Please use this form to clearly and concisely report on project progress. The information included should reflect quantifiable results that can be used to evaluate and measure project success. Comments should be limited to the designated boxes. Technical reports, no longer than 4 pages, may be attached to this summary report.

Project Number:	
Project Title:	Developing and releasing high-yielding soybean varieties /germplasm with climate-resilience and genetic diversity across maturity group 00 to VIII.
Organization:	Virginia Tech
Project Lead Name:	Bo Zhang
Report Date:	June 1, 2024

In the Progress Summary section below, please provide a brief summary of project progress in lay language that will be shared publicly in the National Soybean Checkoff Research Database. Do not include any confidential or proprietary information. If no lay language is provided, the contents of this entire report will be published in the National Soybean Checkoff Research Database.

Progress Summary (in non-proprietary lay language suitable to be shared publicly):

I) Evaluation and release of high-yielding soybean varieties with regional adaptation and climate resilience:

In 2024, five new soybean lines were released V16-0248DI, V19-0064DT, S19-10701, S19-19764HOLL, and S19-12537 across different maturity groups. These lines have demonstrated significant regional adaptation and climate resilience. Additionally, three more soybean lines are under evaluation and may be released by the end of the year.

We have entered over 120 soybean breeding lines into the USDA Preliminary and Regional Uniform trials. Moreover, 200 additional breeding lines are being evaluated for various biotic and abiotic stresses across multiple state trials in the U.S.

II) Development of soybean germplasm with diverse genetic background for climate resilience

For 2024, we are testing 136 diverse soybean breeding lines. These lines are being evaluated in local and regional diversity trials. We are also developing 150 breeding populations with desirable traits and conducting several crosses to introduce related traits into the breeding lines.

III) Discovery of novel genes associated with climate resilience using emerging technologies and methodologies to support breeding efforts

Our team planted over 300 soybean accessions across multiple locations. These accessions will be screened for canopy temperature, yield, and photosynthesis-related traits using drones. Subsequently, the data collected will be used to conduct genomic studies. We are also using genomic prediction models incorporating 6,000 established SNPs and 15 specific markers for abiotic and biotic stress.

Detailed Project Status – Expand upon the above section. What key activities were undertaken and what were the key accomplishments during this reporting period? List each key deliverable from the proposal and describe progress made (or not made) toward achieving it, including metrics were appropriate.

Deliverables

i) **To evaluate and release high-yielding soybean varieties with regional adaptation and climate resilience across MG 00 to VIII**

Virginia Tech (Bo Zhang): V16-0248DI with 25% exotic pedigree from China was released. It is mid-IV MG, and has the potential to adapt the changing environments with a diverse genetic background. V16-0248DI has high protein, and offers Virginia farmers a unique IV conventional variety with a value-added trait. It also outperformed checks AG 3803 and AG 4403 in Virginia Tech Yield trials, and performed strongly in all Mid-Atlantic locations in the Southern Soybean Uniform Trials. It also showed high yields in regional locations: 56.6 bu/ac in Belle Mina, AL, 42.6 bu/ac in McCune, KS, and 59.0 bu/ac in Knoxville, TN, exceeding average yields by 9%, 5%, and 9%, respectively.

Additionally, two breeding lines with 50 % exotic pedigree, V20-1478R2DI derived from PI 547616 and V19-0064DT derived from Fendou 78, are being evaluated at the USDA Preliminary and Regional trial in 2024. V19-0064DT was evaluated last year through the USDA Preliminary trial and showed results in protein and meal above the test mean, 35.5% and 47.6%, respectively.

USDA-ARS, SNFRU (Fallen and Mian): In the 2023 USDA Preliminary Regional Trials three lines yielded above 100% of the test mean and check mean. N17-30715 is derived 50% from PI 407042, which has been reported to show robust germination at low temperatures, with a percent germination of 90% at 11°C. These three lines and additional lines were submitted to the 2024 USDA Uniform Regional Trials.

Yield Performance of High Yielding NC Breeding Lines in the 2023 USDA Preliminary Regional Trials

Line	Test	Environments	% Yield of Test Mean	%Yield of *Check Mean
N19-0820	UP 6	6	104%	103%
N19-0829	UP 6	6	106%	104%
N17-30715	UP 7	5	103%	101%

*UP6 checks: AG64X8RR2X, USDA-N6005, NC-Dunphy, NC-Dilday and P68A07SX
*UP7 checks: SH7418LL, AG72XF0, AGS-738RR, NC-Wilder, AG79X9RR2X/SR and N8002

In the 2023 USDA Uniform Regional Trials five lines yielded 98% to 108% of the test and check mean. NDPJE-14-217 has been extensively evaluated and has performed well across environments and is proposed for release in 2024. The line is particularly adapted to double crop planting. NC has the largest double crop acreage in the US. In the 2023 NC Official Variety Test NDPJE-14-217 was the second highest yielding line in the coastal plain region. The coastal plain is the largest soybean producing region in NC.

Yield Performance of High Yielding NC Breeding Lines in the 2023 USDA Uniform Regional Trials

Line	Test	Environments	% Yield of Test Mean	%Yield of *Check Mean	Potential Release Date
NDPJE-14-217	UT5	16	102%	100%	Fall 2024
N19-0756	UT6	6	102%	98%	
N19-1253	UT6	6	105%	101%	
N19-1468	UT6	6	108%	104%	
N14-7142	UT7	6	106%	102%	Fall 2025

*UT5 checks: S16-14869, AG53XF2, AG55XF0, AG56XF2, TN09-008 and TN11-5140

*UT6 checks: AG64X8RR2X, USDA-N6005, NC-Dunphy, NC-Dilday and P68A07SX

*UT7 checks: SH7418LL, AG72XF0, AGS-738RR, NC-Wilder, AG79X9RR2X/SR and N8002

University of Arkansas (Caio Vieira): Nearly 140 breeding lines are being tested in our final stage across five locations including Marianna, Pine Tree, Rowher, Stuttgart (Arkansas), and Fisk (Missouri). In addition, a seed increase and purity location in Fayetteville is being grown. All breeding lines have been characterized using a proprietary panel of markers linked to major biotic and abiotic stressors, as well as genome-wide molecular markers for genomic prediction purposes. In addition, all final breeding lines are being screened for flooding tolerance in both V2 and R2 growth stages.

A total of 40 pre-commercial lines are being tested across five locations including Marianna, Pine Tree, Rowher, Stuttgart (Arkansas), and Fisk (Missouri). In addition, these are being grown in the Arkansas Variety Testing (12 locations) and the USDA Preliminary or Uniform Test (10-12 locations). Many entries have shown tolerance to flooding stress, as well as various biotic stressors. Two potential releases are being revised by our internal seed committee and may be released in late Summer. It is worth noting that all pre-commercial lines are undergoing herbicide resistance introgression for both Enlist-E3 and XtendFlex technologies.

University of Missouri (Feng Lin): We have released 3 conventional soybean varieties this year: S19-10701 (RM 4.5), S19-19764HOLL (RM 5.1) and S19-12537 (RM 5.0). The S19-10701 has less yield penalty under dryland conditions and is resistant to SC, FLS, SDS and RKN. Conventional soybean variety S19-19764HOLL has high oleic (78.2%) and low linoleic (2.4%) with resistance to multiple diseases including SC, PRR, SDS and SCN. The average yield of these varieties is 61.3 and 61.7 bushels/acre, respectively. Another variety S19-12537 (Indeterminate) is also high yielding (65.6 bushels/acre) and resistant to diseases such as SC, SDS and multiple nematodes- SCN, RKN and RN.

We entered 18 lines in the uniform preliminary yield trials USDA and 6 lines in the uniform yield trials USDA. These lines will be evaluated for their yield performance along different agronomics traits and seed composition in multiple states including Alabama, Arkansas, Kansas, Tennessee, Louisiana, Mississippi, Missouri, North Carolina, Virginia, etc. Based on yield performance, the top yielding lines will be proposed for release in the upcoming 2025.

University of Georgia (Zenglu Li): Based on the 2023 yield results, we advanced 56 elite breeding lines with competitive yield, disease resistance package and improved seed composition into the USDA Southern Preliminary or Uniform Tests in maturity group VI, VII, and VIII, respectively, for yield testing at multiple locations across southeast. These lines are either conventional or possess the herbicide tolerant traits such as RR2X and Enlist E3. Selected top performing lines will be advanced or released as cultivars during the 2024-2025 period. We have advanced 102 breeding lines into our UGA

advanced yield trials at 3 locations with 3 reps per location and 1200 experimental lines for yield testing at 2 locations with 2 reps per location. We are evaluating 9000 plant rows for agronomic traits in 2024. Selected rows will be advanced to the yield trials in 2025. Planting of yield trials has been completed in Athens, GA.

ii)   **To develop soybean germplasm with diverse genetic background for climate resilience**

Virginia Tech (Bo Zhang): In 2024, three preliminary yield trials were initiated to develop climate-resilient soybean germplasm with diverse genetic backgrounds. These trials test 77 soybean breeding lines across maturity groups IV, early V, and late V, aiming to assess their yield performance, agronomic traits, disease resistance, and stress tolerance. As a source of genetic diversity in MG IV, Shennong Black 7 and Shennong 027 were crossed with elite soybean breeding lines from Virginia and other mid-Atlantic locations. For MG V, Shennong Black 9 and Marrof-261 were used. These strategic crosses aim to enhance the genetic variability and resilience of the resulting soybean.

USDA-ARS, SNFRU (Fallen and Mian): In the 2023 Protein Diversity Regional Trials six NC breeding lines yielded 99%-102% of the check mean and 103%-108% of the test mean. N11-10295 is derived 12.5% from a drought tolerant plant introduction (PI). Interestingly, N11-10295 has been shown to exhibit flood tolerance. N16-10756 is derived 25% from wild soybean PI 366122 and is proposed for release in the fall of 2024. N17-30715 and NDPJE-14-217 were also identified as being high yielding in the 2023 USDA Preliminary and Uniform Regional Tests.

Yield Performance of High Yielding NC Breeding Lines in the 2023 Protein Diversity Regional Trials

Line	Test	Environments	% Yield of Test Mean	%Yield of *Check Mean	% Exotic Pedigree
NDPJE-14-194	MG 5	6	106%	101%	12.5%
NDPJE-14-217	MG 5	6	107%	102%	12.5%
N17-30803	MG 6	5	108%	102%	50%
N16-10756	MG 6	5	108%	102%	25%
N11-10295	MG 7	5	103%	99%	12.5%
N17-30715	MG 7	5	106%	101%	50%

*MG5 checks: S16-14869, AG53XF2, AG55XF0, AG56XF2, TN09-008 and TN11-5140

*MG6 checks: AG64X8RR2X, USDA-N6005, NC-Dunphy, NC-Dilday and P68A07SX

*MG7 checks: SH7418LL, AG72XF0, AGS-738RR, NC-Wilder, AG79X9RR2X/SR and N8002

University of Arkansas (Caio Vieira): Approximately 17,000 progeny rows are scheduled to be planted in the following days in Kibler, Arkansas. These are derived from a multitude of genetically diverse pedigrees, including many biotic and abiotic-tolerant parental lines. Selected materials will later be genetically characterized using the previously mentioned panels of molecular markers. In addition, 74 parental lines have been included in the 2024 crossing block. In summary, 25 are resistant to soybean cyst nematode, 19 are resistant to southern root-knot nematode, 52 to stem canker, while 26 are chloride excluders and 32 are excluders for iron chlorosis. Roughly 150 breeding populations will be developed aimed at combining multiple biotic and abiotic stressors under high-yielding genetic backgrounds.

University of Missouri (Feng Lin): This year, we have designed 8 different crosses to introduce the traits related to climate resilience such as drought and heat stress tolerance. The donor parents have

natural tolerance to high temperatures and low moisture conditions. We will introduce these valuable traits into our elite breeding lines.

University of Georgia (Zenglu Li): During 2023 growing season, 19 breeding lines with diverse pedigrees were yield tested in the USB diversity tests in MG VI and VII for evaluation of yield, agronomic traits, seed composition. These lines have a significant portion of exotic accessions in their pedigrees, and also possess enhanced seed composition, disease resistance, as well as climate resilience. Selected 6 lines are yield tested in 2024 and then released as unique germplasm for both public and private breeders to use in their breeding programs. We will have advanced 34 diverse breeding lines into our UGA advanced yield trials at 3 locations with 3 reps per location and 200 diverse experimental lines for yield testing at 2 locations with 2 reps per location. Planting of yield trials has been completed in Athens, GA.

iii) **To discover novel genes associated with climate resilience using emerging technologies and methodologies to support breeding efforts**

Virginia Tech (Bo Zhang): In May 2024, a diverse panel of 311 soybean accessions from maturity groups IV and V was planted at two locations in Virginia. To monitor the environmental adaptability and stress responses of these accessions, a DJI drone will be used to collect canopy temperature data in a time series throughout the growing season for a genome-wide association study.

USDA-ARS, SNFRU (Fallen and Mian): N16-10756 is derived from the backcross of wild soybean PI 366122 to small-seeded recurrent parent MG VII USDA cultivar N7103. N16-10756 is 25% wild soybean by pedigree from PI 366122. For N16-10756, N7103 and PI 366122 genotyping was performed using the Illumina Infinium BARCSoySNP6K BeadChip by the Soybean Genomics and Improvement Laboratory, USDA-ARS, in Beltsville, MD. Marker analysis is underway to detect polymorphisms between the two parents, N7103 and PI 366122 and to determine allelic contribution of each parent to N16-10756.

University of Arkansas (Caio Vieira): A total of 1,279 breeding lines are currently being tested in our preliminary stage. These are derived from a multitude of genetically diverse pedigrees, including many biotic and abiotic-tolerant parental lines. All breeding lines are currently being genotyped with a proprietary panel of markers for a total of 15 biotic and abiotic stressors, as well as a panel of genome-wide molecular markers. Field trials have been planted in Marianna, Pine Tree, and Rohwer, Arkansas. In addition, a seed increase and purity location in Fayetteville is being grown.

University of Missouri (Feng Lin): We have a diverse soybean panel of 300 PI accessions. We will be evaluating this panel for traits related to climate resilience such as high temperature via their photosynthetic performance. We plan to measure the photosynthesis related traits in all these accessions during different growth stages representing moderate and high temperature conditions in southeast Missouri. Then, we will perform genome-wide association studies to identify candidate genes imparting tolerance to high temperatures in terms of improved photosynthetic activity and yield performance.

University of Georgia (Zenglu Li): Over the past several years, we have developed genomic prediction models using genome-wide SNP markers and advanced materials, which have been successfully used to predict the superior cross combinations and select for the yield in early generations. We plan to continue genotyping our 136 advanced lines with 6000 SNP markers and the data set will be added to

the large dataset, which have been yield-tested at the rain-fed conditions to build and optimize the training set for prediction of line performance. The planting has been done in both Athens and Midville, GA. The imaging data will be collected from these fields using drones with multispectral and thermal cameras during the growing season (Late July to October). The imaging data will be associated with the yield and SNP marker data. The results assist us in selecting lines with high yield and better adaptation and climate resilience.