data. A total of 2,618 phenotype trials (containing 818,155 observations) and 38 genotype trials have been uploaded to T3/BreedBase.

SNP Primer Design pages have been ported to T3 Breedbase. A Galaxy project pipeline using PolyMarker developed by Junli Zhang from the UC Davis WheatCAP group is accessible at https://galaxy.triticeaetoolbox.org/. T3 Breedbase also hosts a KASP marker design program, which is a R Shiny program developed by Noah DeWitt from the NC WheatCAP group.

Four large genotype datasets contributed by the Akhunov Lab (2017_WheatCAP, 2019_DiversityGBS, 2019_Diversity GBS Filtered, and 2019_HapMap) are on Breedbase. They are accessed by specifying a range of genome positions, leading to a VCF download. Further, the T3 group is working with the Breedbase developers to modify their code so that it will handle genotype datasets with over 1 million markers, such as those just mentioned. The method will break the data into subsets by chromosome. Access and retrieval of the data will be identical to other genotype data in the database, and therefore totally invisible to the user. Once that feature is complete, access to all genotype datasets will be through the same interface.

The T3 Breedbase platform has a Genomic Selection tool that works in two stages. The first step is to build a prediction model with phenotype and genotype data. The second step is to select entry lists from trials and obtain predictions. The analysis takes 5-10 minutes for each step and the results are permanently cached so that they can be quickly retrieved at a later time.

T3 has ported the T3 Breedbase trial summary tool that generates LSMeans tables with LSDs for a selected group of trials and traits. This tool, for example, allows breeders to customize dynamic cooperative nursery reports.

A new germplasm search tool has been created that allows users to bulk search T3 Breedbase for existing germplasm records by name. This tool uses germplasm names, synonyms and registered accession numbers stored in the database and compares them to the user's search terms using a number of search routines to find similarly named germplasm lines that are likely the same. This tool should help with the perennial problem of germplasm name mismatches in datasets contributed by multiple users.

GrainGenes is working diligently to create and curate JBrowse instances covering a number of reference sequences (https://graingenes.org/GG3/genome_browser). T3 collaborates with GrainGenes to ensure that relevant data sourced from T3 is available on those browsers and links back to correct report pages on T3. The 9 million sequenced EMS mutations in the promoter and coding sequence of tetraploid wheat are now accessible through the GrainGenes JBrowse.

A. 4. Genomics resources

Sequenced tilling populations: The UCD group completed the remapping of the Kronos exome capture to the Chinese Spring RefSeq v1.0 and called mutation effects on all annotated genes. They also established a new error threshold methodology adjusted by individual captures, which improved the quality of the data. The final dataset available in the UC Davis web browser and GrainGenes includes 4,774,529 sequenced mutations with an estimated error rate of 0.33% (99.67% accuracy) and a mutation density of 40 mutations per Kb for the complete population.

The Dubcovsky lab also completed the sequencing of the promoter regions (2 kb) of all annotated high-confidence genes in 1,513 lines of the EMS mutagenized Kronos population using a promoter capture developed by Anthony Hall in the UK. This large sequencing effort resulted in 4,287,361 sequenced mutations with an estimated error rate of 0.21% (99.79% accuracy), and a mutation density of 36 mutations per Kb. The manuscript is still in preparation but all the promoter mutations, together with the re-mapping of the exome capture data, is already publicly available through the Dubcovsky's lab website and the GrainGenes genome browser. WheatCAP continues to distribute mutant seeds to users throughout the world.

Wheat chromatin accessibility data: The chromatin accessibility map of the wheat genome was constructed and results are published (Jordan et al., 2020, see Appendix 2). The KSU group showed that chromatin accessibility is a strong predictor of the effect of SNP variation on phenotype, indicating that the developed map of chromatin states across the genome is useful for prioritizing SNPs for genomic selection experiments, detecting causal SNPs in gene mapping studies, and GWAS. On average, across analyzed traits (plant height, grain filling period, harvest weight, and stress susceptibility), the proportion of phenotypic variation explained by the SNPs located within the most open chromatin regions (0.56) was 3 times higher than that explained by SNPs located in regions with the most closed chromatin (0.17) (Fig. 1). The distribution of chromatin accessibility scores across the genome has been deposited to the T3 database and GrainGenes, and now is being used for developing a tool that will allow for filtering SNPs from the T3 database based on the chromatin accessibility of genomic regions and identifying functional SNPs affecting gene expression or trait variation.
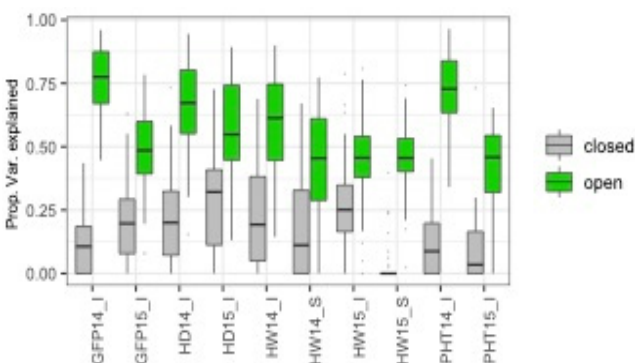

Fig. 1. Proportions of phenotypic variation explained by SNPs located in the genomic regions with closed (grey) and open (green) chromatin. The DNS chromatin accessibility scores were used to assign each genomic region to the top and bottom 20th percentiles of DNS score distribution. The estimates of genetic variance were obtained for the plant height (PHT14_I, PHT15_I), grain filling period (GFP14_I, GFP15_I), harvest weight (HW14_I, HW15_I), and stress susceptibility (HW14_S, HW15_S) traits collected in 2014 and 2015 field seasons.

Regulatory Sequence Capture for a diversity panel of 203 wheat lines: The KSU group used the same regulatory capture assay used in the Kronos EMS population to re-sequence 203 wheat

accessions previously used for eQTL mapping. A total of 9,418,016,463 paired-end 2x150 bp reads were generated for 203 accessions, with the mean of 46,394,170 reads per accession. On average, 87% of all reads were mapped to the genome uniquely with an average of 8% reads failed to map. After SNP filtering, they obtained 3,320,006 SNPs segregating in the regulatory and coding regions of genome. The data was used to identify regulatory SNPs associated with gene expression variation in wheat. This data will be made available through the T3 database by the end of 2020.

Mapping variants (eQTL) controlling gene expression variation in wheat: The KSU group used a panel 198 diverse spring wheat cultivars and landraces to map SNPs associated with variation in gene expression in seedlings and developing spikes. They identified 36,898 and 65,117 eQTL in the RNA-seq datasets from wheat seedlings and spikes, respectively. They found significant enrichment of cis-eQTL among SNPs located in the regions with open chromatin (Fig. 2), as well as SNPs associated with variation in yield component and development traits in wheat. For the majority of collected traits, they found more than 2-fold enrichment of *cis*-eQTL among SNPs identified by genome-wide association mapping. By performing joint analysis of eQTL, GWAS and phenotyping data, they were able to identify candidate genes whose expression is associated with variation in traits (spikelet number per spike, grain size and weight) contributing to yield potential. The KSU data indicates that the eQTL map of wheat genome provides a powerful tool for investigating the mechanistic basis of trait variation, and connecting regulatory variation with genes and pathways controlling agronomic traits.
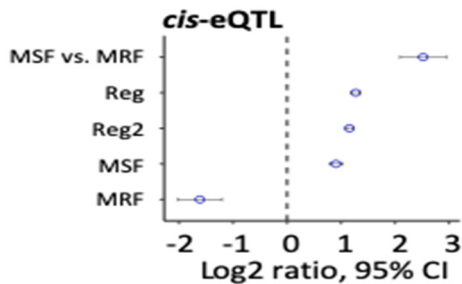

Fig. 2. Enrichment (log2-fold change) of *cis*-eQTL in the MNase Sensitive Footprints (MSF – open chromatin), MNase Resistant Footprints (MRF - closed chromatin), and regulatory regions (Reg and Reg2) identified based on the sensitivity to nuclease treatments, epigenetic variation and open chromatin marks

Developing Practical Haplotype Graph (PHG) tool for wheat: The PHG is an effective SNP data storage and retrieval tool that requires a representative set of wheat lines that capture haplotypic diversity of wheat for predicting missing genotypes. The Akhunov lab collaborates with T3 team and genotyping labs on developing the PHG of wheat. For this purpose, a total of 195 lines have been sequenced with NovaSeq and aligned to Chinese Spring reference. A total of 1,692,264 high quality SNPs and Indels were processed through the GATK pipeline and deposited to the T3 database. Files generated for these lines (gVCF) were used for the Wheat PHG development and assessing the accuracy of genotype imputation in Skim-seq datasets with different levels of genome coverage. The exome capture data generated for WheatCAP parental lines was used to construct a PHG. Then using Skim-seq datasets for another unrelated set of winter wheat cultivars providing 0.01x, 0.1x, and 0.5x coverage of genome, they performed PHG-based genotype imputation. The accuracy of genotype imputation achieved for 0.01x, 0.1x, and 0.5x coverage data was 91%, 95.6% and 96.1%, respectively, suggesting that developed

PHG tool will be a powerful tool for processing, storing and imputing genotypes produced by low-coverage whole-genome sequencing of large wheat populations.

Low-cost genotyping assay for breeding programs: The Akhunov lab have tested molecular inversion probe (MIP) assay for low-cost genotyping in wheat. They selected a set of 363 SNPs including functional markers and SNPs from the 90K iSelect assay. A pool of barcoded MIPs designed in collaboration with NimaGen Company, was used to genotype three wheat accessions that were previously genotyped using the 90K SNP assay. The NGS of pooled MIP amplicons produced data for 287 SNP sites (79%). Comparison with genotyping data generated 90K SNP assay showed 83% concordance rate. Further optimization of MIP pools is being performed to improve performance and accuracy of genotype calling. Overall, these results indicate that the MIP-based genotyping platform could be an effective low-cost genotyping solution for breeding applications, such as low-resolution gene mapping and genomic selection.

A new transformation technology improves regeneration efficiency and editing in wheat. The Dubcovsky lab in collaboration with the transformation facility at UCD developed a new transformation technology using a chimeric protein including the wheat GROWTH-REGULATING FACTOR 4 (GRF4) and its cofactor GRF-INTERACTING FACTOR 1 (GIF1). The inclusion of this chimera increased regeneration efficiency > 7-fold, reduced the transformation protocol from 91 to 56 days, and greatly expanded the number of transformable wheat genotypes. Moreover, *GRF4-GIF1* induces efficient wheat regeneration in the absence of exogenous cytokinins, which facilitates selection of transgenic plants without selectable markers.
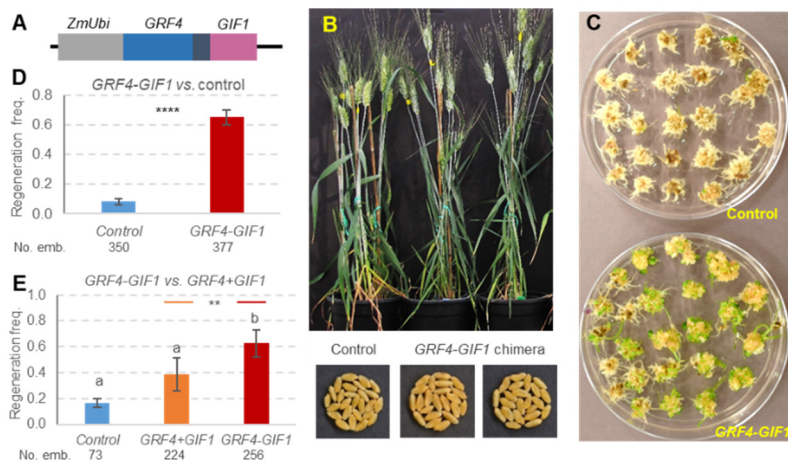

Fig. 3. A) Representation of the *GRF4-GIF1* chimera. **B)** *GRF4-GIF1* transgenic wheat plants were normal and fertile. **C)** Representative transformation showing higher frequency of regenerated shoots during Kronos transformation in the presence of the *GRF4-GIF1* chimera than in the control. **D)** Average regeneration frequency of transgenic Kronos plants from 15 experiments. **E)** The chimera (*GRF4-GIF1*) worked better than *GRF4* and *GIF1* driven by separate promoters (*GRF4+GIF1*).

By combining *GRF4-GIF1* and CRISPR-Cas9 technologies, the UCD group was able to generate large numbers of edited wheat plants. The *GRF4-GIF1* transgenic plants were fertile and without obvious developmental defects, likely due to post-transcriptional regulatory mechanisms operating on *GRF4* in adult tissues (the bioRxiv preprint is available and a Nature Biotechnology paper is in press. See Appendix 2, Debernardi et al. 2020).

A. 5. Genotyping Laboratories

The role of the genotyping labs in the current wheat CAP project is to provide KASP and other marker genotyping services for QTL analysis and high-resolution mapping of candidate genes for yield-related QTL. The NC lab worked with the program at Cornell to develop 28 KASP assays with improved genome specificity that were evaluated on 1,920 lines for a total of 53,760 data points. This work supported fine-mapping of two QTL for kernel weight and kernel width near the centromere of chromosome 5A. Two-enzyme genotyping by sequencing was also performed on a diverse collection of durum wheats submitted by the Cornell University. SNP calling was performed by aligning to the recently published 'Svevo' durum genome sequence and 26,439 variants were identified. In support of the graduate student project at NCSU, forty new genome-specific KASP assays were developed and evaluated on 768 plants for fine-mapping QTL on chromosome 3A, 5A and 3D in the LA95135 x SS-MPV57 population. KASP assays for genes identified as part of the Wheat CAP project, including *B1*, *WAPO-A1*, *TaGW-A2*, *Vrn-A3*, and *FT-A2* were developed and evaluated on 800 eastern winter wheat entries in regional, collaborative nurseries. Entries were also genotyped with an additional 150 assays targeting other traits of agronomic importance. Data are provided to breeders and are being used for analysis of gene/QTL effects across a diverse set of environments.

Research into genotyping technologies: USDA-ARS researchers in collaboration with the Akhunov lab have compiled exome capture sequencing data on a collection of 419 lines relevant to contemporary U.S. wheat breeding efforts. Lines were identified and sequenced by regional small grains genotyping labs in the Pacific Northwest region (Pullman, WA), the Central Plains hard red winter wheat growing region (Manhattan, KS), the Northern Plains hard red spring wheat growing region (Fargo, ND), and the Southeastern soft red winter wheat growing region (Raleigh, NC). Variant calling has identified 1.28 million SNPs and 73,000 indels in this set of lines; currently the read data is being used to prepare a Practical Haplotype Graph, which should help enable the integration of genotypic data across multiple genotyping platforms. These data are the basis for selection of target SNP for a cost-effective mid-density genotyping platform to be deployed for genomic selection strategies.

The Manhattan lab optimized a new next-generation-sequencing based medium- to high-throughput genotyping system called multiplex restriction amplicon sequencing (MRASeq) for Illumina platform. This system, originally developed for Ion Proton sequencer for medium throughput genome-wide SNP analysis, was optimized for use in Illumina NextSeq sequencer. The optimized Illumina sequencer-based protocol generated 115,000 mapped SNPs at 20% missing data and 155,000 mapped SNPs at 80% missing data in an association mapping population of 192 samples from a single run (1x75) of Illumina NextSeq 500. After removing SNPs with >10% heterozygotes and <0.05 MAF in the same population, the total was 4500 polymorphic SNPs at 20% missing data. This genotyping system uses 7 (can be 1-25) well-selected primers and two steps PCR for library construction, which is technically simple and has low cost per sample for library construction (~$1). Number of SNPs can be increased by increasing number of primers used for PCR. Compared to GBS, MRASeq SNPs are more evenly distributed across the wheat genome and have much lower missing data rate. It is also easier to construct MRASeq library, targets a subset of GBS SNPs, and has no patent requirement. SNPs

are called using GBS calling pipeline and previous GBS data can analyzed together with MRASeq data. Therefore, MRASeq is an ideal platform to be used for genomic selection and marker-assisted background selection in breeding programs.

The Manhattan lab also developed three near diagnostic KASP markers for the 1R translocation. By comparison of 1A and 1R GBS-SNPs between wheat and rye association mapping populations, they identified one SNP for separating 1R from 1S, one SNP each for identification of 1B/1R and 1A/1R translocations. These markers were analyzed in more than 1000 wheat lines from different sources and are highly diagnostic for determination of the 1R translocation in wheat. In addition, the lab developed two diagnostic markers for leaf rust resistance gene *Lr42* using RNA-seq, the new markers have been validated in more than 1000 germplasm lines and are highly diagnostic for *Lr42* in different genetic backgrounds. Finally, the Manhattan lab analyzed >8,000 wheat samples from 15 genetics and breeding programs in 2020. These analysis generated about 350 million genome-wide (GBS, GBMAS, MRAseq) and 210,000 sequence-specific (KASP, SSR, STS) data points. About 1,500 wheat lines including parental lines from regional breeding programs and the two HWW regional wheat performance nurseries (RPN) and germplasm observation nursery (RGON) were screened with 125 sequence-specific markers linked to important traits.

The Fargo genotyping laboratory primarily runs Illumina Infinium Assays for genome-wide SNPs and KASP/SSR markers for specific targets. In 2019, they processed 20,000 individual samples and delivered 600M data points to customers (~half of the jobs are wheat). They also updated their liquid handling equipment to increase KASP genotyping capacity, and have started running Semi-Thermal Asymmetric Reverse PCR (STARP) genotyping assays as a service. In FY21, they will evaluate a new Infinium XT design that has the potential to function as a low-cost, medium-throughput genotyping option. They will be also building upon the exome capture genotypes obtained in 2018 with whole genome resequencing of foundation lines of the North American HRSW breeding pool. Integration of the genome-wide polymorphisms in this germplasm will highlight important genetic linkage blocks and will allow researchers to add value to low-density genotyping platforms with imputation. This haplotype information will also be used to guide new targeted amplicon-sequencing-type genotype assays that may also meet the necessary specifications for genomic selection.

Among the WheatCAP-related projects supported by the Western Regional Small Grains Genotyping Laboratory is the development and sequencing of exome capture libraries for lines contributed by the breeding programs, including 127 lines sequenced to an average depth of 42 million reads per sample. They developed a new genotyping technology based on two-step PCR approach that allows for multiplexing thousands of SNP markers for high-throughput genotyping. This method was validated on two recombinant inbred line (RIL) populations that had previous genotyping data from the Illumina Infinium assay and the two data sets were found to be 100% in agreement. The genotyping-by-multiplexed sequencing (GMS) assay includes 1,656 wheat SNP markers, 207 syntenic barley SNP markers, and 49 known informative markers, which generate a possible 2,433 data points (including homeoalleles and paralogs). This protocol is optimized for both the Ion Proton and Illumina High Seq sequencing platforms. In addition, based on the requests from breeding programs, the Western Regional Small Grains

Genotyping Laboratory performed KASP genotyping for introgression of important genes linked with disease resistance (*Yr17*, *Pch1*, and *Fhb1*) and bread baking quality traits.

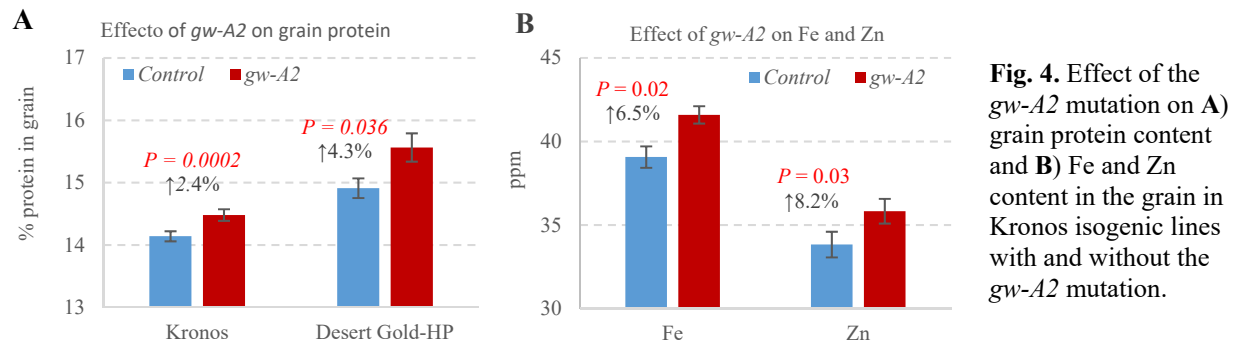### A. 6. CIMMYT HUB. Matthew Reynolds, Sivakumar Sukumaran & Karim Ammar

In the 2019-2020 growing season two experiments were performed in the CIMMYT HUB at Obregon to test the effect of the combined *Elf-A^{m}3* (*T. monococcum*) allele for increased grain number with the *gw-A2* mutant allele for increased grain size. These genes were introgressed into CIMMYT germplasm with high biomass or high grain yield potential. The experiment in hexaploid wheat included BC$_3$F$_3$ and BC$_4$F$_3$ introgression of the *Elf-A^{m}3* allele and the *gw-A2* mutation into the high yielding variety Kingbird and the high-biomass lines HB1 (GID4878569), HB2 (GID4314513) and HB3 (GID4577963). This experiment included 14 genotypes with 10 replications in a RCBD (total 140 yield plots). The second experiment in tetraploid wheat included introgression of the same two genes into the tetraploid wheat varieties Cirno, Kronos, and GID6420253 (4 x 3 = 12 genotypes). This experiment was organized in an RCBD with 8 replications (3.4 m^2 plots) and two levels or irrigation: full irrigation, and reduced drip irrigation. The same experiment was replicated in Imperial Valley CA, but only under full irrigation.

Hexaploid wheat experiment: The hexaploid wheat experiment revealed significant (P = 0.014) increases in grain yield (2.4%) associated with the *Elf-A^{m}3* allele from *T. monococcum.* All four genotypes showed higher yield in the presence of the *Elf-A^{m}3* allele, suggesting that this novel allele may be beneficial in different genetic backgrounds with high grain yield potential or high-biomass. The increase in yield was associated with a 1.7% increase in spikelet number per spike (P = 0.02). The *gw-A2* mutant showed no significant effects on grain yield, but the effect on grain protein is currently being investigated.

Tetraploid wheat experiment: The tetraploid wheat experiment did not detect an overall significant effect on grain yield for either of the two genes. However, both tetraploid experiment detected contrasting effects of *Elf-A^{m}3* depending on the variety in which the gene was introgressed. Analysis by variety in the Obregon experiment showed that the *Elf-A^{m}3* allele from *T. monococcum* had a positive effect on yield in the early flowering variety Kronos but a negative effect in the late flowering variety Cirno. A possible explanation is that the 2 d delay in heading time associated with the *Elf-A^{m}3* allele may have been associated with the differential effect on yield in Kronos (an early variety that can benefit for a few extra days) and Cirno (a late variety that can suffer extreme heat by additional heading delays).

Although the *gw-A2* mutation showed no significant effect on grain yield a positive effect on total protein yield and in nutrient grain content was detected. Introgression of the *gw-A2* mutation in the durum varieties Kronos and Desert Gold-HP showed 2.4% to 4.3% increases in grain protein content respectively. The second result is particularly important since Desert Gold-HP has the *Gpc-B1* allele that was previously shown to increase protein, Fe and Zn content in the grain. In Fig. 4 the higher protein content of Desert Gold relative to Kronos is evident. This result indicates that the two genes have additive effects and that they can be combined to achieve high levels of nutrients in the grain. A significant increases in Fe (6.5%, *P*= 0.02) and Zn (8.2%,

$P = 0.03$) was associated with the presence of the *gw-A2* mutation. However, the effects in nutrient content were dependent on the environment and were not detected in the Imperial Valley experiment.

Fig. 4. Effect of the *gw-A2* mutation on **A**) grain protein content and **B**) Fe and Zn content in the grain in Kronos isogenic lines with and without the *gw-A2* mutation.

New seeds submitted to CIMMYT for isogenic lines including

1. Isogenic lines of *WAPO-A1* allele F47 for high number of spikelets per spike introgressed into CIMMYT high-biomass lines GID3855011, GID4314513, and GID4577963 at UC Davis.

2. Isogenic lines of *QTn.mst-6B* for number of reproductive tillers introgressed from McNeal into CIMMYT high-yielding lines Kingbird and BAJ#1 at Montana State University

3. Isogenic lines of a QTL for spikelet number per spike on chromosome 5A and a QTL for productive tiller number on chromosome 6A from SYC Capstone introgressed into CIMMYT high-biomass line GID3613474 at the University of Idaho.

A. 7. QTL cloning and deployment projects

During the fourth year of the project, candidate genes were identified, validated and/or published for nine QTLs:

1. QTL for number of spikelets per spike on 7AL (*WAPO-A1*, UCD-KSU).
2. Grain size QTL *TaGW7* encoding a TONNEAU1-recruiting motif (TRM) protein (KSU).
3. Grain weight QTL *TaGS3* encoding G-protein subunit (KSU).
4. Awn suppressor *B1* (NCSU).
5. 1RS/1BS QTL for yield under water stress (UCD).
6. 7BL QTL for number of spikelets per spike (Oklahoma State University).
7. 2BL QTL for spikelets per spike (UCD).
8. 3AS QTL for spikelets per spike (*FT-A2*, UCD)
9. Mutations *ful-A2* and *ful-B2* that increase SNS on the long arm of chromosomes of homeologous group 2 (UCD).

2019-2020 progress of individual research projects:

AR. University of Arkansas. Esten Mason

Education: Zachary Winn started on August 21, 2017 as an M.S. student and completed his M.S. in Aug 2019. Zachary was a key member of the positional cloning efforts, including developing new phenotyping methods for spike characteristics. He is attending North Carolina State University for his doctoral research under the direction Dr. Paul Murphy. Dylan Larkin continues to work on cloning the 1AL QTL. He completed his qualifying exams in Mar 2020. Dylan attended and presented about using the results from WheatCAP for genomic selection at the annual WheatCAP session in conjunction with the Plant and Animal Genomics (PAG) Conference in San Diego, CA. He is currently preparing an online seminar for genomic selection with Noah Dewitt for his fellow WheatCAP students. One new M.S. student, Mikayla Hammers, started on Jan 2019 and is assisting with positional cloning efforts by continuing Zachary's research. Mikayla has joined the program at Colorado State University, while Dylan will remain at the University of Arkansas until he graduates in December 2020.

Research project: The University of Arkansas breeding program is cloning a QTL on chromosome 1AL. In the original RIL population, genotypes containing the favorable AGS2000 allele averaged 24.1 g m^{-2} higher grain yield compared to the Pioneer 26R61 allele. In 2018-2019, a field study was conducted in Fayetteville, AR, which included four paired headrow replications of each HIF. This field study was repeated in 2019-2020 with 10 paired headrow replications. A moderate throughput method was developed for quantifying spike characteristics including area spike^{-1} as a surrogate for spike length using image analysis. On average, the AGS 2000 allele was favorable for kernels spike^{-1}, area spike^{-1}, kernel weight spike^{-1}, and 1000 kernel weight in 2019. With the exception of 1000 kernel weight, the additive effect for all yield components was consistent across years and in the combined analysis. Based on current marker density, the AR group was able to narrow down the QTL candidate region to a 10 Mb region between 521.3 and 531.6 Mb.

In Early 2020, the AR team extracted new high-quality DNA for 236 NILs for high-density marker analysis within the QTL region which. Due to the COVID19 shutdown the AR team had limited marker capacity both in house and in cooperation with the genotyping center for the remainder of spring and summer 2020. On Aug 17, 2020, Dr. Esten Mason started as an Associate Professor and Wheat Breeder at Colorado State University and will continue his efforts with the WheatCAP project there and in cooperation with the remaining personnel at Arkansas as necessary.

Deployment: The AR backcrosses are at the BC$_2$F$_1$ stage of introgression of the positive allele of the 1AL QTL into four high-yielding CIMMYT spring wheat lines. Advance was delayed by COVID situation and by the relocation of PI to CSU.

CA. University of California, Davis. Jorge Dubcovsky

Education: PhD students Saarah Kuzay and Priscilla Glenn passed their qualifying exams. Saarah published her paper in TAG as first author on the identification of the 7AL QTL candidate gene and has completed the validation of the candidate gene using mutants and transgenic plants. She will soon start writing her second paper. Priscilla Glenn made good progress in the validation of the *FT-A2* polymorphism associated with SNS and has generated a

first draft of her publication. They both attended the 2020 WheatCAP meeting in PAG in Sand Diego. Saarah Kuzay received the "NAPB 2020 Borlaug Graduate Scholars" funded by the National Association of Plant Breeders (NAPB) and the Agronomic Science Foundation (ASF), for her leadership role in plant breeding training activities.

Research project: The UCD group identified a group of 14 candidate genes associated with the differences in drought tolerances between the Hahn-1RS and Hahn-1RS^{RW} isogenic lines described in previous WheatCAP papers. These genes are all expressed in roots and are deleted in a long-roots 1RS$^{RW-del8}$ radiation mutant (the parental line 1RS^{RW} has short root). The UCD group has initiated the characterization of these candidate genes using RNAseq and transgenic approaches. Preliminary results showed reduced root length for lines overexpressing one of the candidate genes, suggesting that the causal gene has been identified. Validation experiments of this candidate genes using miRNA interference and CRISPR are underway.

Last year, PhD student S. Kuzay published in TAG the identification of *WAPO-A1* as the best candidate for the 7AL QTL for spikelet number per spike (SNS). She showed that only the candidate gene *TraesCS7A02G481600* has non-synonymous polymorphism that differentiated the high-SNS haplotype from the two haplotypes with low-SNS. During 2020, S. Kuzay validated this candidate gene using both mutant and transgenic approaches (Fig. 5).
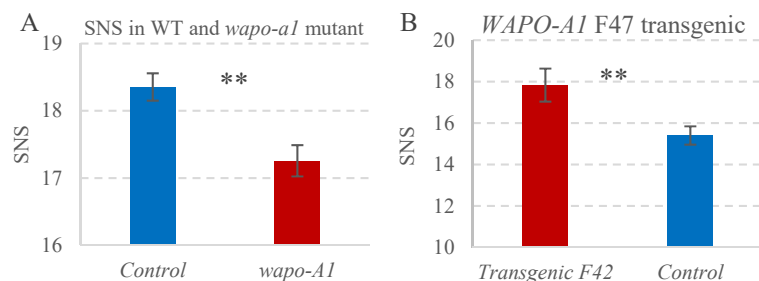

Fig. 5. Validation of the *WAPO-A1* candidate gene. A) A loss-of-function mutation in *Wapo-A1* significantly reduces SNS relative to the WT control. B) A transgenic plant with an additional genomic copy of the *Wapo-A1* F42 allele significantly increases SNS relative to the WT control.

Her results demonstrated that *WAPO-A1* is both necessary and sufficient to modify the number of spikelet per spike, and that therefore it is the causal gene of the SNS QTL on the long arm of chromosome 7AL. Saarah is preparing her second manuscript reporting the validation results.

PhD student Priscilla Glenn completed the high-density mapping of a QTL for SNS on chromosomes 3AS and reduced the candidate region to 8.8 Mb (117.8 to 126.6 Mb). This region includes the *FT-A2* gene that is a strong candidate for the SNS QTL since mutants of this gene increase the number of spikelets per spike. Analysis of the natural variation in *FT-A2* revealed an interesting amino acid change (D10A) that was rare in tetraploid wheat but had a high frequency in modern common wheat varieties, suggesting positive selection for the new allele. Interestingly, she found that the A10 allele had a positive effect on SNS in the fall planted spring varieties but a negative effect in the spring planted spring varieties, suggesting strong epistatic interactions with the genetic background. Priscilla is now analyzing transgenic plants for this gene and exploring the effect of the introgression of the D10 allele into durum wheat.

The UCD group completed the development of the new variety "Yecora Rojo 515" that restores stripe rust resistance into the popular Yecora Rojo variety (Appendix 1) and three germplasm

with mutations in *Glu-B1x*, *Glu-B1y* and one mutant combining both mutations that has no high-molecular weight glutenins. The results were published in the Journal of Cereal Science. The UCD group led five peer-reviewed articles and collaborated in three in 2020 (Appendix 2).

Deployment: In 2020, the UCD lines sent to the CIMMYT hub were tested for grain yield, heading time and SNS in real yield trials including 140 (hexaploid) and 192 (tetraploid) plots. The *Elf-A^{m}3* allele for increased spikelet number from *T. monococcum* and the *gw-A2* mutants for increased grain size were introgressed into tetraploid varieties Kronos, 'Cirno C 2008' and 'GID$_{6420253}$'; and into hexaploid wheat Kingbird HB1 (GID4878569), HB2 (GID4314513) and HB3 (GID4577963). Results for the experiments performed with the UCD seeds are described in the CYIMMYT section (A.6.). Finally, the UCD group introgressed the *WAPO-A1* allele into three CYMMIT high-biomass bread wheat lines GID$_{4314513}$, GID$_{4577963}$ and GID$_{3855011}$ and into the tetraploid variety Kronos (BC$_4$F$_2$). Seeds will be sent to CIMMYT in September 2020.

CO. Colorado State University. Stephen Pearce, Pat Byrne and Scott Haley

Education: PhD student Andrew Katz has completed all course credit requirements for his PhD degree (GPA 4.00) and passed his qualifying exam in March 2020. Andrew has supervised four undergraduate students (Forrest Wold-McGimsey, Mallory Wilemon, Alejandro Benitez and Jack Mentzer) during the project, and presented his research at departmental and university-wide seminars at CSU and at the Texas A&M Plant Breeding Symposium.

Research project: The CO team validated their target QTL for spikelet number on chromosome 6BL (position 492-502 Mb, RefSeq v1.0) across three field seasons in Fort Collins, CO in a Platte/CO940610 RIL population (F$_{5:8}$, n=222), with the Platte 6BL allele conferring an average increase of 0.83 spikelets per spike (% R^2 = 7.6, *P* < 0.0001). They further validated the QTL using eight HIFs (F$_{5:6}$, n=18 sown in 3 replications as headrows). Each HIF was segregating for the 6BL peak marker but fixed for different combinations of the *VRN-D3a/b* and *WAPO-A1a/b* allelic variants, allowing us to account for the confounding effect of these latter alleles on spikelet number. The 6BL QTL was significantly associated with spikelet number (*P* <0.05) in seven of the eight families, with an effect size ranging from 0.25 to 0.50 spikelets per spike.

The CO team screened 2,592 F$_{5:6}$ individuals from these HIFs using 17 KASP markers spanning the peak QTL region and identified 10 critical recombinants to perform progeny tests. For each critical recombinant line in the 2019/2020 field season they derived 100 individual F$_{6:7}$ lines fixed at the 6BL locus which will be planted as head rows in fall 2020 to further delimit the 6BL QTL. They identified a candidate shoot apical meristem maintenance gene that is highly and differentially expressed during the early stages of spike development which they will characterize by CRIPSR/Cas9 knockout.

Deployment: The CO team have introgressed the high-value 6BL and *WAPO-A1b* alleles for greater spikelet number into three CIMMYT high biomass parents; 'Bonsu', 'Nadi', and GID4314513. They developed BC$_3$F$_2$ seed segregating for these alleles in 'Nadi', which will be grown in field trials at CIMMYT during 2021, and BC$_1$F$_{2:3}$ segregating families in 'Bonsu' and GID4314513.

ID. University of Idaho. Jianli Chen and Daolin Fu

Education: Two MS students, Katrina Johnson and Kyle Isham, graduated last December. Kyle Isham was interviewed by several private companies without getting job offers due to COVID-19-related situation. He is currently operating a farm. Katrina Johnson moved to a Ph.D program at OSU. Meng Su started her Ph.D program in 2018 and plans to graduate in December 2021. The OSU group has offered positions to two new MS international students, who could not join the program because of COVID-19 pandemic. Dr. Wang Rui (50% support from the WheatCAP) started a new job in private company in the US. A new postdoc (Rawnaq Chowdhury 50%) was hired in 02/2020.

Research project: The ID team works on cloning a gene underlying the SNS QTL on 5AL using the UI Platinum x SY Capstone mapping population. Ph.D student Meng Su screened 3,615 F_7 plants derived from three HIFs and identified 185 recombinants. Seeds (F_8) from the 185 RILs and the corresponding parental lines (NILs) were increased in greenhouse and, in 2020 field season, evaluated for SNS and HD traits under irrigated conditions in Aberdeen. Thirty-four NIL pairs were also planted in rainfed condition in fall of 2019 and additional nighty-two NIL pairs were planted in spring of 2020 in Moscow and assessed SNS.

In addition, in the flanking region of the 5AL SNS QTL, they mapped a QTL associated with preharvest sprouting (PHS), late maturity alpha amylase (LMA), and falling number FN. This region includes gene *AMY3*, and Meng has initiated a gene editing project for *AMY3* in the background of UI Platinum. The ID team identified a DHL (IDO2102S) that has LMA resistance in the UIP x SYC population which will be released in 2021.

The ID team also mapped QTL on chromosome arm 7DS associated with grain yield, thousand kernel weight (TKW), SNS, and heading date in UI Platinum x LCS Star population (manuscript submitted). *FT-D1* might be the candidate gene with pleiotropic effects on multiple traits. They also identified a DHL (CdDH-266) that has 25 SNS through transgressive segregation. The spike length of this line was longer than that of both parents. They observed that this line has distinct flag leaf morphology, and are going to develop a population from UIP//UIP/CdDH-266. The increasing allele for SNS trait has been introgressed into some elite lines in the program.

Deployment: The UID team will harvest BC_3F_2 lines in the backgrounds of two GID lines (GID3613474 and GID4314513) that contain SNS QTL on 6A and 7A from UI Platinum. They will send seeds to CIMMYT in September. In 2021, the UID team will have BC_3F_2 lines in the background of GID3613474 that contain SNS QTL on 5A and/or PTN QTL on 6A from SYC Capstone.

KS. Kansas State University. E. Akhunov.

Education: The two graduate students from the Manhattan Genotyping lab graduated in 2019. Dr. Yaoguang Li now works as a post-doc in University of Connecticut and Dr. Abdul Hashimi works as an Assistant Professor in Dep. Botany and Microbiology, College of Science, King Saud University in UAE. Students Bliss Betzen and Elina Adhikari from Dr. Akhunov lab are graduating in November 15 and October 15, 2020 respectively. Postdoctoral researcher

Katherine Jordan involved in Wheat CAP joined USDA ARS as Wheat Research Geneticist. Postdoc Fei He is partially supported by the WheatCAP project.

Research: In addition to the contribution made to the development of genomic resources (see A.4), the KSU group performed editing of *TaGS3*, a gene that controls grain weight in wheat. Using CRISPR-Cas9 technology, they modified the *TaGS3* homeologs in all three genomes, and showed that these mutations increase grain weight by ~10%, with relatively small effect of grain dimension traits.

Deployment: Gene editing events for the *TaGW7*, *TaGW2*, *CKX2-1, CKX2-2, TaGS3* and *TaLAC* genes are being introgressed into three CIMMYT high-biomass lines, but phenotypic evaluation of these introgression lines was delayed due to COVID-19 situation. In addition, they crossed lines carrying triple- of double-gene mutations in *TaGW2*, *TaGASR7*, *TaCKX2-1*, and *TaCKX2-2* to produce F_2 populations. Plants carrying mutations in two different genes have been identified by next-generation sequencing and will be used to investigate the effects of multigene editing on yield component traits in 2020-2021 season.

KS. USDA-ARS Manhattan. Mary Guttieri

Education: Mustahsan has completed her coursework toward a Ph.D., with the exception of a seminar requirement. Graduation is anticipated December 2021. She participated at the PAG WheatCAP workshop.

Research: The USDA-ARS Manhattan group targeted a grain yield QTL identified on chromosome arm 2DL in the cross between Overley x Overland. NIL pairs were grown in highly replicated yield trials at two rain-fed Kansas locations in 2020. Analysis of the agronomic data is in progress. Progeny of 32 recombinants identified in 2019 were grown for seed increase in Arizona, and field trials will be established with these 32 lines in Fall 2020. Recombinants belong to two classes: recombination event between 323.6 and 326.2 Mb, and recombination event between 352.0 and 386.2 Mb. Additional HIF plants were screened for recombination in 2020, and 104 recombinants identified. Seed was produced in the greenhouse and will be increased in Arizona in 2020-21.

In addition to the positional cloning project, the KSU group used the winter wheat exome capture pool, to identify a distinctive haplotype in the *Rht24* region. They have isolated HIFs in the region from the Overley/Overland population and, using the pool capture data, designed primers for KASP assays to support better delimiting *Rht24* in hard winter wheat germplasm. A similar analysis has been done for *Rht8* to support marker conversion to KASP. In 2020, the KSU group also brought the field trial recordkeeping of the breeding program into WheatBase, through the support of WheatCAP, to provide a cloud-based breeding management platform for the program. The USDA-ARS Manhattan group provided feedback to the development team to better support wheat breeding activities.

Deployment: *Prl/2*Pastor*: Target *QTL* introgression complete. BC$_3$F$_4$ seed will be increased for distribution. Also *Yr40, Yr17,* and *Yr40+Yr17* introgressions complete.

GID4314513: Target *QTL* introgression complete. BC$_3$F$_3$ seed will be increased for distribution.

Baj, Bonsu, Kingbird: *Yr17-Yr40* introgression complete (individually and in combination). BC₃F₄ seed will be increased for distribution. Not variable in target QTL region.

Chipak, Kachu, Mucuy, Borlaug 100 F2014: *Yr40* introgression complete. BC₃F₄ seed will be increased for distribution. Not variable in target QTL region or *Yr17*.

KenyaSunbird/Kachu is variable in the 2D-QTL region. Unfortunately, no 2D-QTL introgressions were recovered in the third backcross. However, a *Yr17+Yr40* introgression was recovered.

MI. Michigan State University. Eric Olson.

Education: MS student, Jonathan Turkus took a leave of absence from fall 2019 to fall 2020. He has completed a dissertation and will defend in the fall semester, 2020. A second MS student, Tommy Reck, began work on the project in January, 2019. Tommy has made the crosses to introgress the 2DS QTL into CIMMYT backgrounds. He will oversee the planting of recombinant lines in fall, 2020 and will collect phenotypic data on yield components in 2021 yield trials.

Research project: A total of 243 individuals were screened for recombination events from 29 HIFs. A total of 13 recombinants have been identified in the region from 23.3 to 29.4Mb. Recombination events can be divided into four bins across the region:

Bin 1: The recombination bin from 23.3 to 24.9Mb contains two recombinants. The bin contains seven genes with a total of 78 polymorphic SNPs.

Bin 2: The recombination bin from 24.9 to 25.7Mb contains six recombinants. The bin contains 14 genes with a total of 88 polymorphic SNPs.

Bin 3: The recombination bin from 25.7 to 27.9Mb contains six recombinants. The bin contains 23 genes with a total of 154 polymorphic SNPs.

Bin 4: The recombination bin from 27.9 to 29.4Mb contains two recombinants. The bin contains 40 genes with a total of 407 polymorphic SNPs.

All recombinants and lines with complete haplotypes of both mapping population parents were planted in headrows for seed increase. Severe winter conditions and flooding decimated the entire planting in fall 2019 which set the entire project back one year. Recombinants were grown in single rep observation plots in 2020. Yield components were collected including spikelets per spike and tiller number. Seed for 39 genotypes with either recombinant or parental haplotypes across 2DS were harvested in 2020 for yield testing in 2021. Eleven recombinants have been identified across all four recombination bins with at least two recombinants in each bin.

Deployment: The MI group produced BC₁F₁ for the 2DS grain yield QTL in CIMMYT lines Kingbird and Heilo, but backcrossing was halted because markers were monomorphic between donor lines and both recurrent parents Hielo and Kingbird. They anticipate developing new KASP markers using results from the baited SNP sequencing project.

MN. University of Minnesota. Jim Anderson.

Education: PhD student Max Fraser successfully completed his courses at UMN and attended a WheatCAP-sponsored workshop in San Diego, CA. Max completed his written preliminary examinations and is expected to complete his preliminary oral examination this fall. He chaired the 2020 University of Minnesota Plant Sciences Symposium that was unfortunately cancelled due to COVID-19. Undergraduate student Catherine Li remains on the project and has assumed more responsibility for lab and field activities.

Research project: The MN team failed to identify individuals heterozygous for the thousand kernel weight QTL located on chromosome arm 5BS, *QTkw.mna-5B*, previously identified in the G056 population. This resulted in greater emphasis on the 14x111 population (MN10201-4-116/Prosper//Shelly), a multi-parent doubled haploid population. Mapping for yield component traits was conducted using field data collected from seven environments across two years. Two significant QTL influencing spikelet number per spike, *Qsns.mna.4A.1* and *Qsns.mna.4A.2* (LOD=9.0 & 10.2, respectively) were identified on the long arm of chromosome 4A in all seven environments. Biparental populations (MN10201-4-116/Shelly & Shelly/MN10201-4-116) were initiated in summer 2019 in order to dissect and further fine map these QTL. Approximately 800 F_4 individuals were harvested in spring 2020 with the intent of identifying individuals heterozygous for *Qsns.mna.4A.1* and/or *Qsns.mna.4A.2* and developing HIFs. However, due to COVID-19 restrictions, these individuals have yet to be genotyped. Genotyping is expected to be completed in time to select individuals for the fall 2020 greenhouse. Additionally, yield trials of the 14x111 population were sown in summer 2020. The data collected from these trials will be used for mapping and to supplement the yield component data previously collected. Work also continued on 15xR012, an advanced backcross population developed from a hexaploid UMN breeding line MN07098-6 and a tetraploid *T. turanicum* accession, Sun Ray. A genetic map for 15xR012 was constructed using 1443 GBS markers. Consisting of 21 linkage groups, the map spanned a total of 966 cM. No additional phenotyping is expected to be conducted for this population.

Deployment: Crosses of each 14x111 parent were made with GID4313513 during the spring 2019 greenhouse. Backcrossing of the F_1 lines during the fall 2019 greenhouse season failed. COVID-19 prevented a second attempt in the spring 2020 greenhouse, and due to restrictions, a growth chamber could not be secured to conduct the crosses during summer 2020. These backcrosses will be attempted in fall 2020.

MT. Montana State University. Jason Cook

Education: PhD student Brittney Brewer-Jones participated in soft skill building and educational workshops during the 2020 year. Brittney attended a science communication and strengths assessment workshop hosted by Loriana and Patrick Sekarski with Bonsai in San Diego, CA (January 2020). This workshop focused on better understanding individual strength profiles and how to apply these to working in a team setting. Additional topics included having difficult conversations and time management. Brittney is scheduled to graduate with her Ph.D. in May 2021.

Research project: PhD student Brittney Brewer-Jones is fine mapping a QTL, designated *QTn.mst-6B*, for early tiller number (at Zadoks stage 31) located on chromosome 6B. She developed HIFs from heterozygous F_5 individuals derived from biparental crosses between Reeder x Choteau and Vida x McNeal. Reeder and Vida possess the high *QTn.mst-6B* tillering allele. Population size of the HIF families are 540 and 556 F_2 lines from the Reeder/Choteau and Vida/McNeal crosses, respectively. Genotyping has been done using SNPs and markers developed from the WheatCAP Exome Capture Assay. Phenotyping of the HIFs has been done in the greenhouse. Current mapping results place the QTL between 226,868,798 bp and 247,209,591 bp on the short arm of chromosome 6B (IWGSC RefSeq v1.0). This region contains approximately 120 high confidence genes of which only 8 appear to be highly expressed in vegetative tissues (Wheat Expression Database). Brittney has one manuscript under review for publication, and is preparing two more manuscripts for submission in peer-reviewed journals.

QTL deployment: The high tillering allele at *QTn.mst-6B* has been backcrossed into locally adapted Montana varieties McNeal and Duclair as well as CIMMYT high yield lines BAJ #1, Chipak and Kingbird. Seed for BC4F2 (McNeal, Duclair, BAJ #1, and Chipak) and BC3F2 (Kingbird) are currently available. BAJ #1 and Kingbird BC seed has been sent to CIMMYT for seed increase and field evaluation.

NC. USDA-ARS Raleigh. Gina Brown-Guedira

Education: Graduate student Noah DeWitt has completed five semesters of classes and participates in the Wheat CAP student meetings. Noah presented work on the B1 awn suppressor and collaborative genomic selection at the Wheat CAP meeting at 2020 PAG, as well a poster at PAG. He presented work on characterizing QTL effects for yield component traits of wheat during the Fall 2020 NCSU Plant Molecular Biology Seminar Series. Graduate student Daniela Miller has completed two semesters of classes. Daniela completed a second year of replicated field evaluation of 288 RIL of new mapping population LA95135 x AGS 2000 at Raleigh, NC. Lines were rated for level of epicuticular wax (glaucousness) on leaves and spikes, a trait that has been associated with stress tolerance in wheat.

Research: Analysis of the QTL for kernel weight and plant height on chromosome 6A continued. While the centromeric position of this QTL has hindered further fine-mapping, the effect has been well-validated. The results from this research are in the final stages of preparation for submission for publication.

Work in 2020 has focused on analysis and preparation for publication of yield component mapping in the LA95135 x SS-MPV57 (LM) mapping population. This same population was used as an additional population for mapping and candidate gene identification in the cloning of WAPO1 (Kuzay et al. 2019). This population and derived HIFs, along with historical data on diverse material, was used to clone the *B1* awn suppressor (DeWitt et al. 2019). Mapping in this population required screening of 358 individuals with 13 KASP markers and 5691 GBS markers, and phenotyping of the population with 5000 head row plots over five site-year combinations.

Three primary issues were encountered in the analysis of yield component traits: the co-location of yield component QTL with heading date and plant height QTL, pleiotropic effects of QTL for yield component traits, and differential effects of QTL in different environments. Multivariate QTL mapping and analyses methods using structural equation modeling (SEM) have been developed for a holistic approach to detection and analysis of QTL effects (Fig 6).
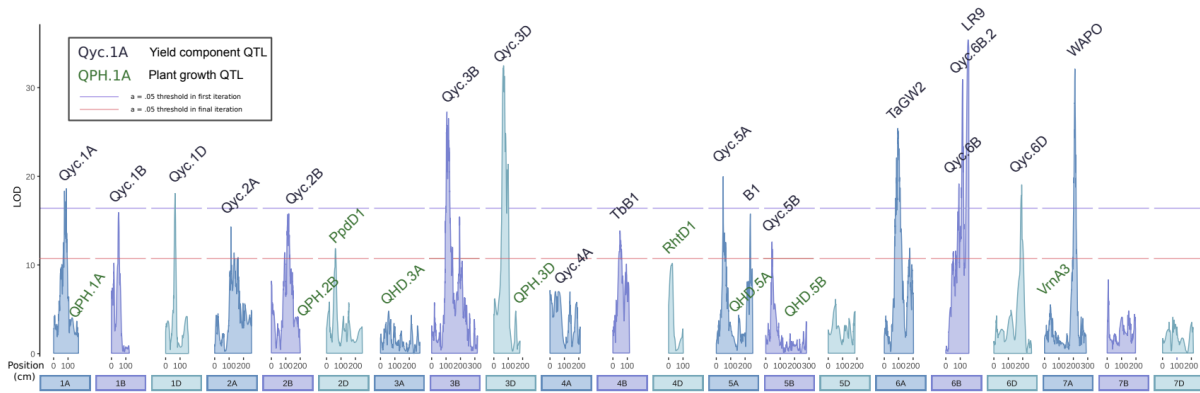

Fig. 6. QTL results from the SEM mapping model in Kinston 2019. All yield component and plant growth (heading date and plant height) phenotypes are considered jointly. Many known and novel yield component QTL are identified, at the same time as QTL for heading date and plant height that may have effects on yield component QTL are not detected.

Path analyses fit with full models have allowed for analysis of environment-specific spike yield effects of know major plant height QTL, and newly cloned yield component QTL segregating in the population *B1*, *WAPO-A1*, and *TaGW-A2*. Trade-offs between yield component QTL effects due to both source limitations and negative pleiotropy often lead to small QTL effects on total spike yield despite large effects on individual yield component traits in this population.

A plant height QTL and a yield component QTL mapped in the LM population on chromosome 3D have been targeted for further fine mapping. The SEM mapping model was used to disentangle the plant height and yield component QTL as two separate QTL, which has been validated in preliminary fine mapping. The LA95135 allele at this QTL has large, stable positive effects on kernel length, and variable negative pleiotropic effects on SPS and kernels per spikelet. NILs planted in the greenhouse were able to confirm the plant height QTL and fine-map the plant height QTL to a region of 36 Mb. A high-throughput genome-specific KASP design pipeline has allowed for the development of over forty KASP markers on chromosome 3D used to screen this population.

Daniela Miller completed the evaluation of the LA95135 x AGS 2000 population at Raleigh for epicuticular wax (glaucousness) on leaves and spikes, a trait that has been associated with stress tolerance in wheat. Multiple QTL were identified for each trait, none of which co-located with the previously cloned regulators of glaucousness. Interestingly, it appears that the major QTL regulating glaucousness for leaves and spikes differ in this population. Twelve KASP assays flanking the QTL were used to identify HIF in the QTL regions for fine mapping. A bi-parental

population (192 RIL) developed from the cross GA06493-13LE6 x Hilliard and a panel of 360 eastern wheat lines were also evaluated in 2020 to validate the glaucousness QTL and identify additional loci affecting the trait.

Deployment: The NC team generated BC$_2$ seed from crosses of awnless wheat cultivar SS-MVP57 with CIMMYT lines GID$_{4314513}$, GID$_{3855011}$ and GID$_{3631474}$. These lines were also crossed with LA95135 to produce BC$_{1\ seed}$ for the kernel weight QTL on 6A and kernel length QTL on 3D. Restrictions on greenhouse work due to COVID-19 resulted in an inability to generate an additional round of backcrossing during spring 2020. Selfed seed was harvested from plants.

ND. USDA-ARS Fargo. Justin Faris

Education: PhD student Amanda Peters Haugrud entered her fourth year as a WheatCAP-funded student, and she has set a tentative graduation date of 12/31/2021. She has completed nearly all of her coursework as well as her written and oral preliminary exams. In the past year, Amanda attended the WheatCAP workshop and the Plant and Animal Genome Conference in San Diego, CA where she presented a poster on her research. Katherine Running has been incorporated as a WheatCAP student for the past year since initiating a research project to evaluate the genetics of seed size in durum. Katherine's major at NDSU is Genomics and Bioinformatics. In addition to completing her courses in genomics, bioinformatics, genetics, statistics, and plant breeding, Katherine attended the WheatCAP workshop and the Plant and Animal Genome Conference in San Diego, CA where she presented a poster on her research.

Research Projects: The group at Fargo is focused on a QTL for kernels per spike (KPS) and grain weight per spike (GWS) on chromosome 2BL in durum wheat. The 2BL QTL was mapped in the RIL population BP025, which was derived from crossing Ben (*Triticum durum*) with the cultivated emmer accession PI 41025 (*T. dicoccum*), and was validated under greenhouse and field conditions. This QTL spans a 38 Mb region at 445 Mb to 483 Mb on the Svevo reference sequence. Two RILs containing PI 41025 alleles in the QTL region were backcrossed to Ben so that the QTL can be studied and validated in isolation. BC$_3$F$_2$ plants were genotyped with two flanking markers about 7 cM on either side of the peak QTL marker region. A total of 108 recombinants out of 1,072 gametes were identified. BC$_3$F$_3$ plants were genotyped to select for homozygous recombinant individuals and were also genotyped with 37 newly developed SSR and STARP markers. BC$_3$F$_4$ plants were grown with five replicates under greenhouse conditions this past spring and phenotyped to narrow down the candidate region. Currently, the Fargo team is are screening additional BC$_3$F$_2$ plants with the flanking markers *Chr2B446082351* and *Chr2B538239714* to identify heterozygous recombinants.

Additional WheatCAP projects at Fargo include mapping yield component and seed morphology traits in three RIL populations derived from crossing different durum varieties with cultivated emmer accessions, and also evaluating seed size and morphology in the global durum panel (GDP). For the durum x emmer RIL populations, the Ben x PI 41025 population was evaluated under field conditions the summers of 2017, 2018, and 2019. The Rusty x PI 193993 population was evaluated under field conditions the summers of 2018, 2019, and 2020. These two

populations were previously studied under greenhouse conditions as well. The third population, Divide x PI 272527, was evaluated under field conditions the summers of 2017, 2019, and 2020, and under greenhouse conditions in 2019 and 2020. For all three populations the following traits have been measured: days to heading, plant height, spikelets per spike, kernels per spike, grain weight per spike, thousand kernel weight, along with the grain dimension parameters including length, width, area, circularity, and length/width ratio. QTL analysis was performed for each trait. The GDP panel was grown in three replications in Casselton, ND in the summer of 2020 and evaluated for heading date and plant height. Other traits including spike length, spikelets per spike, thousand kernel weight, and grain weight, number, length, width, and area will be collected after harvest. The GDP trial will be repeated in the field for two more seasons.

Deployment: The Fargo group has been introgressing this 2BL QTL for kernels per spike (KPS) and grain weight per spike (GWS) into the CIMMYT line GID4878569 and is currently growing the third backcross.

NY. Cornell University. Mark Sorrells

Education: Ellie Taagen is currently supported by the TCAP and is entering the 4th year of her PhD. She passed her candidacy exam in February 2020. Ellie continually presents her research at departmental seminars, lab meetings and will present at the NAPB 2020 annual meeting. The TCAP fine-mapping research has inspired Ellie to further explore the limiting factor of meiotic recombination for her graduate dissertation. In the final chapter she seeks to leverage simulation and bioinformatics tools to better understand the potential for controlled recombination to reveal currently inaccessible genetic diversity and increase control over the inheritance of preferred haplotypes. She received a 2020 Borlaug Scholar award from NAPB. She is on track to graduate in spring 2022. Elizabeth De Meyer completed her undergraduate honors degree in plant sciences from Cornell University in winter 2019. She is starting a PhD program in plant science at University of Missouri in fall 2020.

Research project: The NY team is using the SynOpDH mapping population (162 line subset) and select SynOpRILs to fine map two grain weight and morphology QTL on chromosomes 5AL and 2DS. *QTL 2D*: Originally, 12 seeds from each of 20 selected lines from the SynOpRIL population that were heterozygous at the 2D QTL were advanced to the F6:2 generation (240 F6:2 lines). BLUP values for each SynOpDH line were extracted using random-effect models fitted across six site-year combinations. To fine-map this 2D QTL, they developed a HIF population with increased genetic resolution between 13.9 and 35.2 Mb. The QTL on chromosome 2D increased mean kernel weight by 6.26% and mean kernel length by 4.33%. Fourteen KASP markers have been developed and these markers were tested on SynOpDH DNA and used to genotype the SynOpRIL F6:2s. In January 2019, 50 seeds from each of 14 F6:2 lines heterozygous at the 2D QTL and derived from SynOpRIL F6 line 903 were planted in a greenhouse, along with 22 seeds of each fixed parental control, and 8 seeds of each parent. Final genotyping of the F6:3 progeny was disrupted by COVID-19. This is project will be continued taken on by a new student when Cornell University COVID-19 regulations allow.

QTL5A: The 5AL HIF plants were derived from two F_6 RILs and have been inbred five generations (7,900 total progeny screened for recombination). Graduate student Ellie Taagen planted 11 control HIFs for the Opata allele (positive trait donor), 21 control HIFs for the W7984 allele (negative trait donor) and 96 lines with recombinants between 280-420 Mb. This trial was replicated for validation across years and locations in 2020 at two location in Ithaca, NY, and phenotyped for heading date, anthesis, height, physiological maturity, spikelet per spike, thousand grain weight, grain width and length. Phenotypes will be incorporated to statistical models and R/qtl during fall 2020. Based on 2019 phenotypes the QTL resolved as neighboring peaks for thousand grain weight (TGW) and grain width (GW) on chromosome 5A at 337-349 and 378-385 Mb, respectively. Using this information, in conjunction with the 2019 days-post-anthesis (DPA) time course study, they identified a significant difference in phenotype for the 5A QTL HIF Opata vs W7984 allele starting at 10-16 DPA

The NY team initiated an RNA-seq study including an Opata control, W7984 control and two different recombinants to test the double QTL peak. In a greenhouse they sampled the tissue of maturing grains at 4 and 8 DPA, including three biological reps for each genotype/time-point. The RNA was extracted and the biological reps were sent to Novogene for extraction (24 samples). Ellie Taagen is presently conducting the RNA-seq analysis. Initial findings indicate the population was segregating for presence/absence of 5AS, as previously noted by Gutierrez-Gonzalez et al. 2019. The NY team has a list of candidate genes for the GW QTL 378-385 Mb, based on differential expression at 4 and 8 DPA (TraesCS5A02G181600, TraesCS5A02G184500, TraesCS5A02G183900, TraesCS5A02G177700), but did not detect differential expression for TGW QTL.

Deployment: Unfortunately SynOp is a poor candidate for QTL introgressions with CIMMYT lines as the parental lines were bred by CIMMYT. The Cornell group has discovered no polymorphic markers for the 2D and 5A QTL among the CIMMYT lines, and crosses suffered from necrosis during backcrosses with domestic spring wheat lines.

OK. Oklahoma State University. Liuling Yan and Brett Carver

Education: Forrest C.C. Kan, a Ph.D student, worked on gene mapping on chromosome 1BS in the Duster x Billing population and graduated in December, 2019. He published his results as first author in Molecular Breeding. He was hired as a postdoc in Texas A&M University. Xiaoyu Zhang, the Ph.D. student working on gene mapping on chromosome 7BL in common wheat, graduated in December, 2019 and returned to China. Two new students have been admitted as Ph.D. graduates in OSU and were expected to enroll in fall 2020, but due to the coronavirus, they did not receive visa yet and have deferred enrollment to spring 2021. Dr. Ragu Nagarajan, a current postdoc fellow in my lab, has been assigned to work on the WheatCAP project before new students arrive on campus.

Research projects: *QYld.osu-1BS for increased grain yield*: The extremely low recombination rate in the *QYld.osu-1BS* region has inhibited positional cloning of the gene responsible for the grain yield QTL. The OSU team is using the *Ph1* gene to introduce recombination events for cloning the gene, but it would take several years to purify genetic backgrounds derived from

genetic materials carrying the *Ph1* gene. Nonetheless, this did not prevent the utilization of this QTL in wheat breeding. They have identified unique sequences in the *QYld.osu-1BS* allele, and developed KASP markers for the unique sequences (published in *Molecular Breeding*, 2020). The OSU team used the cultivar 'Duster' containing the *QYld.osu-1BS* to establish the foundation of yield potential, pest resistance, and baking quality and developed two half-sib varieties 'Gallagher' (PI 667569) and 'Iba' (PI 667570) commercially planted in large areas of the southern Plains. They have submitted a manuscript titled "Gallagher and Iba hard red winter wheat: Half-sibs inseparable by yield gain, separable by producer preference" to Journal of Plant Registrations.

QYld.osu-7BL for increased spikelet number per spike (SNS): The gene on chromosome 7BL in CItr17600 is a gene that promotes spike development, thereby increasing grain yield. The OSU team has conducted field experiments on its effects on spike development and grain yield. Although the gene was cloned from a spring wheat cultivar CItr17600, they identified the allele for higher yield in the winter wheat cultivar 'Billings'. The OSU team has also found that OK1059018, a breeding line and well-adapted progeny of Duster/Billings, also carries the desirable allele. Before the cloning of the gene is published, they are using molecular markers to accelerate deployment of this gene in WIT breeding populations.

Deployment: The favorable allele for *QSns.osu-7B* from CItr17600 was crossed with two CIMMYT high-biomass lines (GID: 4577963 and GID: 4314513). The experiments have advanced to BC_2F_2 generation. The favorable allele from *QYld.osu*-1B was backcrossed into six high-yielding lines (NADI, CHIPAK, BONSU, BORLAUG100, KENYA SUNBIRD, KACHU#1) and one high-biomass line (GID:4314513) (PI683503). The experiments have advanced to BC_3F_2 generation with 'GID: 4314513 and BC_3F_2 with 'NADI' (PI683487).

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

Education: Ph.D. student Jyotirmoy Halder is currently supported by the Wheat CAP grant. He is working on the fine mapping, cloning, and deployment of the yield QTL on chromosome 7DS from *Ae. tauschii*. He finished all the necessary coursework and will take a comprehensive exam in the fall semester 2020. He plans to graduate in the summer of 2021. Jyotirmoy participated in the Annual Wheat CAP meeting and Soft Skill Workshop in January 2020. He also participates in monthly online group meetings. Two undergraduate students were trained in wheat breeding during this period and were closely involved in the project developing populations and germplasm focused on yield traits.

Research: The yield QTL was mapped in the distal 6-16 Mb on the short arm of chromosome 7DS. More than 80 KASP markers flanking the 7DS QTL region were evaluated and 15 high-quality co-dominant markers were identified for screening F_6, F_7, and F_8 progenies. The SDSU team screened more than 2,500 progenies with 15 codominant markers and identified 36 recombinants that include both homozygous and heterozygous recombinants. They increased seeds of the recombinant lines in the greenhouse in summer 2019 for field trials. Thirty-six recombinants (8 haplotypes) were planted as single 1m row at two locations in South Dakota in fall 2019. Though considerable winter kill was observed in all recombinant lines, all lines were

successfully harvested from both locations in August 2020. Data on yield and yield contributing trait is being recorded and will be used for fine mapping of 7D QTL. Further, one set of recombinants were also grown under greenhouse condition (bed) to identify which yield contributing traits could be responsible for the yield variation among the recombinants. Eighteen recombinants (out of 36) representing 8 haplotypes and the two parents are presently being genotyped at Arbor Biosciences, MI using myBaits® for fine mapping of QTL region.

A new bi-parental (SD116-28-3/SD18G001) mapping population segregating for various yield contributing traits was developed as a side project. The parents SD116-28-3 and SD18G001 showed variation for spike length (8.62±0.24 cm, 6.18±0.23 cm), spikelet/spike (20.6±0.40, 24.4±0.51), and 1000 kernel weight (36.4±0.48g, 30±0.90g), respectively and preliminary data from F_3 progenies in greenhouse showed large variability. In the 2020 field season, a total of 150 F_4 recombinant lines were evaluated in two replications (1m rows) at two locations in South Dakota. The 25 heads/line/rep/locations were hand-harvested and data on spike length, spikelet/spike, and 1000 kernel weight are currently being recorded. The F_5 lines will be genotyped and phenotyped in a greenhouse to map QTL for yield contributing traits.

Deployment: The DNAM donor line was crossed with CIMMYT lines (GID:3613474 and Kingbird) and markers were used to select for a homozygous *Ae. tauschii* 7D region in BC_2F_2 (GID:3613474). The BC_2F_1 (Kingbird) is being selfed and will also be screened to identify homozygous *Ae. tauschii* 7D region in BC_2F_2. The homozygous lines will be advanced to $BC_2F_{3/4}$ for delivery to CIMMYT in August 2021.

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

Education: ***Smit Dhakal*** finished his Ph.D in December of 2018 and he is a postdoc now working on Sorghum at UIUC. He presented a poster for WheatCAP research progress in the National Association of Plant Breeders (NAPB) meeting in GA in Aug of 2019. ***Jorge Valenzuela Antelo*** will graduate this fall and has taken a job as a breeder lead with Bayer CropScience in Mexico. He presented at the meetings of ASA-CSSA-SSSA in San Antonio, TX in Nov of 2019, Texas Plant Protection Association annual meeting in Dec of 2019 (got 2nd poster award), the WheatCAP annual meeting and soft skill training at San Diego in Jan of 2020, Corteva sponsored TAMU Plant Breeding Symposium on Feb 20, 2020 as a student speaker. Jorge Antelo also worked on a set of 221 RILs from TAM 204/Iba, and he is analyzing the yield components and resistance to Hessian fly. ***Zhen*** joined TAMU since Aug of 2019. He participated the WheatCAP annual meeting and soft skill training at San Diego in Jan of 2020. Zhen presented in the NAPB meeting in Aug of 2020 for genomic prediction and will present at ASA-CSSA-SSSA meeting in Nov of 2020 for yield component mapping, both virtual. Zhen finished courses in College Station and moved to Amarillo to conduct his research on the WheatCAP project. In addition, he learned and practiced the doubled haploid pipeline and genomic prediction and analyzed a set of 356 advanced breeding lines and synthetic derived lines in 2019 and 2020 yield trials. He also analyzed biomass and yield components of other mapping population. Previous WheatCAP postdoc ***Chenggen Chu*** accepted a USDA-ARS geneticist position in Fargo, ND in Feb of 2020 and the Texas team is currently providing some funding form the wheat CAP to postdoc Dr. ***Xiaoxiao Liu*** to contribute to the project.

Research: For the positional cloning of the 2BS QTL for grain weight, the TX group analyzed markers IWB8280, IWB4514, IWB8143 and IWB7072 in 110 plants of two heterozygous F_6 RILs from CO960293-2/TAM 111 and identified 39 heterozygous plants for developing HIFs. Markers covering the whole QTL region were used to analyze 13 HIFs to identify plants with homozygous genotype in QTL region the same as in parents to confirm QTL effect on kernel weight, and heterozygous plants for narrowing down QTL region. From these 13 HIFs, the TX group selected 116 plants with homozygous genotypes in QTL region for comparing kernel weight, 45 heterozygous plants were used to produce recombinants in next generation to narrow down QTL regions. All of these plants are mature in the greenhouse. The seeds are being harvested from the greenhouse and to be analyzed using linked SNPs.

In addition to the positional cloning project, Jackie Rudd evaluated a mapping population of 124 recombinant inbred lines (RILs) from the cross TAM 112/TAM 111. Yield and agronomic traits from 28 environments, yield components from 11 environments, and end-use quality from 7 environments were collected and analyzed. Genetic maps were constructed from 5840 SNPs and two manuscripts were submitted for publication. From TAMU by Jackie Rudd.

Jackie Rudd, Shuyu Liu and Amir Ibrahim tested a nested association panel of 298 synthetic-derived BC_1F_7 lines from a set of 20 synthetics backcrossed with TAM 111 or TAM 112. Data were collected on yield and agronomic traits from 17 environments, yield component from 9 environments, and end-use quality from 7 environments. Significant SNP-trait associations have been identified for all the traits using a 100K SNPs from whole genome genotyping-by-sequencing. Two manuscripts are in preparation.

Finally, Shuyu Liu tested a bi-parental mapping population from TAM 111/TX05A001822 including 179 RILs. Yield and agronomic traits were collected in 6 environments, yield components and end-use quality were analyzed in 3 environments. A set of 3000 SNPs was used for genetics maps and QTL have been analyzed. One manuscript is under preparation.

Deployment: BC_3F_1 plants having the TAM 111 kernel weight increasing loci confirmed with the linked SNPs were developed for doubled haploid (DH). There were a set of 65, 33 and 47 plants derived from 3 CIMMYT lines, GID3855011, GID4314513, and GID4577963. Plants from DH pipeline are growing in the growth chamber and greenhouse now. Fertile plants will be validated using linked SNPs to confirm the QTL introgression and seed will be ready to ship to CIMMYT In Jan of 2021.

WA. Washington State University. Mike Pumphrey & Arron Carter

Education: Ph.D. student Samuel Prather has continued to work on the WheatCAP yield component QTL cloning project with guidance and leadership from Post-doc Tyson Koepke. A new student, Peter Schmuker started on the project in August 2020, to continue this effort as Samuel Prather plans to graduate.

Research Project: The WSU team is focused on a strong QTL on chromosome arm 4AL for kernel weight identified in the cross between elite spring cultivars Kelse and Scarlett. Kelse contributes the positive allele for kernel number and Scarlett the positive allele for kernel weight. In winter/spring 2020, after identification of 119 homozygous recombinants identified from over

2,000 progeny from heterozygous NILs in the Kelse/Scarlet population, 26 unique homozygous recombinants were selected and planted in the greenhouse for phenotyping. With 10 replicates, they measured heading date, spike length, seed number, and seed weight. To repeat phenotyping, a total of 300 homozygous recombinant NILs were evaluated in paired field rows in Pullman WA in 2020. Harvest was completed on August 24, 2020, and they are currently measuring spike length, seed count, seed weight, and heading date from these genotypes. Preliminary analysis places the locus controlling seed number versus seed size between IWB59451 and IWB57074 in this high-resolution mapping population in both greenhouse and field experiments, with an approximately two-day difference in heading date depending on parental alleles.
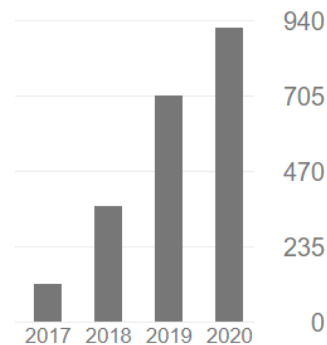
Deployment: The introgression of the 4AL QTL allele from Scarlet into CIMMYT lines PI683500, PI683501, PI683502, PI683503, and PI683504 and from Kelse into PI683501 was advanced to BC_2F_2 and homozygous plants were selected. The WSU team has seed of each line under increase (planted in July 2020), and will ship BC_2F_3 seed as soon as the plants mature.

A. 8. Summary of WheatCAP varieties and germplasm releases

The WheatCAP group released 22 new commercial varieties and four improved wheat germplasm (Appendix 1). Seventeen varieties released in 2019 and reported as pending PVP were assigned PVP in 2020 (Appendix 1). The complete list of released varieties, germplasm and populations is presented in Appendix 1 at the end of this report. By releasing improved wheat varieties in all market classes grown in the US, the WheatCAP group continues to provide a direct contribution to the US economy. Based on the last 2017 survey, the wheat varieties developed by the US wheat breeders and researchers covered 57% of the US wheat acreage and contributed $ 4.3 billion in production value. This value is amplified several times through the milling and baking industries, which contribute additional jobs and value to the economy.

A. 9. Summary of WheatCAP publications

In 2020, WheatCAP participants published 35 peer-reviewed publication acknowledging the USDA-NIFA support for the WheatCAP. The complete list of peer-reviewed publications is presented in Appendix 2 at the end of this report. The WheatCAP publications have been cross-referenced 2,153 times in Google Scholar (9/10/2020) in spite of the short term since their publication. A similar analysis of the publications generated by the previous T-CAP project (2011-2016) indicates 17,146 cross-references in Google scholar until 2020, documenting the high-impact of the publications generated by this group. https://www.triticeaecap.org/publications-and-germplasm/

A. 10. Budget

In 2020, UC Davis completed the subcontracts for the third year for the 19 institutions on time and the funding was available to all collaborators in early 2020. UC Davis has retained the funding for the fifth year from the funding received in years two, three and four, as originally planned. No additional funding is expected. 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 scientist position at Fargo, ND has been filled and the new person, Jason Fiedler, is already interacting well with the WheatCAP PIs. The ND program led by Justin Faris contributed their fourth year funding to the sequencing of the Promoter Capture Tilling population, which was an important objective for year four.

In Montana State University Luther Talbert retired, but Educational Coordinator Jason Cook took over his responsibilities for the project and the supervision of the PhD students in MSU.

Esten Mason (University of Arkansas) moved to Colorado State University, where he replaced the wheat breeder Scott Haley. UCD transferred the AR funds for year five to CSU where he will continue the project with some of the students that moved with him.

B. Prospectus – Plan of Work for Fifth Year

B. 1. Education plans for 5th year (2020-2021).

For the 2020-2021 year, the education group will be adaptive to the evolving situation caused by Covid-19. After the students finish their summer field season, they will recommence online education activities. The first educational activity will occur on Sept. 8-9 where students will participate in an online workshop to learn how to you use 'Breedbase', a data management tool that will be the bases of the T3 database. Members of Jean-Luc Jannink's team will be leading the workshop, and the workshop will include participants from the US Wheat and Barley Scab Initiative. Another education activity, led by Priscilla Glenn (UC-Davis), is a 9-week webinar series slated to start on Oct. 5th. The series will include topics on wheat breeding, pathology, end-use quality, genomic selection and virtual field tours. Speakers will be primarily WheatCAP students plus a few guest speakers who are experts in the various topic areas. Additionally, the education team is exploring the possibility of having webinars with company representatives to give the students an opportunity to learn more about what it is like to work in industry, and to help build networks for career advancement. The original plan was to send the WheatCAP students to company headquarters for this purpose, but it may not be possible due to Covid-19. Lastly, a soft skill training workshop is planned, which will include coaching on how to better cope with the impacts of the Covid-19 pandemic on student education and career advancement.

B. 2. T3 plans for 5th year (2020-20201).

Some of the tools listed below are on T3 Classic and need to be ported to T3 Breedbase. Some are obvious and T3 plans to implement them without additional discussion. Other tools should be

discussed with potential users, specifically WheatCAP graduate students, to determine their priority. Planned activities include

1. Incorporate as many wheat datasets as possible, particularly from cooperative nurseries. In the coming year T3 will be focusing on fusarium head blight nurseries as T3 has some supplemental funding from the scab initiative.
2. GWAS Results. T3 still run automated GWAS on all phenotyping trials in the background. As of yet, T3 has not identified the best interface to present these results through T3 Breedbase.
3. Tutorials. There are quite a number of new functions through T3 Breedbase that need to be documented in a more user-friendly way, specified to the T3/Wheat instance.
4. Adding links from accessions to GrainGenes and GRIN Global. The value of having this data in the cloud is that connections can be made from user data to web resources.
5. Subset markers by Polymorphism. Given a selected set of wheat lines, identify those markers that are polymorphic in the set and select them.
6. Optimize genomic prediction training set. This is needed if the user wants to phenotype a subset of lines such that prediction accuracy for a separate population of lines will be maximized.
7. Variant Effects for specific genotype data sets. Use of algorithms from the literature for VEP and SIFT.
8. Storage of metabolomic and transcriptomic data. These data are challenging because they are very high dimensional and do not have simple ontologies as do typical agronomic traits.
9. Filter Outliers. Curation of phenotypic datasets
10. Canopy Spectral Reflectance. Data from the TriticeaeCAP on CSR is still housed in T3 Classic.
11. Predict cross variance. This can be used as a decision support tool for breeders designing crossing nurseries.

During the 2020-2021 grant year T3 will get a functioning automated imputation engine up and running on T3 using the Practical Haplotype Graph. The main limitation has been that the work of Clay and David goes mainly into making database functions work, rather than developing new functions. Nevertheless, having a working imputation engine is important enough that the project will divert Clay's focus from database maintenance to adding PHG functionality.

B. 3. Genomics Resources plan for 4th year

Plans for 2021

The low-cost medium throughput genotyping assay for mapping and genomic selection applications will be developed and tested in collaboration with genotyping labs. The PHG will be build based on exome capture data generated for US wheat cultivars, and the accuracy of genotype imputation using low-coverage Skim-seq approach will be tested. The PHG resource

along with low-cost medium throughput genotyping assay will be deployed in genotyping labs to accelerate genetic analysis of material from breeding programs. The KSU group will finalize development of the eQTL map of the wheat genome and deposit it to the T3 database. They will collaborate with a T3 development team on setting tools for filtering SNPs in T3 database using functional information from the eQTL and chromatin accessibility maps. They will create tissue-specific gene expression atlases using low-cost 3'-end RNA-seq profiling for parents of Wheat CAP mapping populations to facilitate functional interpretation the yield component QTL mapping results, and also to develop resources for identification of genomic variants predictive of phenotypic trait variation.

In 2020, a KSU team lead by E. Akhunov received funding from USDA NIFA to establish NIFA IWYP Winter Wheat Breeding Innovation (WWBI) Hub. The WWBI Hub is a public-private partnership that evaluates the IWYP research outputs in elite winter wheat germplasm relevant for U.S. breeding programs. In coordination with the consortium of public and private wheat breeders, and geneticists the WWBI Hub will identify and introduce beneficial traits affecting grain yield into elite germplasm. This Hub aims to accelerate delivery of key yield traits to U.S. growers to reverse the declining trend of U.S. winter wheat acreage and add significant value to the U.S. wheat industries. The WWBI Hub leadership will collaborate with Wheat CAP on selecting promising donor germplasm for introgression into winter wheat germplasm and evaluating effects of introgression on yield potential.

In 2021, the UCD lab will complete the publication of the database for sequenced mutations in the promoters of all wheat genes and will generate examples of the application of this database. The UCD lab will also continue distributing the seeds from the EMS sequenced populations and will disseminate the new *GRF4-GIF1* transformation technology and distribute the necessary vectors to accelerate the incorporation of genome editing technologies in wheat. Finally, the UCD group will continue expanding the chromatin accessibility datasets from multiple wheat tissues using ATAC-seq strategy. The data will be combined with already generated MNase chromatin accessibility data, gene expression and promoter sequence variation to develop genomic resources for effective identification of causal variation controlling complex traits in wheat. These resources will contribute to the engineering of the wheat plant by combining beneficial alleles of genes that regulate different agronomic traits.

B. 4. Plans for CIMMYT

In 2021 the CIMMYT hub will repeat the *Elf-A^{m}3* x *gw-A2* filed trials to generate a second year of data that is required for publication. This experiment will be performed as a RCBD with ten blocks using the seed generated in 2019. This is a large experiment including 120 small plots as experimental units.

In addition the CIMMYT hub will initiate preliminary experiments to test and increase the isogenic lines for the:

- *WAPO-A1* QTL high number of spikelets per spike introgressed into CIMMYT high-biomass lines GID3855011, 4314513, 4577963

- Isogenic lines of *QTn.mst-6B* for number of reproductive tillers (MT) introgressed from McNeal into CIMMYT high-yielding lines Kingbird and BAJ#1
- Isogenic lines of a QTL for spikelet number per spike on chromosome 5A and a QTL for productive tiller number on chromosome 6A from SYC Capstone introgressed into CIMMYT high-biomass line. GID3613474

These experiments will be organized as RCBD, but using rows as experimental units due to the limited amount of seed available this year.

B. 5. Plans for the cloning projects

AR: They will work this fall to saturate the genome region containing the QTL with additional KASP markers identified through exome capture. New HIF populations are being developed from identified heterozygous recombinants for screening during the 2020-2021 season. They will attempt a greenhouse experiment in addition to coordinating the field effort with the remaining program associate at Arkansas. This will allow them to work towards phase two of the positional cloning. In addition, the AR group will complete allele introgression into CIMMYT spring wheat, which is currently at BC_3F_1.

CA: In 2020, the CA group will focus on the publication of the *WAPO-A1* validation results and in the completion of the high-density mapping of the SNS QTL on chromosome 3AS. The CA group will also use transgenic approaches to validate the *FT-A2* candidate gene for the 3AS SNS QTL and the candidate for the root architecture and drought resistance QTL on chromosome 1B. The CA group will also continue the introgression of the *FT-A2* and *WAPO-A1* positive alleles for SNS in tetraploid wheat and in the high-biomass and high-yield lines from CIMMYT. Experiments for the four combinations of the *Elf-A^m3* and *gw-A2* alleles in three different tetraploid and hexaploid backgrounds will be repeated one more year at CIMMYT to generate sufficient data for publication.

CO: The CSU group will characterize and phenotype the progeny of 10 critical recombinants in the field and further screen HIFs to identify additional critical recombinants to sow in 2021. They will continue to develop backcross populations segregating for the 6BL QTL in the three CIMMYT backgrounds and the CO wheat varieties 'Monarch' and 'CO15D098R'. To help identify and characterize candidate genes, they will perform RNA-seq using apical tissues from HIFs segregating for the 6BL QTL, and use CRISPR/Cas9 to knockout the identified candidate gene in 'Bobwhite'.

ID: For 2021, the ID group will narrow down the candidate gene region of the 5AL QTL after data is analyzed completely in October. For validation, the student will design more KASP markers for the candidate gene and use it to TILLING in Kronos EMS mutant lines, and an EMS-induced population of UI Platinum as needed. After this validation, the student will do gene editing. They are going to recruit another MS student to screen HIFs to dissect the 7DS region in spring 2021. The ID group identified a DHL (CdDH-028) from this population that has high grain yield, excellent bread baking quality, and good resistance to stripe rust. They are going to release this line in 2021. Another high yielding DHL CdDH-266 has highest SNS, but

smaller TKW and less PTN. They use this line as recurrent parent to introgression a high TKW to increase grain yield. They will use DH system or SSD method to speed the breeding process.

KS: In 2021 the KSU group will complete field evaluation of target QTL NILs and first recombinants. They will increase the second set of recombinants and will identify additional assays to better define the QTL region. They will publish the stripe rust mapping and agronomic analysis of the Overley/Overland population and release the population as germplasm. In 2021 the KSU group will produce seed for distribution from the introgression into CIMMYT backgrounds including GID4314513, Baj, Bonsu, Kingbird.

MI: In 2021, MS student, Tommy Reck will continue the introgression of the 2DS QTL into CIMMYT backgrounds. He will also oversee the planting of recombinant lines in fall, 2020 and will collect phenotypic data on yield components in 2021 yield trials. By July of 2021, the MI group will have a refined position of the 2DS grain yield QTL. The QTL being evaluated confers up to a seven bushel per acre increase in grain yield. In 2021, they will continue evaluating which yield components are affected by the 2DS QTL. The traits to be evaluated in 2021 include photosynthetic parameters, spikelets per spike, tiller number, thousand kernel weight, number of kernels per spike, and kernel dimensions.

MN: The primary goal of the last quarter of 2020 and the first quarter of 2021 is the genotyping of F_4 individuals from biparental crosses of the 14x111 parents. Tissue from approximately 800 individuals was harvested and stored prior to the implementation of COVID-19 restrictions. Individuals identified as heterozygous will be grown in the fall 2020 and spring 2021 greenhouses with the intention of developing heterogeneous inbred families. Testing of the HIFs will be conducted during the second half of 2021. Speed breeding techniques will be employed to make up for crossing failures and COVID-19 restrictions in order to introgress the 4AL QTL identified in the 14x111 population into CIMMYT germplasm. QTL mapping of yield component and disease resistance traits in the 15xR012 population will be done in fall 2020.

MT: Research plans for 2021 include collecting tiller bud and stem axis tissue for RNAseq analysis. The goal is to identify differentially expressed genes in the candidate region that correspond to tiller number variation. Brittney will also continue reducing the size of her candidate gene region using fine-mapping methods. The MT group will continue the introgression of the tiller number QTL on chromosome 6B into CIMMYT high yielding lines Kingbird and BAJ#1 and into MT lines McNeal and Duclair.

NC: Two manuscripts detailing work in mapping plant height and heading date traits, as well as yield component traits, are being prepared for submission. The next generation of HIFs will attempt to validate both the kernel length and SPS, and plant height QTL on chromosome 3D in the field. The pericentromeric location of the yield component QTL may challenge positional cloning of this QTL, but the plant height QTL is a promising target for further fine mapping and cloning. Using a combination of pedigree and genomic information to link multiple unbalanced historic panels, effects of cloned yield component and heading date QTL on yield and their interactions with climate variables will be investigated. Understanding the environmental and genotypic context for yield effects of the QTL identified through Wheat CAP will be critical for useful deployment via MAS.

ND: Once heterozygous recombinant BC_3F_2 plants are identified, the ND group will select BC_3F_3 homozygous recombinant lines from these individuals to fix the recombination event. These BC_3F_3 will be genotypes with internal markers currently being developing based on the exome capture data. Late spring of 2021, they will perform a replicated greenhouse trial using BC_3F_4 individuals to further narrow down the candidate region from where it is currently at. Throughout this process, the ND team will begin identifying candidate genes within the region based on cloned yield component genes in other crops, sequencing these genes in two parental lines and developing markers to add to the high-resolution map if the two genes are polymorphic.

NY: The Cornell group will continue working with the Synthetic W7984 x Opata population for mapping and cloning. They will phenotype both the DH and the RIL populations for mapping and cloning genes for growth rate and biomass yield to characterize the source strength. They will also wrap up the cloning of a second seed size (length and weight) gene on chromosome 2D (positive allele from W7984). This fall Ellie will complete analysis of the transcriptome and candidate genes, in addition to reviewing transcriptome sequence SNPs that may lead to post-transcriptional modifications, as well as investigating the presence/absence of 5AS and potential for homeologous masking or trans-acting factors. The Cornell group intends to publish the fine-mapping and transcriptome results in early 2021.

OK: In 2021, the OKSU team will take two new graduate students on the WheatCAP project. They will also publish the major results on the cloning of the *QSns.osu-7B* and *QYld.osu-1B* for grain yield. They will continue the backcrossing of the *QSns.osu-7B* and *QYld.osu-1B* into the CIMMYT high-yield and high-biomass lines. The OKSU team will use KASP markers to accelerate the development of the introgressed lines. For the *QYld.osu-1B*, they will reduce the Pavon background generated in the crosses with the crosses between Pavon-*ph1b* and Duster or Billings carrying *QYld.osu-1B* to induce recombination in this segment. They will also test genetic effects of *QYld.osu-1B* in Duster x 2174 population to see if there is any crossover in the targeted region. They will use KASP markers to ensure that the genomic region covering the entire *QYld.osu-1BS* from Duster is introduced to novel cultivars. For the *QSns.osu-7B* for grain yield the OKSU team will further test the consistency of the QTL on grain yield when measured across multiple genetic backgrounds and environments. Finally, in September 2020 they will submit five candidates for new variety to the release committee for evaluation.

SD: Genotype and phenotype data from recombinants will be analyzed this fall to fine map the 7DS grain yield QTL from *Ae. tauschii*. An additional greenhouse evaluation will be performed on the selected recombinants for validation. The backcrossing and generation advancement will continue and the homozygous lines ($BC_2F_{3/4}$) with and without 7DS QTL will be delivered to CIMMYT in August 2021.

TX: In 2021 the TX team will work with Guihua Bai to identify and test critical recombinants to narrow down the QTL region. They will also validate the effect of the QTL for kernel weight and its application in breeding. They will complete the introgression of the selected QTL into the CIMMYT lines.

WA: For 2021, the WA group will use exome capture data, newly developed KASPs, and greenhouse phenotyping experiments to further refine and validate the candidate QTL region on

chromosome 4AL, and to seek candidate genes. They have ample seed of heterozygous plants to screen for additional recombinant NILs to further define the region. They will also phenotype the high-biomass CIMMYT NILs that they developed in greenhouse experiments to evaluate the effect in different genetic backgrounds.

C. Deliverables & Other Outputs:

- **Appendix 1.** Germplasm releases
- **Appendix 2**. Publications
- **Appendix 3**. Community resources
- **Appendix 4.** Graduate students.
- **Appendix 5.** Education Survey.

D. Concluding remarks

In 2020, WheatCAP had a very productive year that resulted in new knowledge (35 peer-reviewed publications) and improved wheat varieties (22) with increased yield, resistance to pathogens and/or improved quality. The improved disease resistance of the new varieties will reduce the applications of fungicides, directly benefiting the population and the environment. The increased productivity of these varieties will maintain the competiveness of the USA wheat growers, whereas their improved quality will benefit consumers directly and contribute to the competitiveness of the USA wheat industry. Wheat varieties developed by this group of public breeders cover 57% of the US wheat acreage and contribute $4.3 billion in direct production value (based on 2017 survey).

The genomic tools and databases generated by the WheatCAP team continue to accelerate the pace of discoveries and wheat improvement. Candidate genes for eight QTL for grain yield components were identified in 2020. One of the most important contributions of WheatCAP is the coordination among the major wheat breeding and research programs in the country, which eliminates unnecessary duplication and generates positive and synergistic collaborations. Finally, the training of a new generation of plant breeders guarantees the continuity of the US agricultural enterprise into the future.

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

APPENDIX 1. Varieties and Germplasm releases 2020.
https://www.triticaecap.org/publications-and-germplasm/

2020 New Commercial Wheat Varieties

1. '**Yecora Rojo 515**' (PVP pending) is a hard white spring variety released by the UC Davis wheat-breeding program. It is derived from the popular variety Yecora Rojo by introgression of the stripe rust resistance genes *Yr5* and *Yr15* using marker assisted selection.

2. '**UI Cookie**' (PVP 202000298, filed July 14, 2020) is a soft white spring wheat (*Triticum aestivum* L.) developed and released by the Idaho Agricultural Experiment Station in 2020. UI Cookie has high grain yield, excellent end-use quality, and tolerance to fusarium head blight. It shows also improved resistance to stripe rust and stem rust compared to the widely grown soft white spring wheat cultivar 'UI Stone' (PI 660550). More productive tiller numbers contributed the high grain yield.

3. '**Erie**' (PVP pending) is a soft red winter wheat jointly released by Ohio State University and Cornell University. Erie has very good resistance to Fusarium Head Blight (FHB, caused by the fungus Fusarium graminearum), Powdery Mildew, leaf rust, Stagonospora Leaf Blotch, and Stagonospora Glume Blotch.

4. '**NY99056-161**' is a soft white winter developed by Cornell University. (PVP pending) is a soft white winter wheat variety released by the Cornell small grains breeding program. NY99056-161 has excellent yield and the highest level of resistance to Fusarium Head Blight of any variety grown in NY and is rated as moderately resistant. It is also resistant to Wheat Spindle Streak Mosaic Virus and moderately resistant to powdery mildew.

5. '**Byrd CL Plus**', a hard red winter wheat variety released by Colorado State University, with two-gene Clearfield technology, high drought stress tolerance and excellent straw strength. PVP 201900407.

6. '**Canvas**', a hard red winter wheat variety released by Colorado State University with excellent stripe and stem rust resistance, good test weight and high end-use quality PVP 201900408.

7. '**Crescent AX**', a hard red winter wheat variety released by Colorado State University compatible with the CoAXium wheat production system. Crescent AX has medium-early maturity, very good test weight, wheat curl mite resistance, and good end-use quality. PVP 201900409.

8. '**Monarch**', a hard white winter wheat variety released by Colorado State University in 2018 with excellent straw strength and excellent irrigated yield potential. Monarch has very good stripe rust resistance and quality and very low polyphenol oxidase (PPO) activity. PVP 201900410.

9. '**Snowmass 2.0**', a hard white winter wheat variety released by Colorado State University in 2018, with high yield potential and protein content under dryland and irrigated environments. PVP 201900411.

10. *‘Whistler’*, a hard red winter wheat variety released by Colorado State University with late late-maturity and taller stature. Whistler has excellent resistance to powdery mildew, stripe and stem rust populations in the central plains, while maintaining solid resistance to WSMV and SBMV. PVP 201900412.

11. **‘CO14A055-258’** (AF28/Byrd/3/AF10/2*Byrd), a new high-yielding CoAXium wheat that was approved for release in summer 2020. Variety name pending, PVP not yet submitted.

12. ‘**OK Corral**’ (PVP 202000252 PI 693783) is released as a beardless (awnless) high-quality HRW variety developed by the Oklahoma Agricultural Experimental Station that can be used for all purposes of wheat production, i.e., from silage/hay, or graze-out or dual-purpose, or grain production only. The variety has the potentially unique source of Hessian fly resistance.

13. **‘MN-Torgy’** is a hard red spring wheat variety developed by the University of Minnesota wheat breeding program and released in 2020. MN-Torgy has a balance of high grain yield and grain protein content and is moderately resistant to important diseases including Fusarium head blight and bacterial leaf streak.

14. ‘**SD Andes**’ (9/2020) is hard red winter wheat cultivar developed by the South Dakota Agricultural Experimental Station adapted to the eastern half of South Dakota. It has excellent straw strength and winter hardiness with medium height and late maturity. ‘SD Andes’ had good yielding potential with average protein and test weight and acceptable end-use quality. It is moderate resistant-resistant (MR-R) to stripe rust.

15. ‘**AR06146E-1-4**’ (PVP application pending) is a common wheat variety released by the Board of Trustees of the University of Arkansas from the University of Arkansas in 2020.

16. ‘**KS Hatchett**’ (PVP pending) 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.

17. ‘**KS Hamilton**’ (PVP pending) is a hard red winter wheat cultivar developed by Kansas State University for western Kansas. It has very competitive yield potential. It has good resistances to wheat streak-mosaic virus, stem rust, soilborne mosaic virus, and Hessian fly.

18. ‘**Hedge CL**+’ (PVP pending) is a spring club wheat variety released in 2020 by WSU with two-gene resistance to Imazamox. It is broadly adapted with excellent resistance to stripe rust, very good yield, excellent test weight, and excellent soft white club wheat quality.

19. ‘**MI160898**’ (PVP pending) is a new soft red winter wheat variety developed by Michigan State University Wheat Breeding and Genetics. This variety is ideal for production in Michigan with high yield potential and excellent milling and baking quality. DON mycotoxin levels and visual FHB index are very low in MI16R0898 conferred by the *Fhb1* gene. MI16R0898 is has excellent resistance to Stagonospora Leaf Blotch due in part to the absence of the ToxA receptor *Tsn1*. Soilborne Mosaic Virus resistance in MI16R0898 is conferred by the *Sbm1* gene. .

20. ‘**MI14W0190**’ (PVP pending) is a new soft white winter wheat variety developed by Michigan State University Wheat Breeding and Genetics. This variety is ideal for

production in Michigan with high yield potential and excellent milling and baking quality. Fusarium head blight resistance in MI14W0190 is due in part to the *Fhb1* resistance gene. MI14W0190 also has excellent resistance to Stripe Rust.

21. '**MI16W0133**' (PVP pending) is a new soft white winter wheat variety developed by Michigan State University Wheat Breeding and Genetics. This variety is ideal for production in Michigan with high yield potential (top 10% of commercial wheat varieties) and excellent milling and baking quality. MI16W0133 has excellent resistance to Stagonospora Leaf Blotch due to the absence of the ToxA receptor *Tsn1*. The *Sbm1* gene confers resistance to Soil-borne Mosaic Virus.

22. '**MI16W0528**'is a new soft white winter wheat variety developed by Michigan State University Wheat Breeding and Genetics. This variety is ideal for production in Michigan with high yield potential and excellent milling and baking quality. In 2019, grain yield for MI16W0528 ranked #1 out of 39 entries in the Uniform Eastern Soft WhiteWinter Wheat Nursery tested in Richville, MI and New Haven, IN. MI16W0528 is moderately resistant to FHB and is resistant to Soil-borne Mosaic Virus due to *Sbm1*.

2020 New PVP of varieties reported in previous years

1. **'MN-Washburn'** (PVP 202000190, submitted February 28, 2020) is a hard red spring variety released by the UMN wheat-breeding program that has competitive grain yield and good lodging resistance. MN-Washburn is resistant to prevalent races of leaf and stripe rust and is moderately resistant to Fusarium head blight and bacterial leaf streak.

2. **'UC-Amarillo** (PVP 202000013, submitted October 23, 2019) is a hard white spring variety released by the UC Davis wheat breeding program, which has a unique yellow flower, obtained by the introgression of a functional *PSY1* gene by marker assisted selection.

3. '**Dagmar**' (PVP 201900306, submitted 3/9/2020, Montana State University) is a solid-stemmed hard red spring wheat intended for acreage infested with the wheat stem sawfly. Dagmar has shown excellent dryland yield potential and high gluten strength.

4. '**Winner**' (PVP 202000357, submitted 08/11/2020) is a hard red winter wheat cultivar developed by the South Dakota Agricultural Experimental Station with unusually broad adaptation to the eastern half of the Northern Great Plains. 'Winner' has medium height and medium maturity with higher yield potential, good baking quality, and moderate resistance to stem rust.

5. '**Draper**' (PVP 202000356, submitted 08/11/2020) is a hard red winter wheat cultivar developed by the South Dakota Agricultural Experimental Station with a limited target region, specifically western South Dakota. 'Draper' has improved yield potential with average test weight, grain protein, and good milling and baking quality. It is resistant to soilborne mosaic virus.

6. '**FourOsix**' (PVP 201900053, submitted 12/19/2018). FourOsix is a hard red winter wheat released by Montana State University.

7. '**Ray**' (PVP 201900058, submitted 01/07/2019). Ray is a hard red forage winter wheat released by Montana State University.

8. '**MTF1435**' (PVP 201900073, submitted 01/09/2019). MTF1435 is a hard red forage winter wheat released by Montana State University.

9. '**Bobcat**' (PVP 202000177, submitted 02/03/2020). Bobcat is a hard red winter wheat released by Montana State University.

10. '**Flathead**' (PVP 202000202, submitted 03/09/2020) hard red winter wheat released by Montana State University.

11. '**StandClear CLP**' (PVP 202000183, submitted 02/07/2020. StandClear CLP is a hard red winter wheat released by Montana State University.

12. '**Battle AX**' (PVP 201900406, submitted 9/9/19, CO15A018), a hard red winter wheat released by Colorado State University and marketed by MonTech in Montana.

13. '**AP18 AX**' (PVP 2020000351, submitted 5/28/20, CO14A136), a hard red winter wheat released by Colorado State University and marketed by Agripro-Syngenta.

14. '**Stingray CL+**' (PVP 201900290, submitted 8/13/19) is a soft white winter wheat cultivar released by WSU with two-gene resistance to Imazamox. It also carries the *Pch1* gene and *Yr17* gene for disease resistance. Stingray CL+ has the *Rht-B1b* dwarfing allele and carries the Ax1+Ax2* alleles as GluA1 and the *Dx2+Dy12* alleles *at GluD1*. It is broadly adapted across the Pacific Northwest and has very good end-use quality.

15. '**Scorpio**' (PVP 202000261, submitted 5/4/20) is a hard red winter wheat released by WSU for its excellent tolerance to low pH soils. This line has very good strip rust resistance, and carries the resistance gene *Yr17* among other unknown sources. Scorpio carries the *Rht-B1b* allele for dwarfing and the *Dx5+Dy10* alleles at *Glu-D1*. Scorpio does exceptionally well in no-till production systems.

16. '**Devote**' (PVP 202000262, submitted 5/4/20) is a soft white winter wheat released by WSU for production in <12" rainfall zones of Washington. This line has excellent disease resistance, as it carries resistance genes *Pch1*, *Yr17*, and *Lr68*. It is also tolerant to snow mold and Fusarium crown rot and has very good cold tolerance and end-use quality.

17. '**Purl**' (PVP 201900302, submitted 7/29/19) is a soft white winter wheat variety targeted to the high rainfall production zones of Washington and Northern Idaho. This line has very high test-weight and has the second highest yield average over three years. Purl combines excellent abiotic and biotic stress resistance, being resistant to stripe rust, eyespot foot rot, cereal cyst nematodes, low pH soils, and cold temperatures. The line has good end-use quality for domestic and export markets.

2020 Germplasm

Sr60 introgression. PI 689563. The *Sr60*-resistant haplotype found in *T. monococcum* is not present in polyploid wheat. The UCD group introgressed Sr60 into hexaploid wheat using marker assisted selection and developed a diagnostic molecular marker to accelerate its deployment and pyramiding with other resistance genes.

***Glu-B1x* mutant**: PI 692251, ***Glu-B1y* mutant**: PI 692253 and ***Glu-B1x Glu-B1y* double mutant:** PI 692252. Individual loss-of-function mutants of *Glu-B1x* (ΔBx6) and *Glu-B1y* (ΔBy8) were associated with significant reductions in gluten strength compared to the wildtype, with stronger effects in the ΔBxy double mutant.

2020 Populations

1. Two previously reported DHL mapping populations (UI Platinum x SY Capstone and UI Platinum x LCS Star) generated under support of WheatCAP were deposited in NSGC in the spring of 2020.

2. University of Idaho developed two EMS populations, one from UI Brundage and another from UI Platinum. The two EMS populations will be used in the functional analysis for the identified QTLs.

3. A spring wheat NAM population, consisting of 852 RILs from 10 stem rust resistant sources, all crossed with susceptible line LMPG-6, were deposited in the NSGC and published in the *Journal of Plant Registrations*. The 10 stem rust resistance sources, all with adult plant resistance, consist of 9 Kenyan cultivars and one Minnesota cultivar

4. Wheat D-Genome Nested Association Mapping (NAM) population registered in 2020 and published in the Journal of Plant Registrations by Eric Olson (Michigan State University).

APPENDIX 2. Peer reviewed publications WheatCAP 2020. 35 publications.

- https://www.triticeaecap.org/publications-and-germplasm/
- 2017-2020 WheatCAP publications cross-references in Google Scholar = 2,003 (9/2020).
- 2011-2016 TCAP publications cross-references in Google Scholar = 17,073 (9/2020)

1. Bajgain P., Y. Jin, T.J. Tsilo, G.K. Macharia, S.E. Reynolds, R. Wanyera, and J.A. Anderson. 2020. Registration of KUWNSr, a wheat stem rust nested association mapping population. J Plant Regist. https://doi.org/10.1002/plr2.20043.

2. Bernardo, A., P.St. Amand, H.Q. Le, Z. Su, and G. Bai. 2020. Multiplex restriction amplicon sequencing: a novel next-generation sequencing-based marker platform for high-throughput genotyping. Plant Biotechnol. J., 18:254-265.

3. Bolus, S., E. Akhunov, G. Coaker and J. Dubcovsky. 2019. Dissection of cell death induction by wheat stem rust resistance protein Sr35 and its matching effector AvrSr35. Mol. Plant Microbe Int. 33: 308–319

4. Chen, J., J. Wheeler, N. Klassen, W. Zhao, K. O'Brien, C. Jackson, J.M. Marshall, K. Schroeder, and X.M. Chen. 2020. Registration of 'UI Bronze Jade' hard white winter wheat. Journal of Plant Registration, 1– 8. https://doi.org/10.1002/plr2.20029.

5. Chen, S., M. N. Rouse, W. Zhang, X. Zhang, Y. Guo, J. Briggs, J. Dubcovsky. 2020. Wheat gene *Sr60* encodes a protein with two putative kinase domains that confers resistance to stem rust. New Phytologists. 225:948-959.

6. Cook, J.P., R. K. Acharya, J. M. Martin, N. K. Blake, I. J. Khan, H.-Y. Heo, K. D. Kephart, J. Eckhoff, L.E. Talbert, and J. D. Sherman. 2020. Genetic analysis of stay-green, yield and agronomic traits in spring wheat (*Triticum aestivum* L.). *Crop Science*. (Accepted).

7. Debernardi, J.M., J.R. Greenwood, E.J. Finnegan, J. Jernstedt, J. Dubcovsky. 2019. Wheat *APETALA2*-like genes *AP2L2* and *AP2L5* control the initiation of axillary floral meristems and specify glume-lemma identity. The Plant Journal. 101:171-187

8. Debernardi JM, Tricoli DM, Ercoli MF, Hayta S, Ronald P, Palatnik JF, Dubcovsky J (2020) A chimera including a GROWTH-REGULATING FACTOR (GRF) and its cofactor GRF-INTERACTING FACTOR (GIF) increases transgenic plant regeneration efficiency. Nature Biotechnology In press (bioRxiv = https://biorxiv.org/cgi/content/short/2020.08.23.263905v1

9. DeWitt, N., M. Guedira, E. Lauer, M. Sarinelli, P. Tyagi, D. Fu, Q. Hao, J.P. Murphy, D. Marshall, A. Akhunova, K. Jordan, E. Akhunov, and G. Brown-Guedira. 2020. Sequence based mapping identifies *AWNS1*, a candidate transcription repressor underlying awn suppression at the *B1* locus in wheat. New Phytologist, 225:326-339.

10.   Fang, T., L. Lei, G. Li, C. Powers, P.M. Hunger, B.F. Carver, and L. Yan. 2020. Development and deployment of KASP markers for multiple alleles of *Lr34* in wheat Theor. Appl. Genet. 133:2183-2195.

11.   Guttieri, M.J., R.L. Bowden, K. Reinhart, D. Marshall, Y. Jin, B. Seabourn. 2020. Registration of hard white winter wheat germplasms with adult plant resistance to stem rust, KS14U6380R5, KS16U6380R10, and KS16U6380R11. J. Plant Registrations. 14:210-217.

12.   Halder J., J. Zhang, S. Ali, H.S. Gill, J.S. Sidhu, S. Talukdar, J. Kleinjan, B. Turnipseed, S.K. Sehgal. 2019. Mining and genomic characterization of resistance against to Tan spot, *Stagonospora nodorum* blotch (SNB), and Fusarium head blight in Watkins core collection of wheat. BMC Plant Biology. 19:480

13.   Jones, B.H., N.K. Blake, H.-Y. Heo, J.R. Kalous, J.M. Martin, J.A. Torrion and L.E. Talbert. 2020. Improving hexaploid spring wheat by introgression of alleles for yield component traits from durum wheat. Crop Science 60: 759-771. doi:10.1002/csc2.20011.

14.   Jordan KW, He F, DeSoto MF, Akhunova A, Akhunov E. 2020. Differential chromatin accessibility landscape reveals structural and functional features of the allopolyploid wheat chromosomes. Genome Biol. 21:176.

15.   Kan, C-C, H., Jia, C, Powers, B.F. Carver, and L. Yan. 2020. Genetic characterization and deployment of a major gene for grain yield on chromosome arm 1BS in winter wheat. Mol. Breed. 40:26.

16.   Kippes, N., C. van Gessel, J. Hamilton, A. Akpinar, H. Budak, J. Dubcovsky and S. Pearce. 2020. Effect of *phyB* and *phyC* loss-of-function mutations on wheat transcriptome under short and long day photoperiods. BMC Plant Biology. 20: 297.

17.   Klymiuk, V., A. Fatiukha, D. Raats, V. Bocharova, L. Huang, L. Feng, S. Jaiwar, C. Pozniak, G. Coaker, J. Dubcovsky, T. Fahima. 2020. Three previously characterized resistances to yellow rust are encoded by a single locus *Wtk1*. Journal of Experimental Botany. 71: 2561-2572.

18.   Larkin, D. L., A.L. Holder, R.E. Mason, D.A. Moon, G. Brown-Guedira, P.P. Price, S.A. Harrison, and Y. Dong. (2020). Genome-wide analysis and prediction of fusarium head blight resistance in soft red winter wheat. Crop Science. doi:10.1002/csc2.20273.

19.   Liu, G., X. Liu, Y. Xu, A. Bernardo, M. Chen, Y. Li, F. Niu, L. Zhao and G. Bai. 2020. Reassigning Hessian fly resistance genes *H7* and *H8* to chromosomes 6A and 2B of the wheat cultivar 'Seneca' using genotyping-by-sequencing. Crop Sci. 60:1488–1498

20.   Liu S., G. Bai, M. Lin, M. Luo, D. Zhang, F. Jin, B. Tian, H.N. Trick, L. Yan. 2020. Identification of candidate chromosome region of *Sbwm1* for Soil-borne wheat mosaic virus resistance in wheat. Sci Rep-UK 10:8119.

21. Maulana F., K-S. Kim, J.D. Anderson, M.E. Sorrells, T. J. Butler, **S.-Y. Liu**, P. S. Baenziger, P.F. Byrne, and X-F. Ma. 2020. Genomic selection of forage agronomic traits in winter wheat. Crop Sci**.** https://doi.org/10.1002/csc2.20304.

22. Muleta, K.T., X. Chen and M. Pumphrey. 2020. Genome-wide mapping of resistance to stripe rust caused by *Puccinia striiformis* f. sp. *tritici* in hexaploid winter wheat. Crop Science. DOI:10.1002/csc2.20058.

23. Niu, F., Y. Xu, X. Liu, L. Zhao, A. Bernardo, Y. Li, G. Liu, M. Chen, L. Cao, Z. Hu, X. Xu, and G. Bai. 2020. The Hessian fly recessive resistance gene *h4* mapped to chromosome 1A of the wheat cultivar 'Java' using genotyping-by-sequencing. Theor. Appl. Genet. https://doi.org/10.1007/s00122-020-03642-9.

24. Nyine M, Adhikari E, Clinesmith M, Jordan KW, Fritz AK, Akhunov E. Genomic Patterns of introgression in interspecific populations created by crossing wheat with its wild relative. G3 (Bethesda). 2020 doi: 10.1534/g3.120.401479

25. Shaw, L. M., C. Li, D. P. Woods1, M. A. Alvarez, H. Lin, M. Y. Lau, A. Chen, and J. Dubcovsky. 2020. Epistatic interactions between *PHOTOPERIOD1*, *CONSTANS1* and *CONSTANS2* modulate the photoperiodic response in wheat. PLoS Genetics. 16: e1008812.

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29. Taagen, E., A.J. Bogdanove, M.E. Sorrells. 2020. Achieving controlled recombination with targeted cleavage and epigenetic modifiers. Trends in Plant Science. 25:513-514. https://doi.org/10.1016/j.tplants.2019.12.018

30. Veenstra, L.D., J. Poland, Jannink, and M.E. Sorrells. 2020. Recurrent genomic selection for wheat grain fructans. Crop Science 60:1499-1512. DOI: 10.1002/csc2.20130.

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34.   Zhang, P., C. Guo, Z. Liu, A. Bernardo, H. Ma, P. Jiang, G. Song and G. Bai. 2020. Quantitative trait loci for Fusarium head blight resistance in wheat cultivars Yangmai 158 and Zhengmai 9023, Crop J. https://doi.org/10.1016/j.cj.2020.05.007

35.   Zhang, Y., A. Schonhofen, W. Zhang, J. Hegarty, C. Carter, T. Vang , D. Laudencia-Chingcuanco and J. Dubcovsky, Contributions of individual and combined *Glu-B1x* and *Glu-B1y* high-molecular-weight glutenin subunits to semolina functionality and pasta quality. Journal of Cereal Science 93: 102943.

APPENDIX 3. Community resources generated

2020 Public databases

1. T3 database https://triticeaetoolbox.org/wheat/

2. Promoter and exome sequenced mutant populations https://dubcovskylab.ucdavis.edu/wheat_blast.

3. Expression database. WheatExp. https://wheat.pw.usda.gov/WheatExp/

4. Molecular Marker Protocols. https://maswheat.ucdavis.edu/

2020 Mapping Populations

1.   Two previously reported DHL mapping populations (UI Platinum x SY Capstone and UI Platinum x LCS Star) generated under support of WheatCAP were deposited in NSGC in the spring of 2020.

2.   University of Idaho developed two EMS populations, one from UI Brundage and another from UI Platinum. The two EMS populations will be used in the functional analysis for the identified QTLs.

3.   A spring wheat NAM population, consisting of 852 RILs from 10 stem rust resistant sources, all crossed with susceptible line LMPG-6, were deposited in the NSGC and published in the *Journal of Plant Registrations*. The 10 stem rust resistance sources, all with adult plant resistance, consist of 9 Kenyan cultivars and one Minnesota cultivar

4.   Wheat D-Genome Nested Association Mapping (NAM) population registered in 2020 and published in the Journal of Plant Registrations by Eric Olson (Michigan State University).

APPENDIX 4. Graduate students (12 completed + 23 current = 35 total, 40% female)

Individual student WEB pages at https://www.triticeaecap.org/educational-activities/

Institution	PI	1st Name	Last Name	Deg.	G.	Start Date	Gr.	Current Position
U. of Arkansas	Eston Mason	Dylan	Larkin	PhD	M	9/1/2017		
U. of Arkansas	Eston Mason	Mikayla	Hammers	MS	F	8/1/2020		
U. of Arkansas	Eston Mason	Zachary	Winn	MS	M	8/21/2017	*	PhD student, North Carolina State U.
U. of California-Davis	Jorge Dubcovsky	Saarah	Kuzay	PhD	F	9/1/2016		
U. of California-Davis	Jorge Dubcovsky	Priscilla	Glenn	PhD	F	9/1/2017		
U. of California-Davis	Jorge Dubcovsky	Youngjun	Mo	PhD	M	3/1/2014	*	Breeder in Korea.
Colorado State U.	Stephen Pearce	Andrew	Katz	PhD	M	8/21/2017		
U. of Idaho	Daolin Fu	Katrina	Johnson	MS	F	8/1/2017	*	PhD student, Oregon State U.
Unviersity of Idaho	Daolin Fu	Meng	Su	PhD	F	8/1/2018		
U. of Idaho	Jianli Chen	Kyle	Isham	MS	M	1/1/2018	*	Searching for a job.
USDA-Kansas State U.	Mary Guttieri	Wardah	Mustahsan	PhD	F	6/1/2018		
USDA-Kansas State U.	Guijua Bai	Yuzhou	Xu	PhD	M	8/1/2017		
USDA-Kansas State U.	Guijua Bai	Yaoguang	Li	PhD	F	9/1/2015	*	Post-doc, U. of Connecticut
USDA-Kansas State U.	Guijua Bai	Abdul	Hashimi	PhD	M	9/1/2015	*	Assistant Professor, King Saud U. in UAE
Kansas State U.	Eduard Akhunov	Bliss	Betzen	MS	F	5/1/2018		
Kansas State U.	Eduard Akhunov	Elina	Adhikari	PhD	F	9/1/2015		
Kansas State U.	Eduard Akhunov	Qianli	Pan	MS	F	9/1/2016	*	
Michigan State U.	Eric Olson	Jonathan	Turkus	MS	M	5/22/2017		PhD student, U. of Nebraska - Lincoln
Michigan State U.	Eric Olson	Tommy	Reck	MS	M	1/1/2019		
U. of Minnesota	James Anderson	Max	Fraser	PhD	M	7/1/2017		
Montana State U.-Bozeman	Talbert/Cook	Brittney	Brewer	PhD	F	9/1/2016		
USDA-North Carolina St. U.	G. Brown-Guedira	Eddie	Lauer	MS	M	4/1/2017	*	PhD student, North Carolina State U.
USDA-North Carolina St. U.	G. Brown-Guedira	Noah	DeWitt	PhD	M	1/8/2018		
North Dakota State U.	Justin Faris	Amanda	Peters	PhD	F	6/1/2017		
North Dakota State U.	Justin Faris	Katherine	Running	PhD	F	9/1/2019		
Cornell U.	Mark Sorrells	Ellie	Taagen	PhD	F	6/12/2017		
Cornell U.	Mark Sorrells	Nicholas	Santantonio	PhD	M	8/1/2013	*	Assistant Professor, breeder, Virginia Tech U.
Oklahoma State U.	Liuling Yan	Chia-Cheng	Kan	PhD	M	9/1/2016	*	Post-doc, Texas A&M
Oklahoma State U.	Liuling Yan	Xiaoyu	Zhang	PhD	M	1/1/2017	*	Returned to China
South Dakota State U.	Sunish Sehgal	Jyotirmoy	Halder	PhD	M	8/22/2017		
Texas A&M	Shuyu Liu	Smit	Dhakal	PhD	M	9/1/2014	*	Post-doc, U. of Illinois
Texas A&M	Shuyu Liu	Jorge	Valenzuela-Antelo	PhD	M	8/1/2017		Bayer Crop Science, Breeder
Texas A&M	Shuyu Liu	Zhen	Wang	PhD	M	9/1/2019		
Washington State U.	Mike Pumphery	Samuel	Prather	PhD	M	8/1/2018		
Washington State U.	Mike Pumphery	Peter	Schmuker	PhD	M	8/1/2020		

* = Student has graduated

APPENDIX 5. 2020 Education survey for WheatCAP student

To better understand the needs and interests of the WheatCAP graduate students the education team conducts annual surveys. The complete results are in

, and below is a summary of the responses to some selected questions.

Question 6. How confident are you in the following skill sets?

Skill Sets	Not at All (Rank = 1)	Somewhat (Rank = 2)	Moderately (Rank = 3)	Very (Rank = 4)	Average (1-4)	Total Respondents
Make marker assisted selections	0	0	2	14	3.9	16
Work cooperatively	0	0	4	12	3.8	16
Utilize SNPs	0	0	6	10	3.6	16
Design experiments	0	2	6	8	3.4	16
Manage data	0	0	10	6	3.4	16
Observe and interpret results	0	1	8	7	3.4	16
Molecular techniques	0	1	9	6	3.3	16
Make phenotypic selections	0	3	5	8	3.3	16
Define and solve problems	0	1	10	5	3.3	16
Consider alternative hypotheses	0	1	10	5	3.3	16
Communicate your scientific ideas	0	0	12	4	3.3	16
Statistical analysis	0	2	9	5	3.2	16
Choose parents and make crosses	0	4	6	6	3.1	16
Genomic Selection	3	4	5	4	2.6	16

Confidence level rankings of WheatCAP students regarding different skill sets (1 = no confidence, 4=high confidence).

Question 11. In your opinion, what are the three best methods for educating graduate students?

Education Method	Respondents
One-on-one mentoring	56%
Field experience	50%
Collaboration with faculty other than your advisor	44%
Collaboration with graduate students from OTHER institutions	38%
Independent development of research designs	25%
Exposure to diverse research methods and tools	25%
Experience presenting results (meetings, papers)	19%
Independent development of hypotheses	13%
Laboratory experience	13%
Experience writing grants	13%
Collaboration with other graduate students at your institution	0%
Teaching experience	0%
Exposure to plant breeding students from different ethnic backgrounds	0%

Question 12. Percentage of Wheat-CAP students interested in plant breeding.
85% of the Wheat-CAP students are interested in Plant Breeding.

Question 13. Percentage of Wheat-CAP students who want to pursue a career in plant breeding.

85% of the Wheat-CAP students want to pursue a career in plant breeding.

Question 16. How has Covid-19 impacted your education and research progress?

Student Responses:

1) As we all experiencing, Covid-19 impacting all of us. Beginning of the pandemic, lab and other university facilities were highly restricted and had access for limited hours. All the classes suddenly shifted to online. I had to work mostly alone. But during field season, we are collaborating but maintaining social distance and wear mask all the time.

2) The working time was decreased to half. So many work was delayed.

3) Stop the lab experiment for one semester

4) I stopped my research until phase three. I am leaving one of my project incomplete.

5) "Not too much, but influenced our progress speed"

6) It impacted a lot, I had to drop one of my projects due to the shutdown given the genotyping facility was closed.

7) Research in the lab slowed down significantly. We waited to start new projects and primarily worked from home. Last semester, we had classes online and it was clunky. No interactions between students and teachers or students and students. I am hopeful that by the fall semester the teachers have learned new skills for online teaching! Breakout sessions and just talking to your partner in class are so important. Although, NDSU is going to start with classes in person.

8) I feel it has slowed down my progress a little bit. But doing my best a day at a time.

9) I have been blessed that Covid-19 did not impact my research negatively. It has not stopped any of my projects or greenhouse/field experiments.

10) My ability to perform molecular assays in a timely manner has been reduced dramatically and thus the amount of field data I can collect has also decreased.

11) Thus far my institution has allowed me to do in-person field lab work when it was necessary, so I haven't been negatively affected too badly.

12) For research, it has significantly slowed due to limited time at the lab and less person to person contact with others and my advisor due to shift working in the lab/building. It has also made research more difficult with setting up stuff, communication, etc. My education was slightly impacted because I had lab class last spring that went online and did not gain any of the hands on skills.

13) Working from home provided me with the opportunity to reflect on how my dissertation did and did not match my career goals. It has helped me make adjustments and re-focus my attention on skill building for desired job descriptions.

14) Significantly - no access to lab until this week, much higher workload during field season/harvest/post-harvest this spring and summer with no undergraduate workers. Harder to work on manuscripts with advisor and collaborators.

15) I have had to re-schedule and adapt almost all of my experiments for the last year of my PhD. With these modifications, I can still graduate on-time. All spare storage spaces in my house are also filled with wheat spikes since all characterizing and phenotyping has to be done off campus.

16) Not too much. I'm primarily writing now, so I'm still able to do my work.

Question 17. How can we better serve you in coping with the changes caused by Covid-19?

1) May be more online communication.

2) I need more research instructions on this special period to facilitate my research progress.

3) The writing group is a good idea for me.

4) Maybe we can do more of empowerment and skills development sessions when we are all being stay at home.

5) Hold more seminar to improve our study ability.

6) Probably, having monthly meetings again would help since some of us may be dealing with the same issues and we could advice each other.

7) Tokens of encouragement and moral support

8) I think you were very mindful of adjustments that needed to be made to the program due to

Covid-19. Canceling the CYMMIT trip was huge and saved me many worries. And I am excited to do the seminars over zoom. Will CYMMIT be rescheduled?

9) Social isolation has become an issue - so allowing opportunities for students to get together to socialize would be great.

10) The university is doing the best they can to balance research progress with safety. I have no further suggestions at this time.

11) Continue to support the importance of graduate students being allowed to conduct in-person research. I think at this point myself and virtually every other graduate student I've talked to is way more concerned about our university/institution shutting down our graduate research than any negative effects we might suffer from Covid. As a young health and highly educated person

I wish my university would give me more freedom in deciding my own health risk. Please don't take this message the wrong way, I think my university leadership is full of well-intentioned people who want the best for their students, but I feel they are being overzealous and are hurting us more than they are protecting us.

12) I think the biggest is to help those that keep our progress in check understand that research progress may have slowed due to Covid-19 and that it varies greatly across institutions.

13) We have fewer opportunities to interact with grad students at our institutions (for example running into each other at seminar) and that is a great opportunity for trouble shooting. Could we have a WheatCAP zoom meeting for people to attend if they want to troubleshoot / get some diverse brainstorming perspectives? Different from a research update - the goal is to present a problem.

14) Writing group was a great idea and has been useful! I forget what happened to the online conference/workshop but it would cool to pick that back up, especially if PAG is moved online.

It would be nice to resume monthly or even biweekly WheatCAP meetings where WheatCAP students can present research and get feedback, as I thought this was very valuable.

15) Provide remote networking opportunities and job finding assistance.

16) The inability to communicate with colleagues' in-person a conferences is frustrating.

Question 18. Suggestions for future education opportunities?

1) I think our attempt to include many aspect of skills development is very commendable. We should continuing our academic activities.

2) I think most of us are more familiar about what a career in academia would look like. Maybe career presentations in industry would help familiarize us with industry careers?

3) Having a meeting with advisors and discuss internship opportunities for students. Discuss timeline and encourage it's importance.

4) Genomic selection!!

5) Having more online lecture opportunities this year, like the one on Genomic Selection from

Rex Bernardo.

6) N/A

7) Because many of us have similar experiences and will be looking at jobs soon, a resume/cv workshop may be useful to learn how to tailor our resumes to show off our unique traits.

8) If there is any way for WheatCAP to support more student-interaction that is not based on attending and watching presentations, I would really appreciate that. These can be practical or purely social (eg. Trivia). For example, I really enjoy my little WheatCAP writing group with Brittney and Priscilla. I'm also really interested in hearing about people's "side projects" that are plant breeding related but not about positional cloning.