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
    - T3 database https://triticeaetoolbox.org/wheat/
    - Sequenced mutant populations https://dubcovskylab.ucdavis.edu/wheat_blast
- **Appendix 4.** Graduate students. https://www.triticeaecap.org/educational-activities/

e. Institution name: University of California, Davis

f. Requested amount: $2,500,000

A. Review of WheatCAP past accomplishments

Wheat-CAP overall productivity: During the second year of the WheatCAP, 47 peer-reviewed papers (plus 7 in press) were published acknowledging the USDA-NIFA support for the WheatCAP. WheatCAP breeders have released 14 commercial varieties, 8 improved germplasm, and 5 mapping populations. 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. A report of the economic impact of the public wheat varieties generated by the WheatCAP and previous TCAP projects with the support of the USDA-ARS genotyping laboratories has been included as Appendix 5

Education

A central objective of the WheatCAP project is to train PhD students in molecular plant breeding. By leveraging funds from participating universities, the WheatCAP participants have exceeded the target of 15 students. The WheatCAP is currently training 18 PhD students and 4 MS students (45% female). Three additional students have graduated (1 MS and two students that started their PhD under the TCAP and completed it with WheatCAP support). Student education progress is monitored by annual surveys to assess their educational improvement. The information generated by these surveys helps the education team to adjust the project to the educational needs of the students. Annual survey results are posted online at the following link: https://www.triticeaecap.org/2018-graduate-student-survey/

In 2018, Wheat-CAP students participated in workshops that taught them technical skills required for their positional cloning projects, and soft skills to help enhance their science communication abilities. The first workshop was hosted by Jorge Dubcovsky at UC-Davis (January 8-12) and introduced the students to the overall strategy of positional cloning. The workshop hosted 27 participants from around the country. This workshop was essential to ensure that all the students have a clear understanding of the methods and complexities of the proposed projects.

A second workshop was hosted at Cornell University (June 25-29) to teach the students how to communicate science to the public. This workshop was hosted by Sarah Evanega, director of Alliance for Science, in collaboration with the USDA IWYP funded Gene Editing research project. Seven Wheat-CAP students attended the workshop with several other students from different research projects, and they learned how to relate their research to the public through storytelling methods.

Lastly, a workshop was hosted by Eduard Akhunov and Alina Akhunova at Kansas State University (July 9-13) on the use of RNA-Seq/Bioinformatics to identify candidate genes controlling the student's trait of interest. Twenty-two individuals participated in this workshop. Lectures from the UC-Davis and Kansas State University workshops were recorded and are posted on the PBTN https://passel.unl.edu/communities/pbtn and WheatCAP website. For T3, the link is https://passel.unl.edu/communities/pbtn?idsubcollectionmodule=1130274157&idindependentpage=426.

In addition to the workshops, the students participated in two online courses. The first one was held this summer (June – August) and was designed by Jean-Luc Jannink from Cornell University. The course trained the students on the use of T3 and GrainGenes databases for their research projects. This online course hosted eight online lectures and all lectures are posted on PBTN. Lastly, another online course was hosted this summer (June – August) by Loriana Sekarski (corporate soft skill consultant, Bonsai) to teach soft skills to the WheatCAP students. This course focused on having the students identify their strengths, teaching them how to leverage these strengths, develop their brand, and network efficiently.

Education activities also included the update of the infrastructure of the online PBTN education delivery platform. Leah Sandall upgraded the Plant and Soil Sciences eLibrary (PASSeL), which houses PBTN, to make both sites mobile-friendly. These revisions will result in PBTN being easily accessible by all web-browsing devices. The new target date for completion of the mobile-friendly upgrades is January 2019. Lastly, both Leah and DeAnna Crow, administrative assistant, have been conducting routine maintenance on PBTN, and have been formatting the recorded workshop and online lectures for posting on the website.

The impact of the training activities of the WheatCAP and previous T-CAP projects are described in the economic impact report in Appendix 5 (including current positions of all trained individuals.

T3 database

Education: PhD student Nicholas Santantonio (Mark Sorrells, Cornell) has worked with T3 on data curation over the past six months. He has also participated in initial efforts to develop a wheat Practical Haplotype Graph. He has now completed his PhD and moved on to a postdoc position in quantitative and statistical genetics.

Research: T3 added 24 phenotyping trials including experiments from TCAP, Winter Wheat Scab Nursery, and Mason-Dixon Yield Trials. The 2017_WheatCAP_UCD genotype trial was added, which includes exome capture of all parents in the Wheat CAP project.

The T3 team developed a tool to select markers based on their polymorphism within subsets of lines. In particular, this tool enables users to pick two lines from the Wheat CAP parent dataset and find all polymorphisms between the parents within a specified region of the genome.

A report page was developed to show the Variant Effects Predictor values for the RefSeq_v1 assembly. The Variant Effect Predictor can be used to prioritize genomic variants in coding and non-coding regions. The report also includes links to the Sorting Tolerant from Intolerant (SIFT) score provided by Ensembl Plants.

The T3 team added browse and search functions for genome annotations from RefSeq_v1, TGACv1, and the David Edwards lab Wheat Pangenome. The JBrowse database was updated for RefSeq_v1 and incorporated variety tracks created by the Dubcovsky Lab. T3 has a BLAST server linked to JBrowse showing Variant Effect Predictor values. Scripts for that report were also provided by the Dubcovsky Lab. A JBrowse track was added showing the local recombination rate based on recombination events tallied in wheat NAM populations developed during the TCAP project based on data provided by the Akhunov Lab (Jordan et al., 2018). The T3 team added tutorials for Variant Effects, TASSEL, Flapjack, and R scripts.

An interface from T3 to the graphical genotype viewer Flapjack was developed using Breeding API (BrAPI, https://www.brapi.org/). Flapjack has functionality to analyze and provide decision support for marker assisted backcrossing, which should help students in incorporating their QTL into CIMMYT backgrounds.

Genomics resources

Sequenced tilling populations: WheatCAP has provided access to the sequenced mutant populations of tetraploid and hexaploid wheat including more than 10,000,000 mutations in the coding regions of the wheat genome. In the first 8 month of 2018, WheatCAP distributed 110 samples to 15 laboratories.

Exome capture of parental lines of the WheatCAP mapping populations: The exome capture assay targeting 162 Mb of the wheat genome (Krasileva et al., 2017) was used to re-sequence the coding sequences of 47 wheat lines used as the parents of the Wheat CAP mapping populations. On average, 57 million 150-bp paired-end reads were generated for each line and mapped to the latest version of the wheat genome reference (IWGSC, v. 1.1) providing 50x coverage of the targeted genomic regions. The variant calling using the GATK-based pipeline developed in the Triticeae CAP (Jordan et al., 2015) was used to discover 1,043,576 SNPs in the population. The data was deposited in Grain Genes and T3 databases.

Developing the Practical Haplotype Graph (PHG) tool for wheat: Katherine Jordan from KSU participated in the PHG workshop organized by E. Buckler's group in Cornell. 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 on developing the PHG of wheat. For this purpose, the sequence data generated for 47 Wheat CAP lines is used to start building the first-generation haplotype graph of wheat. To increase the utility of PHG for US breeding programs, KSU team collaborated with USDA genotyping labs to assemble a panel 217 US wheat cultivars that represent genetic diversity of modern US breeding programs. This set of lines is currently being used for exome capture analysis. The exome capture of the first set of 96 wheat lines has been completed.

Low-cost genotyping assay based on rhAmpSeq (IDT): Akhunov lab collaborates with E. Buckler's group to develop a low-cost genotyping assay for wheat based on rhAmpSeq technology developed by IDT. For this purpose, nearly 7 million SNPs obtained for 800 exome-captured accessions representing global genetic and geographic diversity of wheat (He et al., 2018) were used to select 2,999 genome-wide distributed common SNPs. The assay is supplemented with about 120 functional markers associated with various agronomic traits identified by the Wheat CAP or wheat community. The assay will be used for cost-effective genomic selection in breeding programs. A set of 30 rhAmpSeq markers designed from major genes for height, photoperiod, end-use quality were screened in 96 wheat advanced lines in the US hard red winter wheat region by a joint effort from TAMU and IDT.

Exome capture genotype imputation resource: The first generation haplotype map of wheat (Jordan et al., 2015) was used to impute SNPs in the winter wheat association mapping panel to demonstrate that increase in the SNP marker density substantially improves the precision of trait mapping and improves the accuracy of genomic prediction (Nyine et al., 2018, submitted). This

study demonstrates the value of developing a comprehensive haplotype diversity resource for US breeding programs.

Regulatory sequence capture: The design of the regulatory sequence capture targeting 250 Mb of unique genomic regions including predicted miRNA binding sites and 2 kb upstream of each gene model in the wheat genome was completed and tested on a set of 30 wheat lines from the US and UK (Gardiner et al., 2018). The regulatory capture and sequencing have been also completed for 12 Wheat CAP parental lines and 200 diverse wheat accessions. On average, 46.1 million reads were generated for each accession providing about 25x coverage of the wheat promoter regions. The sequencing of remaining lines is underway.

Chromatin accessibility: Akhunov lab optimized the MNase and ATAC-seq chromatin accessibility assays for wheat. The MNase assay was used to identify functionally active regions of the wheat genome. For this purpose, the KSU group have prepared libraries from the MNase treated nuclei isolated from wheat leaves and roots to obtain 10x coverage of the wheat genome. The sequence reads were aligned to the reference genome and used to identify regions with open chromatin. Consistent with expectations, joint analyses of public RNA-seq data generated for cv. Chinese Spring and MNase sensitivity score showed strong correlation (Fig. 1).

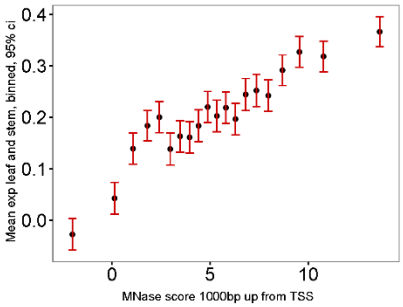

Fig. 1. MNase score 1kb upstream of transcription start sites positively correlates with the levels of gene expression in cv. Chinese Spring. Y-axis - expression average in leaf and stem at Z23 - Z32 development stages.

Wheat NAM population: The spring wheat NAM population was developed, genotyped using 90K iSelect, GBS and exome capture assays and used to characterize the distribution of 102,000 recombination breakpoints across the wheat genome (Jordan et al., 2018). The genotyping data and distribution of recombination breakpoints in the NAM population were deposited to the T3 database. This data will be used by WheatCAP for assessing the number of lines in the progeny required to obtain the adequate number of recombinants for QTL mapping. The NAM population was also used to identify QTL controlling the distribution of recombination along the chromosomes. The identified QTL increasing recombination in pericentromeric regions can be used to reduce linkage drag in these chromosomal regions making them accessible to selection. The seeds of the spring wheat NAM population are deposited to USDA NSGC repository by co-PD Talbert (Blake et al., 2018).

References used in this section:

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Gardiner L, Brabbs T, Akhunova A, Jordan K, Budak H, Richmond T, Singh S, Catchpole L, Akhunov E, Hall A. 2018. Integrating genomic resources to present full gene and promoter capture probe sets for bread wheat. BioRxiv, 2018, doi: https://doi.org/10.1101/363663

Nyine M, Wang S, Kiani K, Jordan K, Liu S, Byrne P, Haley S, Baenziger PS, Chao S, Bowden R, Akhunov E, Genotype imputation in winter wheat using first-generation haplotype map SNPs improves genome-wide association mapping and genomic prediction of traits. 2018 (submitted)

Blake, N. K., M. Pumphrey, K. Glover, S. Chao, K. Jordan, J.-L. Jannick, E. A. Akhunov, J. Dubcovsky, and L. E. Talbert. 2018. Registration of the Triticeae-CAP Spring Wheat Nested Association Mapping Population, (submitted).

He F, Pasam R, Shi F, Kant S, Keeble-Gagnere G, Kay P, Forrest K, Fritz A, Hucl P, Wiebe K, Knox R, Cuthbert R, Pozniak C, Akhunova A, Morrell P, Davies J, Webb S, Spangenberg G, Hayes B, Daetwyler H, Tibbits J, Hayden M, Akhunov E, Exome sequencing reveals the adaptive landscape of the wheat genome. 2018 (submitted)

Genotyping Laboratories

The role of the regional genotyping laboratories in the current Wheat CAP project is to provide KASP and other marker genotyping services for high-resolution mapping of candidate genes for yield-related QTL. The Raleigh lab has provided support for high-resolution mapping for the research projects of students at Cornell and at North Carolina State University. DNA has been isolated from tissue of 2,688 individuals for the high-resolution mapping project at Cornell. Genotypes are being determined for 15 KASP assays targeting QTL regions on chromosomes 5A and 5B. Projects in collaboration with the NCSU graduate student included GBS of a 358 RIL mapping population and development of KASP assays for markers in QTL regions on 5A (*B1* locus), 6A, 3A, and 2D. DNA was isolated from 950 F_2 plants, 288 M2 plants, and 2750 NSGC wheat accessions. All were genotyped with KASP markers in the *B1* region. The Raleigh lab provided genotypic data on vernalization genes for a collaboration with UCD that resulted in a join publication (Kippes et al. 2018).

The Fargo lab has collaborated with researchers at the University of Minnesota, where a population of recombinant lines was screened with SSR markers to identify critical recombinants near their target QTL on chromosome arm 2AL. The lab also collaborated with the Fargo research project by genotyping several populations with the Illumina 90k SNP array for the identification of QTL associated with yield components in durum wheat. In addition, the genotyping lab assisted the Fargo research project in the development of semi-thermal asymmetric reverse PCR (STARP) markers for individual SNPs and used the markers to genotype several backcross generations for the development of a high-resolution mapping population segregating for a single QTL on chromosome arm 2BL that governs seed number and grain weight. The Fargo lab provided the 90K data for a DH population developed at UCD.

The Manhattan lab has collaborated on the graduate student project at Kansas State University in development of a GBS linkage map of the Overland x Overley RIL population used for their gene-cloning project. They have also collaborated on the backcrossing projects by evaluating polymorphism of parents from CO, KS and TX with CIMMYT breeding lines using flanking markers developed for grain yield traits. The Pullman lab has collaborated with the southern Idaho spring wheat-breeding program by evaluating specific markers on wheat CAP material. The Pullman lab has also collaborated with the Washington and UCD breeding program and has run molecular makers for the CAP population.

The genotyping laboratories support the WheatCAP activities via the provision of genotyping services to breeders and researchers who seek to improve the productivity and quality of wheat varieties. Since the WheatCAP project was initiated, the Fargo lab has provided services for processing Illumina 90k SNP arrays for 30 projects consisting of over 8,000 samples and generating 736 million data points for wheat. The labs at Manhattan and Raleigh have produced similar numbers of data points. The Pullman lab has developed primer pools for amplicon sequencing of hundreds of markers across the genome. Each of the regional labs is collaborating with the Akhunov lab at KSU and USDA ARS at Ithaca, NY to expand exome capture data for elite US cultivars and to develop inexpensive haplotype-based approaches to genotyping. The genotyping labs also provide genotyping services using SSRs and KASP markers for marker-assisted selection of specific agronomically important traits to all breeding programs in their respective regions. Of the 33 publications reported in Appendix 2, the leaders of the genotyping labs are co-authors in six of them, documenting the integration of the genotyping laboratories with the research and breeding programs of the WheatCAP.

CIMMYT HUB. Matthew Reynolds

The CIMMYT hub tested Kronos homozygous mutants with four different allelic combinations of *Elf3* allele from *T. monococcum* for increased spikelet number and the *gw-A2* mutant allele for increased grain size. The four lines - (1) *GW2A*-WT, *ELF3*-WT (2) *GW2A*-MUT, *ELF3*-WT (3) *GWA2A*-WT, *ELF3*-MUT and (4) *GW2A*-MUT, *ELF3*-MUT along with four checks (entries 5 to 8) were evaluated in a randomized complete block design with three replications, planted in January 2, 2018. Each entry was planted in two rows of 2 m.

Genotype	Yield gr	SE	TKW	SE
Gw-A2$_{WT}$/*Elf3*$_{WT}$	346.2	43.2	49.2	1.2
gw-A2$_{mut}$/*Elf3*$_{WT}$	338.5	5.2	51.8	0.4
Gw-A2$_{WT}$/*Elf3*$_{Tm}$	364.7	31.9	47.1	1.8
gw-A2$_{mu}$t/*Elf3*$_{Tm}$	379.0	39.1	51.3	0.2

The lines carrying the *ELF3* allele from *Triticum monococcum* accession DV92 showed an 8.6% higher yield than the lines carrying the wild type allele. The lines carrying the *Gw-A2* mutation showed a 7% increase in kernel size, which is consistent with previous results reported in CA and the UK (Simmonds et al. 2016 TAG129:1099). The line combining the *ELF3* allele from DV92 and the *Gw-A2* mutation showed the highest yield. Analysis of variance indicated the entries were significantly different for grain yield and TKW. Duncan's multiple range test comparison indicated that entry 4 was significantly different from the other three lines.

In July 2018, UCD sent to the CIMMYT hub seeds for the four *GW-A2/ELF3* combination introgressed in the genetic backgrounds of top CIMMYT lines CIRNO and GID 6420253. These lines will be evaluated in the 2018-2019 growing season at the CIMMYT hub.

The five CIMMYT high-biomass lines were evaluated at UC Davis and compared with local high yielding genotypes UC1767 and UC1817. Four of the five CIMMYT lines showed high total biomass, but their grain yield and harvest indexes were lower than the adapted UC varieties. The high biomass CIMMYT lines were taller than the UCD lines and one showed high values for spikelets per spike (SPS, GID3613474) and one for grains per spike (GPS, GID 4577963).

Entry	Protein	Biomass /row	Grain /row	Straw /row	HI	No of Spikes	TKW (g)	Height cm	SPS	GPS

GID3855011	14.0	2.015	0.481	1.534	0.24	298.3	47.9	113.8	20.7	45.4
GID3613474	14.5	1.958	0.499	1.458	0.26	290.0	44.3	106.3	23.9	57.3
GID4577963	13.7	1.583	0.504	1.078	0.33	275.5	38.6	101.3	21.6	61.7
GID4314513	14.9	2.048	0.588	1.460	0.29	420.5	42.1	107.5	19.5	45.3
GID4878569	14.4	2.029	0.381	1.648	0.19	256.6	48.1	111.9	21.0	59.2
UC1767	14.1	2.158	0.733	1.424	0.34	384.3	42.0	100.0	21.6	51.2
UC1817	14.9	1.920	0.651	1.269	0.34	370.8	38.4	91.3	21.8	54.0

QTL cloning projects

AR. University of Arkansas. Esten Mason

***Education*:** PhD student Dylan Larkin (start 8/2017) is focusing on the 1A QTL for grain yield, spike weight and thousand-kernel weight. MS student Zachary Winn (start 8/2017) is working on the 6B yield QTL. Both students attended the WheatCAP workshops at UCD and KSU and made presentations. Andrea Acuna, who assisted with the project from 12/2016, completed her PhD in July 2018. Dennis Lozada completed his PhD in Aug 2018 and published a marker validation study on grain yield QTL in soft winter wheat using a CIMMYT spring wheat panel. Paul Wolf is an undergraduate honors student who works as a research assistant on the project.

***Research project*:** the AR group targeted two QTL from the winter wheat line AGS2000, located on chromosomes 1A and 6B. In Year 2, they used the greenhouse to grow out 303 individuals to identify homozygous recombinants for markers flanking the QTL. KASP markers *IWA7173*, *IWA3477, IWA339, IWA1081, IWA531* along with SSR markers *gwm135* and *cfa2129* are being used to delineate the 1A region and *gwm193, IWA755, IWA6428* and *IWA2830* the 6B region. The AR group is using the exome capture data to design new markers to screen for additional recombinants, which will be planted in fall 2018 for field phenotyping.

The AR group completed the initial crosses of AGS2000 with CIMMYT spring wheat lines lacking the favorable alleles in the 1A QTL ($GID_{4878569}$, Kenya Sunbird, Kingbird, MUTUS#1) or the 6B QTL ($GID_{3613474}$, $GID_{4314513}$, $GID_{4577963}$, BAJ#1, BONSU, CHIPAK, KINGBIRD, KUTZ, M1SR1). Since AGS2000 is a winter wheat, the production of the first F_1 required vernalization, which delayed progress (Table 1). However, once these lines are converted to a spring-wheat background, the backcrossing process will be faster.

In addition to the cloning efforts, the AR group published a study validating winter wheat QTL on chromosomes 3A (*IWA3560*), 4B (*IWA1818*), and 6B (*IWA755*). The marker *IWA755* is the same 6B QTL targeted in the cloning study. They also published a genomic selection study showing the importance of using vernalization and photoperiod loci as covariates to improve yield prediction accuracy. In total, the AR group published three manuscripts in 2018.

CA. University of California, Davis. Jorge Dubcovsky

Education: PhD students Saarah Kuzay and Priscilla Glenn made significant progress in the thesis projects. They defined the candidate regions of the QTL for spikelet number and identified putative candidate genes. Saarah has completed her courses and is preparing her qualifying exam and Priscilla Glenn completed her first year courses successfully. They both attended WheatCAP workshops in UC Davis, KSU and Cornell. Youngjun Mo and Nicolas Cobo, who initiated their

PhD supported by the T-CAP, completed their PhD with WheatCAP support. They published their results, and are now working as breeders.

Research project: Wheat CAP coordinator Dr. J. Zhang refined the map of a QTL for grain yield and root length on a segment of chromosome arm 1BS introgressed on the rye 1RS arm ($1RS^{RW}$). The normal 1RS arm is associated with long roots and high yield, whereas the 1BS introgression results in short roots and reduced yield (Figure 1). Using radiation mutants, he identified a 1.46 Mb deletion in 1BS that restored the long roots (Fig. 1). Four candidate genes have been identified in the 1.46 Mb region and CRISPR Cas9 and overexpression validation experiments have been initiated.

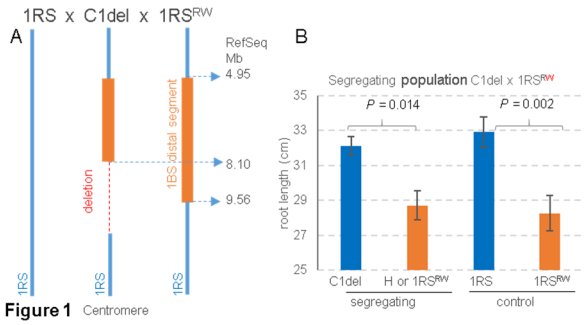

Figure 1

PhD student S. Kuzay completed the high-density mapping of the 7AL QTL for spikelet number and delimited a 0.86 Mb candidate region including eight annotated genes. She used exon capture data to identify potential causal polymorphisms and, based on these results, she prioritized three genes for validation. She identified truncation mutants for the A and B genome homeologs in the sequenced TILLING population and initiated backcrosses to Kronos to reduce the load of background mutations. She will then intercross the A and B genome BC_1 lines to evaluate the effect of the double mutants on spikelet number.

PhD student Priscilla Glenn identified two QTL for spikelet number per spike on chromosomes 3AS and 2BS and delimited the QTL regions to 6.3 Mb and 4.7 Mb intervals respectively. Candidate genes have been identified for both QTL. She initiated screens of larger HIF populations to reduce the candidate regions.

Seeds were sent to the CIMMYT hub in 2018 (BC_4F_2) combining the *Elf-A^{m}3* allele for increased spikelet number from *T. monococcum* and the *gw-A2* mutants for increased grain size into the CIMMYT tetraploid varieties 'Cirno C 2008' and '$GID_{6420253}$'and the hexaploid variety Kingbird (BC_4). The 7AL QTL for increased spikelet number was introgressed by four backcrosses into CYMMIT high-biomass bread wheat lines $GID_{4314513}$, $GID_{4577963}$ and $GID_{3855011}$ (Table 1).

The UCD group completed the development of two new commercial bread wheat varieties using marker-assisted selection. 'Desert Gold' is a high-yielding durum line with QTL for reduced cadmium, improved semolina color and pasta color stability. 'Central Red' is a high-yielding HRS with excellent breadmaking quality and stripe rust resistance gene *Yr15* (Appendix 1). The UCD group published nine peer-reviewed articles in 2018 acknowledging USDA-NIFA (Appendix 2).

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

Education: PhD student Andrew Katz has completed successfully his 2018 courses (GPA 4.00). Andrew attended the WheatCAP workshops at UC Davis, Cornell, and KSU, and participated in the online workshops offered by the T3 Database and WheatCAP Soft Skills. Three undergraduate students (Mallory Wilemon, Alejandro Benitez and Jack Mentzer) have supported

the project, and gained experience in general molecular biology techniques, genotyping, and field-based phenotyping.

Research project: The CO group identified a QTL for spikelet number on chromosome arm 6BL (503Mb) by GWAS on the Hard Winter Wheat Association Mapping Panel. They validated this QTL in an $F_{5:6}$ Platte/CO940610 RIL population (n=224) during the 2016/2017 field season. The Platte allele showed a positive effect of 0.78 spikelets per spike (R^2=11.8, $P < 0.0001$). The CO group developed nine KASP markers spanning the peak region and identified 19 heterozygous $F_{4:5}$ individuals. They genotyped each individual for three other segregating alleles: *VRN-D3a/b*, *PPD-B1a/b*, and a 7AL QTL for spikelet number, which is significantly associated with spikelet number in this population and is similar to the QTL targeted at UCD.

To introgress the 6BL QTL into elite materials, the CO group generated F_1 seed from crosses between Platte (carrying the favorable 6BL and 7AL alleles) and five CIMMYT lines (Bonsu, PRL/2*Pastor, Nadi, Mucuy, and $GID_{3855011}$) and Colorado advanced breeding line CO13D1383, which carries the 6BL allele for low spikelet number (Table 1).

In 2018, the CSU wheat-breeding program released the two winter wheat varieties 'Breck' and 'Incline AX' and six winter wheat breeding lines: Snowmass 2.0, Canvas, Whistler, Monarch, Byrd CL Plus and Crescent AX. The CO group also generated two peer-reviewed publications.

ID. University of Idaho. Jianli Chen and Daolin Fu

Education: The UI team includes one postdoc (50%) and two MS. Students (Kyle Isham and Katrina Johnson). They attended the WheatCAP training workshops at UC Davis and KSU and made good progress in their course work. Dr. Rui Wang and Mr.Kyle Isham attended the 20th Int. Smut conference in UT, the Western Wheat Workers in ID, and a growers' field day in Aberdeen. When Katrina finishes her MS, her project will be continued by new PhD student Meng Su.

Research project: The UI team is working on two different QTL, one for number of spikelets QTL on chromosome arm 5AL, and the other one, for productive tiller number on chromosome 6A. In 2018, they conducted two greenhouse and one field trial experiments for both QTL.

QSNS.ui-5A. KASP markers were developed for flanking markers located at 631 and 643 Mb (peak marker at 636 Mb). Eight families carrying recombination events between the flanking markers were identified and sown this spring. Preliminary results indicate that the gene is located within a 7-Mb region of chromosome arm 5AL between 636 and 643 Mb.

QPTN.ui-6A. KASP markers were developed based on flanking markers located at 91 and 198 Mb (peak marker at 107 Mb). Five families ($F_{5:3}$ or $F_{6:3}$) carrying recombination events within the target region were identified and sown in the spring. Data is being analyzed.

The two QTL have been backcrossed into four CYMMIT high-biomass lines and BC_2F_1 were obtained. The two QTL will be advanced to BC_3 this fall (Table 1). The ID group selected three lines for release in 2019: IDO1405S, IDO1603S, and IDO1706 and developed two EMS populations in UI Platinum and Brundage. Mutant lines with spike-related phenotypes have been selected to investigate in the WheatCAP project. The ID team published four peer-reviewed papers in 2018.

KS. USDA-ARS Manhattan.

Education: MS student Quanli Pan and PhD student Elina Adhikari are involved in the WheatCAP project in Dr. E. Akhunov laboratory. Both attended the WheatCAP workshops at UC Davis and KSU, and the Nebraska Plant Breeding Symposium (where they made presentations). Graduate student W. Mustahsan (PhD) started in June 2018 with Mary Guttieri and attended the KSU RNASeq Workshop. Undergraduate student Emma Purvis is managing the introgression into CIMMYT germplasm. E. Akhunov and Alina Akhunova organized a successful workshop on the production and analysis of RNA-seq data for 22 graduate students and postdoctoral researchers at the KSU Integrated Genomics Facility.

Research project: A grain yield QTL was identified on chromosome arm 2DL in the cross between Overley x Overland. Exome-capture based SNPs spanning the target region were converted to KASP markers and used to identify $F_{3:4}$ families segregating for the QTL. F_4 sib pairs for the QTL are being planted for seed increase in Arizona, and the resulting seed will be used for yield testing in the Great Plains. F_4 individuals heterozygous for the KASP markers were self-pollinated, and > 2000 F4:5 progeny are presently being screened for recombinants within the region. Non-recombinant $F_{4:5}$ progeny of both parental classes are being identified as NILs for a greenhouse experiment to assess the effect of the QTL region on yield component parameters. The Overley/Overland RIL population was yield tested at Manhattan and Hays, KS in 2018. The exome capture SNPs have been evaluated on the Overley/Overland population and are presently being integrated into the GBS-based genetic map.

The donor parent KS11WGRC53-O is the source of the 2DL QTL, the 2NS/2AS translocation and the $5M^g$ translocation including *Yr40, Lr57,* and *Sr53*. All three regions are targets for introgression using molecular markers. The 2DL allele for high yield is being introgressed into 11 high-yielding CIMMYT lines that carry the 2DL allele for low yield (BC_2F_{1S}, Table 1). BC_1 bridge crosses will be required for three lines that showed hybrid necrosis. KASP marker *khw37* will be used to screen against the $2Ne^m$ allele from KS11WGR53-O in the progeny. Three of the CIMMYT lines (PBW/2*Pastor, Kenya Sunbird/Kachu, and Borlaug100) also were positive for the *Lr13*-$2Ne^m$-associated marker.

The KSU team released the variety ‘KS Venada’ and the germplasm ‘KS05HW14’ (Appendix 1) and generated eight peer-reviewed publications (Appendix 2).

MI. Michigan State University. Eric Olson.

Education: PhD student Jon Turkus is leading the MI project. Jon completed successfully his courses and attended the WheatCAP workshops at UCD and KSU. Participation in a wheat field day provided Jon the opportunity to interact directly with wheat growers and industry. An undergraduate student researcher, Marcy Stephens, has also been provided training through this project. Marcy plans to attend graduate school in fall, 2019.

Research project: The MI project is focused on a QTL for grain yield located on chromosome arm 2DS derived from KS05HW14. They genotyped the progeny of F_5 plants derived from F_4 lines segregating for the target QTL to identify HIFs. The F_6 progeny from heterozygous F_5 plants were then evaluated with KASP markers across the QTL interval to identify 12 target recombinant genotypes for the development of HIFs. From ~1,500 progeny, 13 recombinant F_7 genotypes have been identified. Homozygous recombinant plants are being increased in the greenhouse and will then be increased in the field. Using the exome capture SNPs, six KASP

markers were developed, five codominant and one dominant. All markers are unique to chromosome 2DS from 22.1Mb to 29.5Mb.

The MI group produced BC_1F_1 for the 2DS grain yield QTL in CIMMYT lines Kingbird and Heilo backgrounds (Table 1), and released the new soft white winter wheat variety 'Whitetail' through Michigan Crop Improvement Association (Appendix 1).

MN. University of Minnesota. Jim Anderson.

Education: PhD student Max Fraser completed successfully his courses at UMN and attended WheatCAP sponsored workshops at UCD and KSU. In addition, Max participated in a small grains field day highlighting new variety releases and developments from the UMN wheat-breeding program. Undergraduate student Catherine Li was hired in February 2018. She has gained experience in molecular markers, field phenotyping, and greenhouse activities.

Research project: Previously, the MN team was working to characterize a thousand kernel weight (TKW) QTL, *QTkw.mna-2A*. However, this work was suspended when they discovered that this QTL was centromeric and that the interval included a previously cloned and characterized polymorphism affecting TKW. The objective of the MN team has shifted to the characterization of a thousand kernel weight QTL located on chromosome arm 5BS, *QTkw.mna-5B* (LOD = 3.90, $R^2 = 10.50$) identified in the population MN98550-5/MN99394-1. This QTL resides on a ~32 Mb region of the short arm of chromosome 5B. Heterozygous RILs were identified in the fall of 2017. Development of heterogeneous inbred families for the 5BS QTL will start in fall 2018.

Max Fraser has developed BC_2F_2 introgressions of *QTkw.mna-5* from MN99394-1 into CIMMYT line $GID_{4314513}$. Additional crosses with CIMMYT line $GID_{4314513}$ will be made with the parents of the 14x111 population (Shelly, Prosper, and MN10201-4-116) during the upcoming greenhouse season. Additional CIMMYT lines have been abandoned due to severe and hybrid necrosis.

Additionally, the UMN team has begun the process of identifying novel yield component QTL in two genetic populations. The first, 14x111, is a double haploid population developed from the three-way cross MN10201-4-116/Prosper//Shelly. Population 14x111 was grown in three locations in 2017 and four locations in 2018. The research on 14x111 is a collaborative effort with the NDSU WheatCAP student, Amanda Peters. The second population, 15xR012, is an advanced backcross population developed by USDA-ARS Geneticist Matt Rouse from UMN breeding line MN07098-6 and a *T. turanicum* accession, Sun Ray. 15xR012 was planted in replicated field trials in three locations in 2018. Genotyping of both populations by GBS is currently underway. Linkage mapping will be completed by spring 2019. The MN group published five peer-reviewed papers in 2018.

MT. Montana State University. Luther Talbert

Education: Graduate student Brittney Brewer completed the second year of her PhD program and participated in the positional cloning workshop at UC-Davis and the RNA-seq workshop at KSU. She presented a poster on related research at the Plant and Animal Genome Conference in San Diego (https://pag.confex.com/pag/xxvi/meetingapp.cgi/Paper/32300).

Research Project: Phenotyping trials showed that the allele differences for the targeted 6B QTL for number of reproductive tillers were detectable under greenhouse conditions by counting early

tiller number. This trait correlated with final number of reproductive tillers only under favorable growing conditions. The MT group screened 2,100 lines from three HIF segregating for *QTn.mst-6B*. Primers for KASP were designed based on exome capture SNPs for fine mapping the QTL region centered at 430 Mb on chromosome 6B. More than 50% of the KASP markers mapped to the target region and were suitable for characterizing the candidate region.

The introgression of *QTn.mst-6B* into four CIMMYT lines was continued to the BC_2 generation (Table 1). Verification yield trials with NIL for six yield-component QTL identified in a durum wheat by hexaploid wheat population were conducted at three sites. In 2018, the MT group deposited the TCAP NAM population consisting of 2400 RIL in the NSGC and generated six peer-reviewed publications.

NC. USDA-ARS Raleigh. Gina Brown-Guedira

Education: Graduate student Eddie Lauer works on the NC project to validate and fine map the kernel weight QTL on chromosome 6A. He completed his MS degree during December 2017. New graduate student Noah DeWitt (1/ 2018) completed his first semester of classes and participated in the Wheat CAP student meetings. Noah attended the WheatCAP workshops at UCD and KSU.

Research project: The initial focus of the NC team was a QTL for kernel weight and plant height on chromosome 6A identified in the population from the cross SS-MPV57 x Massey (MM). Inbred lines selected from five F_5-derived heterozygous inbred families were evaluated in the field at Raleigh, NC during 2018. The effects of the chromosome 6A QTL region on both kernel weight and plant height were confirmed, with good expression in all HIF. After the positive effect of the 6A QTL was confirmed, the NC group made crosses between the donor of the positive allele (Massey) and the HB/HY CIMMYT lines selected as recurrent parents in this project (Table 1). However, lack of recombination in the 6A QTL region limited progress in the fine mapping of this QTL and prompted the exploration of a second segregating population.

Two sets of NIL (one with awns and one awnless) were developed from a single F4-derived HIF from a cross between LA95135 x SS-MVP57 (LM) and evaluated in the field. Significant differences in kernel weight were observed in lines contrasting for awns, with awned NIL having larger kernels. The 358 RIL of the LM population were grown in replicated experiments in the greenhouse and at two field locations in NC. Multiple QTL were identified, including a region of chromosome 5A for kernel weight that encompassed the *B1* awn suppressor. In addition, GWAS in a panel of soft winter wheat lines identified a highly significant association between a 5A SNP and the awn phenotype and test weight. New markers were developed to fine map the *B1* locus in the LM population and in 950 F_2 segregating for awns. Expression of candidate genes was evaluated by qPCR and using data from the WheatExp database. The NC group is collaborating with Daolin Fu at the University of Idaho to analyze awned mutants of the awnless cultivar Brundage.

The NC group demonstrated that the *B1* locus is significantly associated with kernel weight in their RIL population and with test weight in a GWAS of eastern US wheat. These results are consistent with reports that awns can contribute to improved grain yield in wheat. As a result, the efforts of graduate student Noah DeWitt have been focused on identifying the underlying mechanism of awn suppression. Noah has narrowed the region by fine mapping and identified a promising candidate gene using mutants. The NC group will introgress the *B1* awn-suppressor

into the CIMMYT lines to generate awned and awnless NILs to test the effect of this trait on yield at the CIMMYT hub (Table 1). The NC group generated four peer-reviewed publications.

ND. USDA-ARS Fargo. Justin Faris

Education: PhD student Amanda Peters is entering her second year as a WheatCAP-funded student. She completed her MS degree in Plant Sciences at NDSU in May 2017. She has completed her 2018 courses at NDSU and attended the WheatCAP workshops on positional cloning (UCD) and RNA sequencing (KSU). She presented a poster at the Plant and Animal Genome XXVI Conference in San Diego, CA.

Research Projects: The group at Fargo has replaced their target QTL for grain yield QTL on chromosome 3A in winter wheat with a QTL for kernels per spike (KPS) and grain weight per spike (GWS) on chromosome 2BL in durum wheat. They will continue to narrow down the 3A QTL region while focusing on the new 2BL project.

The 2BL QTL was first mapped in the RIL population BP025, derived from crossing Ben (*Triticum durum*) with the cultivated emmer accession PI 41025 (*T. dicoccum*), grown under greenhouse conditions. A field experiment conducted in the summer of 2017 showed the QTL was expressed under field conditions as well. Currently, the 2BL QTL spans a 38 Mb region (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. Currently, BC_3F_1 seed is growing, and heterozygous plants in this target region will be selected and self-pollinated to obtain BC_3F_2 seed for high-resolution mapping.

Additionally, the Fargo group has begun introgressing the 2BL QTL into multiple CIMMYT lines and generated F_1 plants from crosses between Ben and $GID_{4878569}$, $GID_{4577963}$, $GID_{3613474}$, and Kingbird; and will soon make the first backcross (Table 1). The ND group has also crossed Ben to Fielder to use it as a bridge in crosses showing hybrid necrosis.

Additional projects of the Fargo group related to the WheatCAP objectives include mapping yield component and seed morphology traits in three RIL populations derived from crossing different durum varieties by cultivated emmer accessions. These are being grown under both greenhouse and field conditions.

NY. Cornell University. Mark Sorrells

Education: Four Ph.D. students that benefited from the TCAP and WheatCAP support graduated in 2018: Nicolas Santantonio, Lisa Kissing Kucek, Lynn Venstra and Itaraju Brum. PhD student Ella Taagen, who is currently supported by the WheatCAP, completed the first year courses successfully and participated in the 2018 WheatCAP workshops. She attended PAG 2018 and will present a poster at the ASA/CSSA conference in November 2018. She was invited to participate in the Tri Societies Congressional Visit Days during March 2018 and has developed an interest in agricultural policy. Ella seeks out opportunities to participate in seasonal extension days for NY small grains and meet local supply chain stakeholders.

Research project: The Cornell Small Grains research program is using the SynOpDH (200) and SynOpRIL (2000) mapping populations to fine-map three QTL for grain-size and grain-shape. The primary targets are a QTL on 5AL for kernel width and TKW at 66 cM, and a QTL on 5BL for kernel length at 40.5 cM. In the past two years, these two QTL have been validated in five different environments. A secondary target is the seed size QTL positioned more distally on

chromosome arm 5BL at ~75 cM. The donor of the positive allele for the 5AL QTL is Opata whereas the donor for both 5BL QTL positive allele is the synthetic parent W7984. The 5AL QTL may be homoeologous to one of the 5BL QTL.

HIF were developed from RILs with heterozygous QTL peak flanking markers and self-pollinated for three generations to reduce genetic variability. Phenotypes and genotypes from a 2017 greenhouse planting validated previous results. Three HIFs were selected per QTL (9 total) for 2018 spring field plantings. A total of 232, 370 and 15 recombinant individuals were found for 5AL, $5BL_1$ and $5BL_2$ respectively, all of which were phenotyped for TKW, seed length, width, area and perimeter. Individuals with homozygous flaking markers served as parental checks. Fifty seeds from homozygous parental checks or a single heterozygous flanking marker, and 100 seeds from individuals where both flanking markers are heterozygous were field planted in May 2018 for all 9 HIFs. During the summer of 2018, tissue was harvested from 2,600 HIF plants. Fifteen new KASP primers were developed and mapped on the DH population in the three QTL regions on interest.

- *5AL QTL flanking KASP:* KS0617_566068 (50.4 cM), KS0617_550080 (66.7 cM),
- *$5BL_1$ QTL flanking KASP:* KS0617_598686 (29.6 cM), KS0617_611864 (56.4 cM)
- *$5BL_2$ QTL flanking KASP:* KS0617_613479 (62.3 cM, KS0617_627763 (95.8 cM)

Elle Taagen will analyze genotypic and phenotypic data using R/QTL this fall. Phenotyping of HIFs and SynOpDH population has been expanded by using a new WinSEEDLE scanner.

The NY group is backcrossing the positive alleles from the DH population as donors and recurrent parents Opata, Tom and Glenn, as well as five CIMMYT high-biomass lines and selected high-yielding lines (Venda, Kingbird #1, Mutus #1, PRL/2*Pastor, Borlaug100 & Kachu #1). BC_3 plants from backcrosses to Opata, Tom and Glenn have been genotyped using the recently developed KASP primers and selected individuals will be planted for the fourth round of backcrossing in October 2018. In addition, CIMMYT high biomass lines and CIMMYT high yielding lines will be planted and crossed to produce their BC_2 and BC_1 generations, respectively (Table 1).

OK. Oklahoma State University. Liuling Yan and Brett Carver

Education: PhD student Forrest C.C. Kan thesis project is focused on the cloning of the *QYld.osu-1B* gene in the 'Duster x Billing' population (positive allele contributed by Duster). PhD student Xiaoyu Zhang thesis project is focused on the cloning of a major gene for spikelet number on chromosome 7BL (positive allele contributed by CItr17600). Both Forrest and Xiaoyu attended the WheatCAP workshops at UCD and KSU.

Research project: For the grain yield QTL *QYld.osu-1B*, the OK team screened 2,200 F_4 plants and discovered 24 lines with recombination events between the flanking markers. The recombinant plants were phenotyped and seeds were increased for field trials. Using these recombinant lines, the candidate region for *QYld.osu-1B* was narrowed down from 164 Mb to 25 Mb in 2018. To test if the low recombination rate observed in this region was due to the introgression of an alien segment, the *ph1b* mutation from Pavon is being introgressed in a line heterozygous for the 1B QTL region.

For the spikelet number QTL on chromosome arm 7BL, the OK team screened 1,875 F_4 plants derived from WF112 F_3 line and identified 21 recombination events between the flanking

markers. Phenotypes and genotypes from these 21 F_4 recombinant plants confirmed that the spikelet number QTL was genetically controlled by a single locus on chromosome arm 7BL located within a three Mb candidate region.

Donor lines Duster (*QYld.osu-1B*) and CItr17600 (7BL QTL) have been crossed with CIMMIT wheat lines and Oklahoma wheat breeding lines (Table 1). The OK team generated four peer-reviewed publications and released four commercial wheat varieties in 2018.

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

Education: PhD student Jyotirmoy Halder is working on the fine mapping and deployment of a yield QTL on chromosome 7DS from *Ae. tauschii*. He completed his expected coursework and attended the WheatCAP workshops at UCD, Cornell and KSU. Jyotirmoy also participated in monthly group meetings and online learning modules. Two undergraduate students were also trained in wheat breeding during this period and were closely involved in the project developing populations/germplasm focused on yield-related traits.

Research project: The yield QTL targeted by SDSU was mapped on the distal 6 -16 Mb region of the short arm of chromosome 7DS. The parents of the mapping population, KS05HW14 (HWWW) and TA1615 (*Aegilops tauschii*) were genotyped by exome capture. The SD team identified 800 potential SNPs in the target region among the parents. Forty-three SNP based KASP markers flanking the QTL region were evaluated and several co-dominant markers were identified for screening HIF families to identify recombinants. Jyotirmoy has identified 15 potential recombinants from HIFs U6711-B-50 and U6712-148. The SD team is also growing HIF progenies, which were heterozygous in the target region to identify additional recombinants in the next generation.

The favorable allele from the yield QTL on 7D was crossed with CIMMYT lines Kingbird, $GID_{4314513}$ and $GID_{3613474}$, and with locally adapted cultivars Ideal and Overland (Table 1). The SD team generated one peer-reviewed publication in 2018.

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

Education: PhD student Smit Dhakal working on the TX project is assisted by undergraduate student Jackie Avila from Amarillo College. Associate Research Scientist Chenggen Chu also collaborates with this project. Smit has finished his course work and attended the WheatCAP workshop at UCD, Cornell and KSU. He also attended the online WheatCAP update meeting, T3 training series and soft skill development series.

Research Project: The target of the TAMU group is a major QTL for grain yield and kernel weight on chromosome arm 2BS (*Qgy.tamu.2BS*). This QTL is associated with peak markers *IWB4514* (152.9 Mb) and *IWB8143* (65.0 Mb), and explains up to 25% of the variation in grain yield and 19.5% of the variation in kernel weight. The TAMU group designed five new KASP primers based on the exome capture data, which were mapped to the expected positions. Combined with the previously developed five KASP from the 90K SNP array, these markers were used to reduce the *Qgy.tamu.2BS* candidate region from 37 Mb to 14 Mb.

Three F_7 HIFs were harvested and germinated to genotype and phenotype kernel weight in the greenhouse. Three KASP markers in the re-defined QTL region were used to screen additional 90 F_7 plants, and 11 recombination events between the flanking markers were identified.

Together with the four recombinant lines identified in the previous screen, these 15 recombinant lines will be used to define more precisely the candidate gene region.

In addition, the TAMU group initiated the genotypic and phenotypic characterization of other four mapping populations (TAM 112/TAM 111, TAM 112/Duster, TAM 111/TX05A001822, TAM 204/IBA) to determine if *Qgy.tamu.2BS* is also segregating in these populations. This information would be useful to determine the haplotypes associated with the *Qgy.tamu.2BS* alleles and to identify other major QTL for grain yield components.

The TAMU group harvested F_1 seeds from crosses between two homozygous for the positive *Qgy.tamu.2BS* allele with four high-biomass CIMMYT lines and seeds were germinated to generate BC_1F_1 (Table 1).

WA. Washington State University. Mike Pumphrey

Education: Graduate student Sam Prather started this summer in the first year of his PhD program. Even though the WSU team was not able to recruit a PhD student during the first year of the project, they were able to keep the project moving. Therefore, Sam will start with germplasm that is comparable to the other students. Sam will begin his research on the project by using markers to select near-isogenic lines polymorphic for the 4AL QTL for grain weight and number of grains per spike.

Research Project: The WSU team is focused on a strong QTL for kernel weight (LOD=6.5; R^2=11%) and kernel number (LOD=6.6; R^2=13%) 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, suggesting a negative correlation between the two traits. Marker analysis of the 4AL QTL region was performed using six KASP markers. Of the 190 Kelse x Scarlet RIL, two lines were identified as heterozygous for the 4AL region. These two lines were validated and used to create heterozygous inbred families (HIF). Four lines from each of the two HIF families were selected based on background homozygosity at non-target regions to speed up the process of creating isogenic lines at regions apart from the 4AL locus. For each HIF, 1000 seed will be planted (total 2,000 progeny) to screen for recombination events between the flanking markers.

The introgression of the 4AL QTL allele from Scarlett into CIMMYT lines carrying the Kelse allele was continued to the BC_2 generation. BC_2F_1 seed will be harvested shortly, advanced to the BC_2F_2 generation, and then markers will be used to select lines homozygous for the 4AL QTL alternative alleles to compare their effect in these CIMMYT lines.

Summary of WheatCAP varieties and germplasm releases

The WheatCAP group released 14 new commercial varieties and eight improved wheat germplasm (Appendix 1). Five varieties released in 2017 and reported as pending PVP in the 2017 WheatCAP report were assigned PVP in 2018 (Appendix 1). The spring wheat TCAP NAM population consisting of 2,400 RIL was deposited in the NSGC and four new RIL and doubled haploid populations were generated. The complete list of released varieties, germplasm and populations is presented in Appendix 1 at the end of this report.
https://www.triticeaecap.org/publications-and-germplasm/

Summary of WheatCAP publications

In 2018, WheatCAP participants published 47 peer-reviewed publication (plus 7 in press) 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. These 2018 publications were already cross-referenced 327 times in Google Scholar 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 11,207 cross-references in Google scholar, documenting the high-impact of the publications generated by this group.

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

Budget

The subcontracts for the second year for the 19 institutions was completed on time and the funding was available to all collaborators in early 2018. The 2018 financial report covers expenses up to July 31, 2018 so there are still 4.5 months of spending this year. The current spending is at 37% of the budget but, in reality, it is closer to 50%. This distortion is due to the forward funding received in year two, which is being saved for the fifth year of the project as originally planned.

There have been no changes in the budgets or original objectives. The budget of USDA-ARS Ithaca will continue to be transferred to Cornell University to provide T3 more flexibility and to simplify administration as approved last year for the complete duration of this grant. The only minor change in personnel was the retirement of Dr. Shiaoman Chao, who was in charge of the USDA-ARS small grains genotyping laboratory in Fargo, ND. Currently, Dr. Justin Faris is overseeing the laboratory. The scientist position was posted this past July and the interview and hiring process will be ongoing this fall to fill this position.

B. Prospectus – Plan of Work for Second Year

Education: In 2019, the Wheat-CAP students will host a Pioneer Symposia in San Diego, CA on January 11th, a day before the 2019 PAG conference begins. The topic of the Pioneer Symposia will be focused on how genomic technology is being used to increase yield. Jean-Luc Jannink is scheduled to host a workshop at Cornell University this upcoming summer that will be focused on database management, and he will introduce the students to new informatics tools being developed by the Genomic Open-source Breeding Informatics Initiative (GoBii) project. The soft skill training will continue in year three with Sarah Evanega leading another Science Communications workshop, and Loriana Sekarski continuing to lead the online soft skill course.

***T3*:** The T3 group will collaborate with that Edward Buckler lab and the Akhunov Lab in bringing the genome data storage and imputation method called PHG to wheat. Previously, the T3 team tested the 62 wheat-exome reference of Jordan et al. (2015) for imputation using Beagle4 (Browing & Browning, 2009). The collaboration with the Buckler lab will expand the reference set used for imputation and will facilitate the comparison of the two methods (Beagle4 and PHG). When new wheat lines are uploaded to T3 with genotype data of adequate density, they will be imputed. The imputed data will be available for download along with imputation statistics summarizing the reliability of imputed scores.

Internally, the imputed scores will be used for GWAS analyses. GWAS analyses using imputed scores will take the reliability of those scores into account, as advocated by Guan and Stephens (2008). To date, all T3 functions (e.g., clustering by genotype, genomic prediction, haplotype tracking), have been run on original genotypes. Genotype imputation will be initially most important for T3 for the GWAS function, and that will be implemented first. Later, users will have options for downloading imputed genotypes and for applying other functions using genotypes on imputed rather than original genotypes. Thus, imputed genotypes will be stored in parallel tables to the original genotypes, but functions will query the relevant tables, as requested by users.

The T3 team is developing a report to provide links from T3 to Knetminer / Wheat (http://knetminer.rothamsted.ac.uk/). The report will enable T3 users interested in a particular gene to explore knowledge on that gene culled from the literature and assembled into a network that helps identify if a the gene can be considered a likely candidate affecting a trait.

Ricardo Ramirez-Gonzalez of the Cristobal Uauy lab at John Innes in the UK is currently running analyses to design PCR primers for polymorphisms identified among Wheat CAP parents. Links to those primers will be made available through T3.

When the Akhunov Lab releases new data from either exome or regulatory capture assays, T3 will make those available through T3. Likewise, T3 will incorporate data from MNase and ATAC-Seq into new JBrowse tracks, giving users prior information on which variants are likely to be exposed to DNA regulatory and transcription machinery.

***Genomics Resources*:** In the next year, the KSU group will continue its focus on re-sequencing the regulatory regions of a diverse set of wheat lines using the newly designed capture assay for wheat promoter regions. They will compare chromatin accessibility profiles obtained using ATAC-seq and MNase approaches. Chromatin accessibility profiles for developing spikes and embryos of hexaploid wheat and their relationship to gene expression will be obtained.

The analyses of regulatory capture data generated for Wheat CAP parental lines and diversity panel will be completed and deposited into T3. The information about regulatory sequence variation will be integrated with gene expression, with a focus on candidate genes for the grain yield components targeted in this study.

To connect the expression and diversity data, RNA-seq profiling of developing spike tissues will be implemented across several wheat accessions in collaboration with KSU IGF. The KSU group will collaborate with the T3 team on the analyses of genetic diversity, chromatin accessibility and gene expression data and in the development of bioinformatics tools to facilitate the access of this data to users.

In collaboration with the genotyping laboratories, the KSU group will develop an updated rhAmpSeq assay. This assay will incorporate SNPs relevant for US breeding programs selected from the next-generation Practical Haplotype Graph (PHG) constructed using a representative sample of exome-captured data from 217 US wheat lines.

Plans for the cloning projects

AR: The AR group plans to evaluate homozygous individuals with and without the target QTL (++, --) in highly replicated field headrow trials using an augmented design with replicated check lines. Recombinant lines will be phenotyped for all major yield components, agronomic traits

and physiological traits. Data from exome capture will be used to target additional polymorphic markers within the delineated QTL regions. In addition, heterozygous individuals (+/-) will be identified for continued selfing to improve the isogenic background and move toward stage 2 of cloning. The AR group will continue the backcrossing effort into CIMMYT spring lines.

CA: In 2019, the CA group will focus on the validation of the candidate genes identified in 2018 high-density mapping projects. First, they will validate which of the four candidate genes identified in a 1.46 Mb region on chromosome 1BS is responsible for the observed differences in grain yield and root length. Second, they will validate a promising candidate gene for the plant height locus *Rht25* identified in a 4.3 Mb region on chromosome arm 6AS. Finally, they will validate the candidate genes identified for three QTL for number of spikelets per spike on chromosomes 7AL (0.86 Mb), 2BS (4.7 Mb) and 3AS (6.3 Mb). Validation activities will include a reduction of the candidate regions by screening larger segregating HIF populations, the characterization of mutants, and complementation experiments using transgenics.

To determine if the candidate genes are essential for the observed phenotypes, the CA group will screen the sequenced EMS mutant population for loss-of-function mutations in the A and B genome homoeologs of the candidate gene and they will then combine those mutations to generate complete loss-of-function mutants. If no loss-of-function mutations are identified, knock out mutations will be generated using CRISPR-Cas9. If feasible, CRIPR-Cas9 will be used to edit the same polymorphisms as the one observed in nature, to validate the causal polymorphisms. Finally, they will complement the phenotype in the mutant lines by transformation of the functional allele under its natural promoter.

CO: The CO team will characterize the interaction between the 6BL QTL and *VRN-D3*, *PPD-B1* and the 7AL QTL for spikelet number using the $F_{6:7}$ Platte/CO940610 RIL population. They will evaluate the effect of the 6BL QTL in eight $F_{5:6}$ HIFs representing each combination of *VRN-D3a/b*, *PPD-B1a/b*, and 7AL QTL alleles. In 2019, they will identify critical recombinants among the $F_{5:6}$ HIFs using KASP markers for high resolution mapping and perform RNA-seq to identify differentially expressed genes at two stages of spike development between HIF individuals divergent for the 6BL QTL. Finally, they will continue to backcross the 6BL QTL into advanced Colorado and CIMMYT high biomass lines.

***ID*:** In FY19, the *QSNS.ui-5A* and *QPTN.ui-6A* regions will be refined to less than one Mb by designing additional markers and screening larger populations (> 2000 plants) for additional recombination events. The backcrossing of the two QTL into CYMMIT high-biomass lines will be advanced to BC_{4-5}.

KS: A second year of yield trials of the Overley/Overland RIL population will be conducted in 2018-2019. Kernel size characteristics will be measured on the 2018 Manhattan trial. A greenhouse experiment to evaluate yield component characteristics will be conducted on $F_{4:5}$ NILs for the QTL region. Seed of $F_{3:4}$ NILs will be increased in Arizona for 2019-20 yield trials in the Great Plains. Recombinants will be identified and self-pollinated. A final cycle of crossing will be completed on most CIMMYT introgressions, and BC_3F_2 seed will be produced

MI: In 2019, the MI team will increase the HIFs in the field. Sufficient seed will be available to plant four replicates of each genotype in five locations. This is expected to generate sufficient information to generate a refined position of the 2DS grain yield QTL. The MI team will characterize recombinants across the 2DS region and add additional markers to dissect better the regions between markers. The targeted QTL confers up to a seven bushel per acre increase in

grain yield, but the yield components involved are currently unknown. Therefore, one of the objectives for 2019 is to determine which yield components are affected by the 2DS QTL. The traits to be evaluated in 2019 include photosynthetic parameters, spikelets per spike, tiller number, thousand kernel weight, number of kernels per spike, and kernel dimensions.

MN: Development of HIF families for *QTkw.mna-5B* will commence in fall 2018. Additional tasks related to *QTkw.mna-5B* include molecular marker development and QTL introgression into CIMMYT germplasm. In addition to the fine mapping of *QTkw.mna-5B,* the 14x111 and 15xR012 populations will be genotyped using GBS methods. Yield component data for both populations will be collected starting in late August 2018 using a MARVIN Seed Analyzer. Analysis and linkage mapping is expected to be complete by spring 2019 for 14x111. The 15xR012 population will be grown in three locations in 2019.

MT: KASP primers designed from exome capture will be used to fine map *QTn.mst-6B* using recombinant lines from three HIF families. Lines showing recombination in the critical region will be phenotyped in the greenhouse to identify recombinants between the markers and *QTn.mst-6B*. Protocols for RNA-sequencing experiments will be developed for existing NIL and potentially useful recombinants. Introgression of *QTn.mst-6B* into four CIMMYT lines will be completed. Data for the yield component QTL in durum wheat will be analyzed and tabulated in order to prepare a final manuscript.

NC: The NC group will publish the fine mapping of the *B1* locus and continue characterization of the candidate gene. They will obtain seed of mutant lines and initiate experiments to determine the effect of deletion of the *B1* suppressor on final awn length and kernel size. In addition, attempts at fine mapping the 6A QTL will continue. Heterozygous plants derived from MM RIL 58 will be grown to develop a large segregating population. In addition, HIF for other QTL regions will be identified in the LM population, including a 3A QTL with effects on spike characteristics. The exome capture database will be inspected for differences in the QTL regions and KASP assays developed for screening large populations.

ND: BC_3F_2 plants will be genotyped with flanking markers to identify recombinants within the QTL region. Then BC_3F_3 plants derived from heterozygous recombinant plants will be screened to identify homozygous recombinants and to fix the recombination event. These plants will be grown in the greenhouse next summer to determine phenotypes. Additionally, internal markers (STARP or KASP) within our target region will be developed using exome capture data and 90k SNP data previously obtained. The backcrossing of the selected QTL into the CIMMYT lines will be advanced, along with building a bridge for future hexaploid crosses if hybrid necrosis occurs when hybridizing across ploidy levels.

NY: The immediate goal is to correlate the 2018 SynOpDH and HIF field phenotypes with genotype scores from the newly developed KASP primers. This will help to decrease the number of HIFs per QTL and the number of head rows that will be planted during the 2019 field season. The upcoming data analysis will reduce the QTL candidate region to an adequate size for the identification of candidate genes. These candidates will be validated using mutant and transgenic approaches. A visiting scientist in the NY lab has been developing CRISPR transformations with Glenn and Medina wheat varieties and the *TaGW2* gene, and has been able to regenerate plants from callus with both wheat cultivars. The NY group will also continue advancing the backcrosses of the targeted alleles to generate BC_4 and BC_5 lines in the recurrent parents Tom,

Glenn and Opata, BC_2 and BC_3 in the CIMMYT high-biomass lines, and BC_1 and BC_2 in CIMMYT high yield lines.

OK: For the *QYld-osu-1B* region, the OK team will work on understanding the cause of low recombination in in the region. Recombination rates will be determined in the presence and absence of the *ph1b* mutation. For the spikelet number QTL on chromosome 7BL, they will phenotype and genotype 21 progeny plants that have recombination events in the 3 Mb candidate genomic region. They will characterize the allelic variation in candidate genes for the number of spikelets per spike and will validate them using transgenic wheat plants. For both QTL, they will develop molecular markers and introgress the QTL into CIMMIT wheat lines.

SD: The SD team goals for next year include the development of new KASP markers to saturate the QTL region and the generation of sufficient seeds of the recombinant lines in the greenhouse to be used in field trials in the fall of 2019. Additional objectives include the identification of additional recombinants from advanced generation, and the development of larger mapping populations for the 7DS QTL. Finally, the SD team will continue the backcrossing of the 7DS QTL in CIMMYT lines and local cultivars.

TX: More HIFs will be screened to find additional recombinants. Homozygous recombinant lines and non-recombinant lines will be developed and confirmed with KASP markers. Seed will be increased to test them in the greenhouse for grain yield and kernel weight. Genotyping will be conducted between two parents and bulk to find polymorphic markers for the distal region of the QTL. The TX team will continue the backcrossing of *Qgy.tamu.2BS* to the selected CIMMYT lines.

WA: 2,000 lines from the two HIF will be screened with KASP markers associated with the 4AL QTL to identify near-isogenic lines with recombination events in the target region. These lines will then be planted and screened in the field in the spring of 2019, and data will be collected on spike length, kernels per spike, and kernel weight to begin estimating the effect of the QTL region. Backcross introgression of the Scarlet 4AL alleles into CIMMYT germplasm will be completed.

C. Deliverables & Other Outputs:

- **Table 1**. BC in CIMMYT and local lines
- **Appendix 1.** Germplasm releases https://www.triticeaecap.org/publications-and-germplasm/
- **Appendix 2**. Publications https://www.triticeaecap.org/publications-and-germplasm/
- **Appendix 3**. Community resources
- **Appendix 4.** Graduate students. https://www.triticeaecap.org/educational-activities/

D. Concluding remarks

The 2018 year has been very productive to the WheatCAP that resulted in new knowledge (54 peer-reviewed publications) and improved wheat varieties (14) and germplasm (8) with increased yield, resistant to pathogens and/or improved quality. The improved disease resistance of the new varieties to pathogens will reduce the applications of fungicides benefiting directly 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.

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

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

Table 1. Traits, QTL, donor alleles, CIMMYT recurrent parents and status of crosses.

State	Trait	QTL/Gene	Donor allele	CIMMYT Background [1]	Status
AR	Yield	1A (IWA7173)	AGS 2000	4 HY CIMMYT lines	BC_1
	Yield	6B (IWA755, IWA6428)	AGS 2000	9 HY CIMMYT lines	BC_1
CA	Spikelet No.	7AL 670-680 Mb[2]	Berkut	HB (GID 3855011, 4314513, 4878563)	BC_4
	Spikelet No.	$1A^mL$. *Elf3 =Eps-A^m1*	*T. monococcum*	Kingbird / 5 HB CIMMYT	BC_4/BC_2
	Grain Size	6AL *gw-A2*	EMS mutant	Kingbird / 5 HB CIMMYT	BC_4/BC_2
	Combined	*Eps-A^m1 + gw-A2*	Same as above	Cirno, Kronos, GID 6420253	BC_4F_2
CO	Kernel weight	6BL 493-503 Mb	Platte	5 HB CIMMYT / CO13D1383	F_1
	Spikelet No	7AL 670-680 Mb	Platte	5 HB CIMMYT / CO13D1383	F_1
ID	Spikelet No.	5AL 631-643 Mb	UI Platinum	4 HB CIMMYT	BC_3
	Productive tillers	6A 91-198 Mb	Capstone	4 HB CIMMYT	BC_3
KS	Yield & diseases	2DL QTL, *Sr57/Yr40,* 2NS	KS11WGGRC53-O	11 HY/HB	BC_2
MI	Yield	2DS 22.1-29.5Mb	KS05HW14	Kingbird & Heilo	BC_1F_1
MN	Grain size	5BS *QTkw.mna-5B*	MN99394-1	HB (3855011, …13, ...63, ...69)	BC_2F_2
MT	Productive tillers	6B *QTn.mst-6B* 150Mb	Reeder	HB (GID 3613474)	BC_2
NC	Grain weight	6A	Massey	HY/HB	F_1
	Awns	5A, *B1* awn suppressor	Multiple	HY/HB	F_1
ND	Grain wgt./spike	2BL *QGws.fcu-2B*	Ben	Kingbird, GID4878569, 4577963, 3613474.	F_1/BC_1
NY	Grain wgt./width	5AL (66 cM)	Opata	6 HY/ HB CIMMYT, Tom, Glenn	$BC_{1\text{-}2}$
	Grain length	5BL1 (40.5 cM)	Synthetic W9784	6 HY/ HB CIMMYT, Tom, Glenn	$BC_{1\text{-}2}$
OK	Yield	*QYld.osu*-1B (25 Mb reg.)	Duster	HY/ HB CIMMYT	F_1
	Spikelet No.	7BL, 650-700 Mb	CItr17600 (L20)	HY/ HB CIMMYT	F_1
SD	Yield	7DS, 6-16 Mb	*Ae. tauschii* TA1615	Kingbird, GID4314513,3613474, Ideal	F_1
TX	Grain weight	2BS, 65.5 Mb	TAM 111	4 HB CIMMYT	F_1 /BC_1
WA	Grain No/weight	4AL	Scarlett grain wgt.	HB CIMMYT[3]	BC_2

[1] CIMMYT recurrent parents for high biomass =HB and for high yield =HY.

[2] Coordinates are from the new released reference genome IWGS RefSeq v1.0

[3] Scarlett carries the positive allele for grain weight and Kelese the positive allele for grain number. The CIMMYT lines have the Kelese allele.

APPENDIX 1. Varieties and Germplasm releases 2018.
https://www.triticeaecap.org/publications-and-germplasm/

The economic impact of the WheatCAP and TCAP public wheat varieties is described in Appendix 5.

Variety releases with PVP

1. UC-Lassik-RS is a hard red spring variety with five *sbeII* mutations that result in a 42-53% increase in amylose and 880-905% increase in resistant starch. UC-Lassik-RS performs well agronomically in Sacramento, San Joaquin and Imperial valleys of California and has good breadmaking quality characteristics. PVP application 201800070 (11/22/2017).

2. UC-Patwin-RS is a hard white spring variety with five *sbeII* mutations that result in a 69-77% increase in amylose and 1034-1102% increase in resistant starch. UC-Patwin-RS has excellent breadmaking quality characteristics and high yield potential in the San Joaquin and Imperial valleys of California. PVP application 201800058 (11/22/2017).

3. UC-Desert King-RS is a Desert Durum® variety with four *sbeII* mutations and a 41-58% increase in amylose and 900% increase in resistant starch. UC-Desert King-RS showed a 55% reduction in cadmium content in the grain and excellent pasta quality. PVP application 201800069 (11/22/2017).

Variety releases with pending PVP

4. Desert Gold is a Desert Durum® variety with reduced cadmium (*Cdu1* gene), increase yellow pigment (two QTL for semolina yellow pigment) and color stability (*lpxB1.1* mutation) and increased gluten strengths. It showed very high grain yield in the San Joaquin and Imperial Valleys and excellent pasta quality. PVP submission pending.

5. Central Red is a hard red spring wheat variety with one of the highest yields in the Sacramento and San Joaquin valleys and excellent breadmaking quality. It was selected with molecular markers for s resistance gene *Yr15* effective against stripe rust, strong gluten allele *Glu-D1d*, and the 2NS/2AS translocation from *Aegilops ventricosa.* PVP submission pending.

6. 'Showdown' (OK12716) hard red winter wheat (PVP application pending), developed by the Oklahoma Agricultural Experimental Station, will be targeted for statewide adoption with improved yield potential, stripe rust resistance, Hessian fly resistance, and test weight over the recently released HRW cultivar, Bentley.

7. 'Green Hammer' (OK13209) hard red winter wheat (PVP application pending), developed by the Oklahoma Agricultural Experimental Station, has a more limited target region, specifically southwest, central, and north central Oklahoma, with elevated grain protein content, superior test weight, and exceptional protection against leaf rust and stripe rust. Yield responses to fungicide treatments in OSU variety trials have routinely been neutral.

8. 'Baker's Ann' (OK13621) hard red winter wheat (PVP application pending), developed by the Oklahoma Agricultural Experimental Station, will be intended solely for contracted production and direct shipment to end-users with a need for elevated dough strength in the HRW class.

9. 'Skydance (OK13625) hard red winter wheat (PVP application pending), developed by the Oklahoma Agricultural Experimental Station, will be targeted to those environments which may transiently lack for soil-available nitrogen, combined with broad and effective foliar disease resistance and exceptional milling and baking quality. An apparently higher nitrogen-use efficiency level was discovered from research at Tipton, OK originating from a previous CAP project emphasizing this trait in collaboration with UN-L.

10. ‘KS Venada’ (PVP application pending) is a hard white winter wheat cultivar developed by the Kansas State University. It has competitive yield in central Kansas and good disease package with improved straw strength and pre-harvest sprouting tolerance. PVP pending.

11. ‘Purl’ 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. PVP pending.

12. ‘Breck’ (CO12D2011), a hard white winter wheat, released fall 2017. Markers for *Glu-B1al* (HMWG Bx7oe+8), *Glu-D1d* (HMWG 5+10), PHS3AS, *Lr24*/*Sr24*, and *Lr37*/*Yr17* confirmed by USDA genotyping lab in Manhattan KS.

13. ‘Incline AX’ (CO14A065), hard red CoAXium winter wheat, released fall 2017. The first wheat variety released compatible with the CoAXium wheat production system. Markers for *Lr46* and *Glu-D1a* (HMWG 2+12) confirmed by USDA genotyping lab in Manhattan KS.

14. ‘Whitetail’ is a new soft white winter wheat variety release through Michigan Crop Improvement Association.

Varieties with pending PVP in 2017 report that received PVP in 2018

1. ‘Smith’s Gold’ (PVP201800136, 1/24/2018) is a hard red winter wheat cultivar developed by the Oklahoma Agricultural Experimental Station and designated as a potential replacement for ‘Gallagher’ with improved stripe rust resistance and baking quality.

2. ‘Spirit Rider’ (PVP201800137, 1/24/2018) is a hard red winter wheat cultivar developed by the Oklahoma Agricultural Experimental Station with elevated total dietary fiber in the grain and was selected with the aid of DNA marker assays for *Lr34* and *Rht8*. It was also found to carry the *Wx-B1b* allele, and it apparently has gene(s) conferring strong acid-soil tolerance different from *ALMT1*.

3. ‘Lonerider’ (PVP201800135, 1/24/2018) is a hard red winter wheat cultivar developed by the Oklahoma Agricultural Experimental Station with unusually broad adaptation to the southern and central Plains. Critical to its release was using marker assays to select for the absence of 1RS and presence of *Glu-D1d* in a genetic background prone to weaker gluten.

4. ‘Lang-MN’ (PVP201800165, 3/8/2018) is a hard red spring variety released by the MN wheat-breeding program in 2017. Lang-MN has competitive grain yields, high grain protein. Lang-MN has good resistance to Fusarium head blight, leaf rust, stripe rust, and bacterial leaf streak.

5. ‘Thompson’ (PVP 201800429, 8/22/2018) is a HRS wheat released by SDSU that has an excellent combination of high yield and disease resistance. Thompson has medium height and medium maturity with average protein content, test weight and grain quality. It is moderately resistant to leaf rust, stem rust and FHB.

Germplasm releases

1. Induced mutant *RHT-B1*$_{E529K}$ (PI 687144) confers reduced height by partially suppressing the semi-dwarf phenotype of *Rht-B1b*. This mutation is also associated with length increases in coleoptiles, seedling shoots, and stem internodes relative to the *Rht-B1b* allele

2. KS05HW14 is a hard white winter experimental line developed by the Kansas State University. It has good crossability with *Aegilops tauschii*, a very important genetic resource that could contribute various traits of agronomic importance for wheat.

3. Six winter wheat germplasm from CSU: Snowmass 2.0, Canvas, Whistler, Monarch, Byrd CL Plus and Crescent AX.

Population releases

1. The spring wheat TCAP NAM population consisting of 2400 RIL was deposited in the NSGC.

2. South Dakota State University. RIL population SD52/SD1001, 92 F_5 RILs, genotyped by GBS SNPs and evaluated for Bacterial Leaf Streak resistance.

3. South Dakota State University. RIL population 2 - Lyman/Emerson, 92 F_5 RILs for FHB resistance, will be genotyped soon.

4. A doubled haploid population (140 DH lines) from the cross between UC-Lassik-RS c UC-Patwin-RS, two lines that share loss-of-function mutations in five of the *sbeII* genes. Developed by the University of California, Davis was genotyped with the 90K Illumina. Assay in the ND genotyping laboratory. The objective is to identify loci that help ameliorate yield penalties in line with increased levels of amylose and resistant starch.

5. CO960293-2/TAM 111 mapping population with 217 RILs developed by Drs. Shuyu Liu and Jackie Rudd from Texas A&M. A QTL for yield on chromosome 2B and a QTL for TKW have been already identified.

APPENDIX 2. Peer reviewed publications WheatCAP 2018. 47 published + 7 in press (total 54).

- https://www.triticeaecap.org/publications-and-germplasm/
- 2017 WheatCAP publications cross-referenced in Google Scholar 327 times.
- 2011-2016 TCAP publications cross-referenced in Google Scholar 11,207 times

1. Anderson, J.A., J.J. Wiersma, G.L. Linkert, S. Reynolds, J.A. Kolmer, Y. Jin, M. Rouse, R. Dill-Macky, G.A. Hareland, and J.-B. Ohm. 2018. Registration of 'Norden' hard red spring wheat. J. Plant Registrations. 12:90–96.

2. Anderson, J.A., J.J. Wiersma, G.L. Linkert, S. Reynolds, J.A. Kolmer, Y. Jin, M. Rouse, R. Dill-Macky, G.A. Hareland, and J.-B. Ohm. 2018. Registration of 'Linkert' spring wheat with good straw strength and adult plant resistance to the Ug99 family of stem rust races. J. Plant Registrations 12:208–214.

3. Anderson, J.A., J.J. Wiersma, G.L. Linkert, S. Reynolds, J.A. Kolmer, Y. Jin, M. Rouse, R. Dill-Macky, G.A. Hareland, and J.-B. Ohm. 2018. Registration of 'Bolles' hard red spring wheat with high grain protein concentration and superior baking quality. J. Plant Registrations 12:215-221.

4. Ando, K., S. Rynearson, K. T. Muleta, J. Gedamu, B, Girma, N. Bosque-Pérez, M. S. Chen, M. O. Pumphrey. 2018. Genome-Wide Associations for Multiple Pest Resistances in a Northwestern United States Elite Spring Wheat Panel. Plos One 13: e0191305.

5. Ayana GT, Ali S, Sidhu JS, Gonzalez Hernandez JL, Turnipseed B and Sehgal SK (2018) Genome-wide association study for spot blotch resistance in hard winter wheat. *Front. Plant Sci*. 9:926. *doi:10.3389/fpls.2018.00926*.

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10. Chen, S., Y. Guo, J. Briggs, F. Dubach, S. Chao, W. Zhang, M.N. Rouse, J. Dubcovsky. 2018. Mapping and characterization of wheat stem rust resistance genes *SrTm5* and *Sr60* from *Triticum monococcum* Theor. Appl. Genet. 131: 625-635.

11. Chen, S., W. Zhang, S. Bolus, M.N. Rouse, J. Dubcovsky. 2018. Identification and characterization of wheat stem rust resistance gene *Sr21* effective against the Ug99 race group. PLOS Genetics. 14: e1007287.

12. Cook, J.; Heo, H.-Y. Varella, A., Lanning, S., Blake, N, Sherman, J. D, Martin, J., See, D. R, Chao, S., L. Talbert. 2018. Evaluation of a QTL mapping population comprised of hard red spring and winter wheat alleles using various marker platforms. Crop Sci. 58:701-712.

13. Dong H, R. Wang, Y. Yuan, J. Anderson, M. Pumphrey, Z. Zhang, J. Chen. 2018. Evaluation of the potential for genomic selection to improve spring wheat resistance to Fusarium head blight in the Pacific Northwest. Frontiers in Plant Science. 9: 911.

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15. Elbasyoni I.S., A.J. Lorenz, M. Guttieri, K. Frels, P.S. Baenziger, J. Poland, E. Akhunov. 2018. A comparison between genotyping-by-sequencing and array-based scoring of SNPs for genomic prediction accuracy in winter wheat. Plant Sci. 270:123-130.

16. El-Feki, W.M., P.F. Byrne, S.D. Reid, and S.D. Haley. 2018. Mapping quantitative trait loci for agronomic traits in winter wheat under different soil moisture levels. Agronomy 8: 133.

17. Frels, K., M. Guttieri, B. Joyce, B. Leavitt, P.S. Baenziger. 2018. Evaluating canopy spectral reflectance indices to estimate nitrogen use traits in hard winter wheat. Field Crops Research 217:82. *DOI : 10.1016/j.fcr.2017.12.004*

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APPENDIX 3. Community resources generated

2018 Public databases

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

2. Sequenced mutant populations https://dubcovskylab.ucdavis.edu/wheat_blast

2017 Mapping Populations

The spring wheat TCAP NAM population consisting of 2400 RIL was deposited in the NSGC.

Drs. Jianli Chen and Daolin Fu from the University of Idaho developed tilling populations in UI Platinum and Brundage and screened the population for spike phenotypes.

Dr. Dubcovsky from UC Davis distributed the sequenced TILLING population of Kronos (110 samples to 15 laboratories in 2018).

APPENDIX 4. Graduate students

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

Institution	Last Name	First Name	Degree	Gender	Start Date – Graduation*
University of Arkansas	Dylan	Larkin	PhD	M	9/1/2017
	Winn	Zachary	MS	M	8/21/2017
University of California-Davis	Kuzay	Saarah	PhD	F	9/1/2016
	Glenn	Priscilla	PhD	F	9/1/2017
	Mo	Youngjun	PhD	M	9/1/2014 - 5/1/2018*
Colorado State University	Katz	Andrew	PhD	M	8/21/2017
University of Idaho	Isham	Kyle	MS	M	1/1/2018
	Johnson	Katrina	MS	F	8/1/2017
USDA-Kansas State University	Mustahsan	Wardah	PhD	F	6/1/2018
	Xu	Yuzhou	PhD	M	8/1/2017
Kansas State University	Qianli	Pan	MS	F	9/1/2016
	Adhikari	Elina	PhD	F	9/1/2017
Michigan State University	Turkus	Jonathan	PhD	M	5/22/2017
University of Minnesota	Fraser	Max	PhD	M	7/1/2017
Montana State University	Brewer	Brittaney	PhD	F	9/1/2016
USDA-N. Carolina State Univ.	Lauer	Eddie	MS	M	12/1/2016 - 12/31/17*
	Dewitt	Noah	PhD	M	1/1/2018
North Dakota State University	Peters	Amanda	PhD	F	6/1/2017
Cornell University	Taagen	Ellie	PhD	F	6/12/2017
	Santantonio	Nicholas	PhD	M	8/1/2013 – 8/31/2018*
Oklahoma State University	Kan	Forrest	PhD	M	9/1/2016
	Zhang	Xiaoyu	PhD	M	7/1/2017
South Dakota State University	Halder	Jyotirmoy	PhD	F	8/22/2017
Texas A&M	Dhakal	Smit	PhD	M	9/1/2014
Washington State University	Prather	Sam	PhD	M	6/1/2018

APPENDIX 5
Economic impact report of WheatCAP, TCAP and USDA-ARS genotyping labs

Economic impact of public wheat varieties in 2017: $ 4.3 billion/year

Wheat ranks third among U.S. field crops in planted acreage, production and gross farm receipts, behind corn and soybeans. In 2015, 21 million full- and part-time jobs were related to the agricultural and food sectors (11.1 % of total U.S. employment). Wheat is an important component of the economic contribution of agriculture to the US economy. In 2017, 46 million acres of wheat were planted in the US, resulting in production valued at $ 8.14 billion dollars (USDA-NASS 2017 statistics).

To study the contribution of the public wheat breeding programs, we completed a survey that includes wheat planted acreage and production value for 34 states, covering 98.4% of the US wheat acreage (Appendix I). Based on this survey, public varieties accounted for 56.9% of the 2017 wheat acreage and contributed $ 4.3 billion in value of production. These numbers document the importance of the public wheat breeding programs to the US economy.

The public wheat breeding programs are an example of a successful collaboration between the private and public sectors. Growers provide funding for the core breeding activities and USDA provides support to these activities through the NIFA-USDA CAP grants and the USDA-ARS high-throughput genotyping laboratories and quality laboratories.

The $4.3-billion value of the wheat produced from public wheat varieties is amplified several times through the milling and baking industries, which contribute additional jobs and value to the economy. In 2017, the Bureau of Labor Statistics reported 210,000 jobs in bakeries and tortilla manufacturing, 291,000 in retail bakeries and 60,140 in milling (including grains and oil seeds) https://www.bls.gov/cps/cpsaat18b.htm. Another amplification factor of the value of the public wheat varieties is their frequent use by private breeding companies in their crosses, which transfers part of their value to the private sector and multiplies the economic benefits from the public breeding activities.

Public varieties yield additional economic benefits through their improved disease resistance and quality, but those are difficult to quantify. The use of molecular markers has enabled breeders to pyramid multiple resistance genes improving resistance durability and minimizing the use of pesticides and potential negative impacts on people and the environment. In addition, the ability of the public sector to emphasize socially desirable quality and nutritional traits for which the market may provide limited economic incentives, provides a more desirable and nutritive product to US consumers and improves the value of US wheat internationally. We include at the end of this report a letter from the National Association of Wheat Growers documenting the value of the WheatCAP research and training for US wheat growers.

Impact of CAP projects on production values of wheat varieties

The genetic information and molecular assays generated by the WheatCAP projects and USDA-ARS genotyping labs during the past 10 years have become an essential part of the breeding efforts in most public wheat breeding programs in the US. This is documented by the increase in the proportion of planted wheat varieties that benefited from these technologies. In 2012, roughly 20% of the US wheat acreage included varieties that benefited from marker technologies

provided by WheatCAP and USDA-ARS genotyping labs (2013 Economic Impact report TCAP). This percentage doubled in 2017, and represented 41% of the wheat acreage planted in the USA ($3.1 billion in direct production value). In 2017, 72% of the public varieties benefited in some degree from the support provided by the WheatCAP and USDA-ARS genotyping labs.

To estimate how much of the $3.1 billion value of those varieties was added by the WheatCAP and USDA-ARS genotyping labs, we made the following assumptions:

1) If a variety is grown commercially there must be a perceived increased value compared to other available varieties. Thus, we assumed that the currently grown varieties developed by these projects have at least a 5% advantage in production values to justify the grower's decision to buy seed for a new variety. Therefore, we calculated first the 5% of the production value of the public varieties that benefited for the WheatCAP-genotyping labs support (5% of 3.1 billion= $156.6 million).

2) Public wheat varieties differ in the proportion of funds received for their development from WheatCAP and local growers' support. A survey including CA, KS, MT, ND, OK, and TX showed that the funding provided by the WheatCAP (direct costs) and USDA-ARS genotyping labs represented between 20% and 40% of the combined funding received by these public wheat breeding programs in 2017. To be conservative, we estimated that 10% of the variety development cost was contributed by the support of the current and past CAP and the USDA-ARS genotyping labs. Therefore, we applied this 10% to the $156.6 million, resulting in an estimated $15.7 million value added by the USDA funding support.

The estimated $15.7 million return is roughly 2.3-fold the amount provided in 2017 by USDA-NIFA to the WheatCAP and five satellite IWYP (International Wheat Yield Partnership initiative) projects (~$3.5 million) and by USDA-ARS to the genotyping labs (~$3.2 million). This positive return should be consider with caution because the 5% and 10% estimates used in the calculations are speculative. However, this result is consistent with previous studies. For example, Hurley et al. (2016) reported an estimated return to research and development investments in wheat to be on average 47.4% per year (based on 221 studies).

The returns on the investments in the WheatCAP, TCAP and genotyping labs are complicated by the different contributions of research, extension and breeding investments to the development of specific public wheat varieties, and by the long time it takes for breeding investments to materialize in economic returns. However, the exact return rate of these particular projects does not affect the fact that the public wheat varieties contributed $4.3 billion production value to the US economy in 2017.

Economic impact of the information and technological tools generated by WheatCAP and USDA-ARS genotyping labs

In addition to the value captured directly through production using the public wheat varieties, additional value is generated by the transfer of improved public varieties to the private sector to be used as parents for their crosses and by technology transfer. The maps, marker information, and marker technological developments (ISelect 9K and 92K chips, exome capture platforms, maps, etc.) are actively used by the wheat breeding programs in the US private sector. Many private companies use markers developed by the public sector, and some use the USDA marker labs. For example, most wheat breeding private companies in the USA have requested the KASP

assays developed by the USDA-ARS genotyping laboratory located at Raleigh, NC. Private companies also use the MASWheat site for MAS protocols. Many "private" varieties actually originate from public institutions (e.g. Purdue University and the University of Illinois release most varieties for licensing to private companies). The genes and linked markers identified by the WheatCAP and the genotyping labs accelerates the deployment of useful traits into the breeding programs. The WheatCAP grants have been transformative for the wheat breeding enterprise in the USA by generating marker densities and imputation strategies that have made genomic selection possible in several wheat breeding programs.

In summary, the WheatCAP and USDA-ARS genotyping labs wheat varieties and research results serve well the entire US wheat industry as indicated at the end of this report by a positive support letter from the National Association of Wheat Growers.

Economic impact of the training provided by the CAP grants

In addition to the wheat varieties and technological developments, the WheatCAP projects have made a significant contribution to train the next generation of plant breeders. The previous decade has witnessed limited training opportunities for students interested in plant breeding, and has resulted in a shortage of plant breeders nation-wide. The wheat breeding programs represent one of the last reservoirs of active breeding programs in the public sector to provide hands on training to the students. Previous and current WheatCAP projects have supported the training of multiple graduate and undergraduate students and postdocs (Appendix 2). The CAP grants have also provided training opportunities by providing seminars, workshops and online courses.

The value of this training is documented by the demand of industry for the students trained by the WheatCAP projects, which have been rapidly incorporated into different breeding industries in the US and abroad. To document this impact, we performed a survey of the jobs filled by the people trained during previous WheatCAP projects (Appendix 2). Among the 168 individuals trained in the WheatCAP and TCAP projects, 79% work in the US and 21% abroad, 60% are males and 40% female, and 49% work in academic or government positions and 51% in the private sector. This data confirm the large and balanced contribution of the WheatCAP projects to train the people required by the public and private sector in the agriculture and food sectors.

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Appendix I. Acreage and production from wheat public varieties supported by WheatCAP and USDA-ARS genotyping labs

State	Acres Planted	Public var. ac planted	%	Ac public var. suppoted by CAP & genotyping labs	%	Production in $	$ Production Public Varieties	$ Production supported by CAP & Genotyping labs
ALABAMA	150,000	62,400	41.6%	62400	41.6%	35,420,000	14,734,720	14,734,720
ARIZONA	115,000	37,500	32.6%	37,500	32.6%	72,912,000	23,775,652	23,775,652
ARKANSAS	200,000	65,400	32.7%	65400	32.7%	28,600,000	9,352,200	9,352,200
CALIFORNIA	420,000	175,560	41.8%	124,740	29.7%	67,854,000	28,362,972	20,152,638
COLORADO	2,260,000	2,000,100	88.5%	2,000,100	88.5%	328,529,000	290,748,165	290,748,165
DELAWARE	75,000					22,918,000		
FLORIDA	20,000	18,000	90.0%	18,000	90.0%	2,072,000	1,864,800	1,864,800
GEORGIA	160,000	128,000	80.0%	128,000	80.0%	13,489,000	10,791,200	
IDAHO	1,165,000	435,710	37.4%	388,295	33.3%	415,657,000	155,455,718	138,538,478
ILLINOIS	500,000	125,000	25.0%	125,000	25.0%	162,526,000	40,631,500	40,631,500
INDIANA	290,000	156,600	54.0%	156,600	54.0%	84,360,000	45,554,400	45,554,400
IOWA	16,000					2,067,000		
KANSAS	7,600,000	3,868,400	50.9%	3,245,200	42.7%	1,334,400,000	679,209,600	569,788,800
KENTUCKY	480,000	100,800	21.0%	100,800	21.0%	109,802,000	23,058,420	23,058,420
LOUISIANA	20,000	16,000	80.0%	16000	80.0%	2,512,000	2,009,600	2,009,600
MARYLAND	410,000	164,000	40.0%	102,500	25.0%	60,421,000	24,168,400	15,105,250
MICHIGAN	480,000	229,800	47.9%	181,000	37.7%	151,088,000	72,333,380	56,972,767
MINNESOTA	1,170,000	698,490	59.7%	667,756	57.1%	436,548,000	260,619,156	249,151,913
MISSISSIPPI	45,000	12,420	27.6%	12420	27.6%	6,018,000	1,660,968	1,660,968
MISSOURI	640,000	161920	25.3%	161920	25.3%	161,568,000	40,876,704	40,876,704
MONTANA	5,140,000	3,727,000	72.5%	1,285,000	25.0%	674,243,000	488,891,763	168,560,750
NEBRASKA	1,120,000	840,000	75.0%	756,000	67.5%	185,334,000	139,000,500	125,100,450
NEVADA	29,000					4,925,000		
NEW JERSEY	23,000					5,005,000		
NEW MEXICO	330,000					17,010,000		
NEW YORK	140,000	42,000	30%	42,000	30%	38,106,000	11,431,800	11,431,800
NORTH CAROLINA	450,000	148,500	33.0%	148,500	33.0%	95,906,000	31,648,980	31,648,980
NORTH DAKOTA	6,680,000	3,392,310	50.8%	2,105,000	31.5%	1,384,140,000	702,908,977	436,169,865
OHIO	460,000	69,000	15.0%	69,000	15.0%	157,731,000	23,659,650	23,659,650
OKLAHOMA	4,500,000	3,690,000	82.0%	3,240,000	72.0%	379,610,000	311,280,200	273,319,200
OREGON	775,000	523,900	67.6%	514,600	66.4%	238,654,000	161,330,104	158,466,256
PENNSYLVANIA	210,000	63,000	30.0%			56,700,000	17,010,000	
SOUTH CAROLINA	90,000	18,000	20.0%	18,000	20.0%	15,986,000	3,197,200	3,197,200
SOUTH DAKOTA	1,887,000	1,175,601	62.3%	1,175,601	62.3%	233,464,000	145,448,072	145,448,072
TENNESSEE	370,000	50,000	13.5%	0	0	87,588,000	11,836,216	0
TEXAS	4,700,000	2,270,100	48.3%	1,175,000	25.0%	255,563,000	123,436,929	63,890,750
UTAH	134,000					28,954,000		
VIRGINIA	210,000	31,500	15.0%	31,500	15.0%	44,979,000	6,746,850	6,746,850
WASHINGTON	2,195,000	1,212,200	55.2%	420,000	19.1%	680,266,000	375,680,385	130,164,793
WEST VIRGINIA	8,000					1,297,000		
WISCONSIN	210,000	44,100	21.0%	44,100	21.0%	46,818,000	9,831,780	9,831,780
WYOMING	135,000					11,025,000		
TOTAL	**46,012,000**	**25,753,311**	**56.9%**	**18,818,908**	**40.9%**	**8,142,065,000**	**4,288,546,961**	**3,131,613,371**

Appendix 2. Current positions of people trained during previous WheatCAP and TCAP projects. Total 168.

- 79% working in US and 21% working abroad
- 49% working in academia and government, versus 51% in private industry
- 60% male and 40% female

State	Trainee	Current position
AR	Dennis Lozada	Postdoc at Washington State University
CA	Malena Faricelli	Pioneer USA
CA	Iago Hale	Professor at the University of New Hampshire
CA	Juan Carlos Brevis	Onion Breeder Bayer
CA	Cristobal Uauy	Project Leader at the John Innes Centre, UK
CA	Kati Wu	Amyris Biotechnologies Associate scientist
CA	Marco Maccaferri	Researcher University of Bologna
CA	Juan Sanchez	Monsanto
CA	Eligio Bossolini	Bayer Europe
CA	Rebeca Turner	Onion Breeder Bayer
CA	Tyson Howell	Molecular Breeder Bayer
CA	Nicolas Cobo	Strawberry breeder UCD
CA	Josh Hegarty	Triticale breeder UCD
CA	Brittany Hazard	Project Leader Institute of Food Research, UK
CA	Youngjun Mo	Researcher in NICS Korea
CO	Kelsey Salvo	U.S. Peace Corps, Senegal
CO	Jessica Davis	USDA, Pullman
CO	Elizabeth Bloetvogel	Eurofins STA Labs, Longmont, CO
CO	Beth Econopouly	Gates Foundation, Seattle
CO	Erena Edae	USDA-ARS, Manhattan, KS
CO	Anna Pranger	Syngenta, Longmont, CO
CO	Annie Heiliger	Cargill, Fort Collins, CO
CO	Shusong Zheng	Academy of Sciences, Beijing
CO	Wahid El-Feki	University of Alexandria, Egypt
CO	Melaku Mekonnen	Syngenta, Junction City, KS
CO	Joshua Butler	Busch Agricultural Resources
CO	Sally Clayshulte	Bayer Crop Science
CO	Ben Beyer	Advanta US
CO	Jennifer Andeway	Monsanto
CO	Victoria Valdez	Colorado State Univ.
CO	Karla Rippe	Pioneer
CO	Nelson Hevner	Monsanto
CO	Steve Becker	Corn breeder, Beck's Hybrids
CO	Hung Dao	Agricultural Hi-Tech Park, Vietnam
CO	Grogan Sarah	Bayer Biologics
CO	Melaku Mekonnen	Syngenta lettuce breeder, CA

CO	Erena Edea	Research Associate Univ. of Minnesota, St. Paul
CO	Jessica Moore (Cooper)	GS specialist at Cargill Specialty Oils, Fort Colins, CO
CO	Wahid Awad	Professor Cairo Univ. Egypt / CILcare (French company)
CO	Susan Latshaw	BASF, wheat breeder
IA	Shenqiang Zhong	Monsanto
IA	Elliot Heffner	Pioneer Hibred Intl.
IA	Yi Jia	Dow Agrosciences
IA	Aaron Lorenz	Associate Professor, University of Minnesota
IA	Jesse Poland	Professor, Kansas State Univ., Manhattan, KS
IA	Victoria Blake	Geneticist, USDA-ARS, Albany, CA
IA	Deniz Akdemir	Postdoctoral Fellow, Cornell University, Ithaca, NY
IA	Martha Hamblin	Senior Research Associate, Cornell University, Ithaca, NY
ID	Reuben Mclean	Production manager at Pendleton Flour Mill, Blackfoot, ID
ID	Maqsood Rehman	DowAgscience, leader Soybean breeding for North America
ID	Mackenzie Ellison	DowAgscience wheat breeding Pullman, WA. Research tech
ID	Justin Wheeler	Support scientist at University of Idaho
ID	Junli Zhang	Project Scientist, University of California, Davis
ID	Ping Li	Assistant Professor, Huazhong Agric. Univ. Wuhan, China
ID	Brian Bowman	Sweet corn breeder, HM Clause USA
ID	Yuxiu Liu	Assistant Professor, Northwest A&F Univ. China
KS	Xiaofei Wang	Bioinformatician University of Kansas
KS	Shubing Liu	Research Scientist in KSU
KS	Amy Bernardo	Research Scientist in KSU
KS	Irazema Fuentes-Bueno	USDA-ARS, Manhattan, KS as technician
KS	Jin Cai	Jiangsu Academy of Agricultural Science in China
KS	Meng Lin	Postdoc Cornell Univ.
KS	Yue Lu	Postdoc in Yangzhou Univ. China
KS	Fatima Nosheen	Professor Nat. Univ. of Science and Technology, Pakistan
KY	Lloyd May	Monsanto
KY	Beiyan Zeng	Monsanto
KY	Virginia Verges	Don Mario Seeds
KY	Andres Agostinelli	Limagrain
KY	Ana Balut	Monsanto Argentina
KY	Carrie Knott	UK faculty
KY	Herry Utomo	LSU
KY	Katlyn Hitz	Barley breeder MillerCoors
KY	Kathleen Russell	Colorado State Univ. Station Manager
MN	Xiuling Zhang	Corn Breeder, Pioneer Hi-Bred, Mankato MN
MN	Alex Rigor	Rice Breeder, Pioneer Hi-Bred, Philippines
MN	Toi Tsilo	Wheat Geneticist, Agricultural Research Council, South Africa
MN	Ed Quirin	Marker Analytics, Pioneer Hi-Bred, Johnston IA
MN	Godwin Macharia	Kenya Agricultural Research Institute, Kenya
MN	Brian Seda	Corn Breeder, Syngenta, Brookings, SD

MN	Trevor Keith	Research Associate, Pioneer Hi-Bred
MN	Jon Massman	Research Scientist, Pioneer, Johnston, IA
MN	Carol Powers	Coordinator, Grad Student Prof. Dev., Oklahoma State Univ.
MN	Vikas Vikram	Trait Assessment & Deployment, Bayer
MN	Warren Kruger	N. America Soybean, Cotton and Wheat Breeding Lead, Bayer
MN	Hongyun Wang	Pioneer Hi-Bred
MN	Michael Van de Weghe	Pioneer Hi-Bred Intern
MN	Prabin Bajgain	Postdoc Univ. of Minnesota, St. Paul
MN	Kathryn Turner	Research Associate, The Land Inst. KS.
MT	Hussein Abdul-Haleem	University of Georgia
MT	Jeremy Jewell	Washington State University
MT	Deven See	Washington State University
MT	Steve Larson	USDA-Logan, Utah
MT	Don Lee	Univ. Nebraska, Lincoln
MT	Jeong Shin	Seoul University
MT	Jason Cook	Monsanto
MT	Yukiko Naruoka	Washington State University
MT	Gail Sharp	Monsanto
MT	John Erpelding	USDA Scientist
MT	Megan Hartzell	Forage Genetics
MT	Peng Wah Chee	University of Georgia
MT	Xueyan Shan	Misissippi State University
MT	Eric Storlie	Colorado State University
MT	Yukiko Naruoka	Hybrid Wheat Breeder, Syngenta
MT	Andrea Varella	Limagrain, wheat breeder
MT	Jay Kalous	Limagrain, wheat breeder
MT	Afaf Nasseer	Scientist, Iraq Ministry of Agriculture
NY	Chiranth C. Rajashekar	Sathguru, India
NY	Keith Williams	PepsiCo Inc.
NY	Emily Combs	DuPont Pioneer
NY	Nick Santantonio	Postdoc at Cornell Univ.
NY	Jessica Rutkoski	Assistant professor IP-CALS, Research scientist IRRI
NY	Lynn Veenstra	Heinz, tomato breeder
ND	Ana Correa-Heileman	Monsanto
ND	Magan Lewis	Dow AgroSciences
ND	Fabio Pedraza	Seeds 2000
NE	Nicholas Crowley	Corn Breeder, Pioneer
NE	Neway Mengistu	Corn Breeder, Pioneer
NE	Kayse Onweller	Station Manager, BASF
NE	Ali Bakhsh	Professor, College of Agriculture Dera Ghazi Khan
NE	Anyamanee Auvachanon	Professor, Kasetsart University at KPS, Thailand
NE	Ibrahim Salah El-Baysoni	Professor, Damanhour University, Egypt
NE	Mary Guttieri	USDA-ARS Manhattan Research Geneticist

NE	Katherine Frels	Postdoc Univ. of Minnesota, St. Paul
NE	Hussain Waseem	Mahyco wheat breeder / postdoc UNL
NE	Tadele Kumssa	Postdoc Noble foundation
NE	Kayse Onweller	BASF, station manager
NC	Jared Benson	Molecular Breeding Scientist, Pioneer Hi-Bred
NC	Leandro Perugini	Research Scientist, Pioneer Hi-Bred
NC	Tristan Coram	Agronomic & Phenotyping Group Leader at Dow AgroSciences
NC	Raja Kota	Senior Scientist, Syngenta
NC	Eric Olson	Professor, Wheat Breeding Michigan State University
NC	Marla Hall	Wheat Breeder, Limagrain Cereal Seeds
NC	Eddie Lauer	PhD student, North Carolina State Univ.
NC	Martin Sarinelli	GDM Seeds, soybean breeding manager
OH	Mao Huang	Post-Doc at Ohio State University
OH	Amber Hoffstetter	Post-Doc at Michigan State University
OH	Antonio Cabrera	Scientist at BASF Bayer Crop Science
OH	Nafeti Mheni	Wheat breeder, Tanzania Agricultural Research Institute
OH	Elias Balimponya	Manager, Tanzanian Official Seed Certification Institute
OK	Chor_Tee Tan	Texas A&M University - Texas AgriLife
OK	Tilin Fang	Oklahoma State University
OK	Tianrong Huang	Inst. Grain Crops, Xinjiang Acad. Agric. Sci., P.R. China
OK	Xinkai Zhu	Yangzhou University, P.R. China
OR	Juan Rey	Dow Agrosciences
OR	Scott Fisk	Oregon State University
OR	Alfonso Cuesta-Marcos	Oregon State University
OR	Natalie Graham	Cos County, Oregon
OR	Yada Chutimanitsakun	Kasetsart University
OR	Kelley Richardson	USDA/ARS
TX	Silvano Ocheya Assanga	Corn breeder, Monsanto
TX	Chor-Tee Tan	Greenhouse Manager, Australia
TX	Yan Yang	Postdoc in Joint Genome Institute
VA	Greg Berger	Partner in Hopkins Ag Research in Portland, TX
VA	Mark Christopher	Assistant Wheat Breeder, KWS-U.S., IL
VA	Pat O'Boyle	Sugar Beet Breeder, Betaseed, Inc., Shakopee, MN.
VA	Sam Markell	Assistant Professor, North Dakota State University, Fargo, ND
VA	Jianli Chen	Associate Professor, University of Idaho, Aberdeen, ID
VA	Jafar Mammadov	DOW Agro Sciences, Indianapolis, IN
VA	Robert Paris	High School teacher, Xenia OH
VA	Sixin Liu	Molecular Biologist, USDA-ARS, Kearneysville, WV
VA	Young-Soo Chung	Professor, Korea University, Seoul, South Korea
WA	Jayfred Godoy	Wheat breeder, Australia
WA	Shiferaw Gizaw	Quantitative geneticist, Sakata Seed
WA	Megan Lewien	Onion breeder, Bayer Crop Science
WA	Bryn Hulbert	Monsanto

WA	Kendra Jernigan	Assistant Professor, Abilene Christian University
WA	Weizhen, Liu	Post-Doctoral Researcher, Cornell University
WA	Graham Ellis	PhD Candidate, potato breeding WSU
WA	Carter, Arron	Associate Professor / breeder, Washington State University

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National Association of Wheat Growers

Dr. Jorge Dubcovsky,
Project Director of the USDA-NIFA WheatCAP Grant
Distinguished Professor, University of California-Davis
Dept. of Plant Sciences, One Shields Ave.
University of California, Davis, CA 95616

Dear Dr. Dubcovsky:

The National Association of Wheat Growers (NAWG), its member states and state wheat organizations across the country have long supported the USDA-National Institute of Food and Agriculture (NIFA) WheatCAP grants efforts to improve wheat. We appreciate the copy of the second year WheatCAP report and, based on the reported progress and excellent work, we are pleased to reiterate our support for this vital work.

We are impressed by the progress achieved in such a short period and by the National scope of the project. In particular, we would like to recognize the WheatCAP for the release of 42 new wheat varieties and improved germplasm in the first two years of the project. These improved varieties are essential to maintain the competitiveness of the wheat crop and wheat growers. Improved varieties from the current WheatCAP and previous USDA-funded CAP projects are having a positive economic impact on our industry. It has long been recognized that the release of a new cultivar represents a significant return on investment. An economic analysis of Kansas wheat breeding by Barkley (1997) estimated a return of 39% on investment of public dollars (KAES Progress Report 793). Thus, it is clear that the economic impact of the new variety releases is significant.

We are very interested in the WheatCAP focus on grain yield and grain yield components, and hope that the discoveries in this area can accelerate the rates of grain yield improvement. We are happy to see that the increased yield of the new varieties has been accompanied by continuous efforts to increase resistance to different wheat pathogens and pests. This has enormous agronomic, environmental and economic benefits, since it reduces the need for expensive fungicides and increases the productivity and profitability of the wheat growers.

We also recognize the long-term impact of the WheatCAP project's emphasis on training new wheat breeders. The list of trained people presented in your economic impact report is

impressive. It documents well the positive impact that this training has had in both the academic and private industry. Wheat growers understand that wheat research is a long-term proposition that requires an investment in the development of human resources. The ability of the WheatCAP participants to work closely with the next generation of breeders may be one of the most significant contributions of this project to the overall economic health and longevity of the wheat industry.

In summary, we continue to be grateful for the WheatCAP project's focus on wheat improvement as well as the significant economic impact that this project is already having on the wheat industry. We look forward to continued work together with you and your colleagues.

Sincerely,

Jimmie Musick
President
National Association of Wheat Growers