Project Title: Germplasm evaluation for fruit quality and post-harvest traits

Report Type: Final Project Report

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Cooperators: None

Project Duration: 3 Year

Total Project Request for Year 1 Funding: $ 33,000
Total Project Request for Year 2 Funding: $ 12,000
Total Project Request for Year 3 Funding: $ 10,000

Other related/associated funding sources: Requested
Funding Duration: 2025 - 2029
Amount: $ 4,000,000+
Agency Name: USDA SCRI
Notes: Title: Integrating multidisciplinary and translational approaches to manage postharvest rots on apples and pears in major U.S. pome fruit growing regions. All three PIs are listed as co-PIs on this project.

Other related/associated funding sources: Requested
Funding Duration: 2025 - 2028
Amount: $640,000
Agency Name: USDA NIFA

Notes: Title: Leveraging diverse germplasm resources to develop breeding tools for postharvest rot resistance in pome fruit. PI Gottschalk is lead PI for this proposal and co-PI Collum is listed as co-PI.

WTFRC Collaborative Costs:

Item	2022	2023	2024
Salaries			
Benefits			
Wages			
Benefits			
RCA Room Rental			
Shipping	$6,000.00	$6,000.00	$6,000.00
Supplies	$4,000.00	$4,000.00	$2,000.00
Travel	$3,000.00	$2,000.00	$2,000.00
Plot Fees			
Miscellaneous			
Equipment	$20,000.00		
Total	$33,000.00	$12,000.00	$10,000.00

Footnotes:

Budget 1
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Benefits			
Wages			
Benefits			
RCA Room Rental			
Shipping			
Supplies	$1,700.00	$3,400.00	$1,700.00
Travel	$3,000.00	$2,000.00	$2,000.00
Plot Fees			
Miscellaneous			
Equipment	$18,500.00		
Total	$23,200.00	$5,400.00	$3,700.00

Footnotes:

If project duration is only 1 year, delete Year 2 and Year 3 columns.

Budget 2
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Item	2022	2023	2024
Salaries			
Benefits			
Wages			
Benefits			
RCA Room Rental			
Shipping	$6,000.00	$6,000.00	$6,000.00
Supplies	$2,300.00	$600.00	$300.00
Travel			
Plot Fees			
Miscellaneous			
Equipment	$1,500.00		
Total	$9,800.00	$6,600.00	$6,300.00

Footnotes:
Objectives: Our project has four objectives that complementarily address the evaluation of pear germplasm for post-harvest traits. The first objective is to evaluate the USDA Pear Collection for optimal harvest and storage time for 50 high-value genotypes. We proposed using two germplasm sources to acquire 50 genotypes: 1) USDA Pear Collection at the USDA ARS National Clonal Germplasm Repository (NCGR) in Corvallis, OR, which contains nearly 2,300 unique pear cultivars, breeding lines, and hybrids that represent 36 species and 2) the USDA ARS Appalachian Fruit Research Station (AFRS) breeding program in Kearneysville, WV. The aims are to evaluate the lines for harvest dates, storage requirements, and the presence/absence of post-harvest diseases. We are approaching the disease evaluations in a two-step process. First, evaluate the fruit for natural infections and the classification of pathogens present. Second, conduct resistance testing by inoculating the genotypes found to be free of natural infection for resistance to the identified pathogens. The second objective is to characterize the 50 high-value genotypes for fruit quality, attributes including total soluble solids, acidity, polyphenolic content, texture, peel and flesh color, and overall grade. This objective aims to characterize fruit quality traits using two approaches, destructive and non-destructive, correlate their measures, and develop models used to predict the destructive trait measurements using the non-destructive equipment in the future. The third objective is to challenge the 50 high-value genotypes in simulated supply-chain stress to document resistance to bruising, scuffing, and puncturing. This objective aims to identify germplasm that can withstand the intense forces that are exerted on the fruit during the supply-chain process. However, we have found that fruit received from NCGR pear collection undergoes shipping stress and upon receipt can exhibit real-life damage. We have deviated from our initial objective here to take qualitative measures from the NCGR fruit since it has already been subjected to the planned stresses. Genotypes that exhibit

damage are noted and the damage type is described. The fourth objective is to document and distribute findings through publications and presentations regarding the resistance of the 50 high-value genotypes to storage disorders and diseases. The aim here is to provide communication with the stakeholders and provide any products developed from the analyzes as impactful tools for evaluation of post-harvest traits in pear.

Significant Findings

Objective 1:

- Evaluated over 100 unique genotypes for harvest date and conditioning requirement.
- Evaluated 50+ genotypes for susceptibility to *Penicillium expansum* and *Colletotrichum fioriniae* (45 from NCGR and 46 from AFRS).
- Identified seven genotypes that were significantly less susceptible to *P. expansum* and *C. fioriniae* compared to 'Bartlett' and 'Gem' in 2024.

Objective 2:

- Identified numerous genotypes associated with large fruit size, high sugar content, and high acidity.
- Identified the range of tannic acid in *Pyrus communis,* including content levels associated with standard cultivars.

Objective 3:

- Conducted a first of its kind phenotyping assay to determine supply chain resilience, which identified a two potential sources of resiliency.

Methods

Objective 1: We identified high-value germplasm from historical texts, the USDA GRIN database, and recommendations from germplasm curators and previous breeders. The terms that were used as queries in the literature search for desirable genotypes included disease-resistance (fire blight, *Monolinia*, and post-harvest pathogens), ships well, excellent flavor, keeps well, fruit quality, acidic, phenolic (non-perry), early ripening, late-ripening, and tree-ripe. Following bloom and prior to the fruit ripening period, crop load was estimated from each tree to determine if the minimal fruit number need for all analyses was available. For harvest timing, our initial approach was to select five randomly selected fruit from each tree were collected weekly. Each fruit was cataloged for color development and underwent firmness testing using a penetrometer with a measurement taken from the sun-exposed and shaded side of the fruit following removal of the peel. A genotype will be determined as harvest-ready when firmness decreases to an average of 20 lbf, and color development has reached its peak. We have found that the simple approach of lifting the pear(s) on a branch from the bottom of the fruit, with a minimal force that resulted in release, the pear was determined as harvest ripe. Several of the AFRS breeding lines correlated with known harvest dates using this approach as opposed to decreases in firmness. Moreover, during the first year of harvest date phenotyping, we found many of the varieties when picked at 20 lbf did not ripen in storage to a sufficient lower firmness level (3 lbf). This result suggests that we were picking fruit too immature. We have modified our harvesting approach to using this more simplistic ease-of-release from the branch to indicate harvest timing. Potentially, this result is due to the hybrid (*Pyrus* spp.) origins of many of the breeding lines at AFRS. We have applied this approach to the NCGR sourced fruit as well which were collected and phenotyped during the 2023 and 2024 seasons.

Each genotype then had 75 fruits, or the maximum available, harvested and packed into 40 lbs fruit boxes and stored at USDA AFRS in a new cold storage unit. For the NCGR fruit, harvested pears were wrapped in a Styrofoam fruit wrapper and placed into trays and packaged into boxes for shipping. Overall, this approach maintained the integrity of many of the shipped genotypes. However, some genotypes were found to still be susceptible to the shipping forces (bruising, scuffing, and punctures) and were damage upon receipt even though significantly protected during the shipping

process. The boxes of fruit were kept in cold storage at 30˚F and 90-98% relative humidity. At ten days to biweekly intervals, starting at two weeks in storage to 12 weeks or until ripe, three randomly selected fruit will be taken out of storage and rested at room temperature for 24 - 48 hours. Following the acclimation period, the selected fruit was tested for firmness using a penetrometer. The genotypes were considered ripe when average firmness reaches 3 lbf or less.

A total of 91 pear genotypes (45 from NCGR and 46 from AFRS) were directly challenged with *Penicillium expansum* or *Colletotrichum fioriniae* using a wound inoculation method. Depending on fruit availability ten or twenty fruits from each genotype were inoculated with each pathogen. Fruits were harvested at maturity and inoculated within a week of harvest. On the day of inoculation, fruits were removed from cold storage and allowed to acclimate to room temperature. All fruits were surface sterilized with 70% ethanol and allowed to dry in a laminar flow hood. For *P. expansum* experiments, fruit was wounded with a 3 mm x 3 mm wounding tool and the plug was removed. A conidial suspension was prepared from a 7-day culture of *P. expansum* isolate MD-8 by flooding the plate with sterile distilled water plus Tween-20 and the concentration was adjusted with a hemacytometer to $1x10^4$ conidia/mL. 25 µl drops of the suspension were placed in the wounds with a repeating syringe. For *C. fioriniae* experiments, fruit was wounded with a 4 mm cork borer and the plug was removed. Corresponding plugs were punched from a 7-day culture of *C. fioriniae* isolate WV-223 with the same 4 mm cork borer. *C. fioriniae* plugs were placed mycelium side down into the fruit wounds. For all experiments, inoculated fruits were stored in covered fruit bins at room temperature and lesion diameters were measured at 3-, 5-, and 7-days post inoculation.

Objective 2: We originally proposed using twelve randomly selected pears from each genotype, that are identified as at an optimal eating quality following storage, to be used to evaluate fruit quality traits. However, limited crop loads, higher soft scald incidence, an outbreak of *Fabraea* leaf spot at AFRS, and longer cold condition sampling time points than anticipated required the decrease of the number of replicates to five for this objective. The five fruits first underwent size (length, diameter, and weight) and shape (qualitative) measures. Following non-destructive measurements, all five of the replicate fruit per genotype were analyzed using Near-infrared (NIR) Produce Quality Meter (Felix Instruments). After NIR measurement, each replicate pear was processed to extract juice using a Good Nature M-1 Fruit Grinder and Press. The extracted juice was frozen and underwent measurements for TSS (ATAGO PAL-1), TA and pH (Orion Star T910 Autotitrator), and total polyphenolic content (Folin-Cointreau; absorbance using a spectrometer) using industry-standard measurement methods during the winter months. The data obtained from the NIR meter and industry-standard methods will be inputted into Felix Instrument's model-building software to develop and validate models for the NIR meter for future use. Our initial plan was to use the NIR meter as the sole instrument used to determine all fruit quality metrics except for a juice extraction to determine polyphenolic content in years two and three. However, due to limited availability of fruit from each genotype consistent between years we continued to perform the destructive phenotyping. By collecting more of the ground truth measurements through destructive sampling will only increase our power in training accurate and predictive models using the NIR meter. Due to the limited replicate fruit, we were unable to conduct a sensory evaluation using a trained three-person panel consisting of staff at AFRS.

Objective 3: We will evaluate each genotype for resilience to stress associated with the supply chain including bruising, puncturing, and degradation severity estimation. This objective began during the 2024 season due to the limited fruit available during the 2022 and 2023 seasons and the need to identify the cold conditioning requirements for each genotype across two consecutive years to predict the timing more accurately for evaluations. Additionally, we have found the fruit shipped from NCGR is already subject to real-world shipping stress. As a result, we are modifying this objective to quantitively document damage to fruit received from NCGR. As for fruit obtained from AFRS, when a genotype has acquired one or two year of storage data, it will be selected for evaluation when excess

fruit is available. We were able to repair and utilize a robot arm to simulate container loading and unloading which would cause bruising along with puncture wounds. The robotic stress was applied by having the robot's arm traverse a horizontal space at speed setting that mimics truck movement on the roadway and a drop treatment that covers a distance of 600 mm in < 1 sec. The robotic-associated testing occurred at AFRS under the guidance of Dr. Amy Tabb who has performed similar simulations. To evaluate the fruit under these two conditions, eight replicated fruits were randomly selected for each genotype. Fruit was then placed into a cardboard box with a trimmed down cardboard fruit insert on both the top and bottom sides (clam shell). On top of the upper fruit insert, a sheet of one cm diameter bubble wrap was used to serve as an additional cushion. Fruit was then enclosed in the box with the packaging and placed onto the robot arm. The fruit was then subjected to 30 mins of the shaking and five simulated drops in succession. Following the stress, the fruit was rested for four to five days at room temperature and then evaluated for presence/absence of bruising, puncture, and degradation severity. The same quantitative measures were taken from the NCGR shipped fruit.

Objective 4: The results gained from Objectives 1-3 will be presented and distributed to the research community and stakeholders.

Results and Discussion

Objective 1: The identification of 50 high-value varieties from historic literature was successful. We additionally, were able to properly re-identify 60+ genotypes in the historic AFRS germplasm. Unfortunately, in year one, a minor frost in the spring of 2022 and biennial bearing habits extremely limited the fruit available for the NCGR. In 2022, we obtained harvest dates for 43 genotypes all sourced from AFRS. In 2023, we obtained harvest dates for 69 genotypes. Of those 69, 29 were collected from the NCGR and remaining 40 from AFRS. In 2024, we obtained harvest dates for 113 genotypes. Of those 113, 49 were collected from the NCGR and remaining 64 from AFRS. Across the three years of this project, 43 genotypes were collected for a single season and 76 genotypes were collected over two or three seasons. In total, we evaluated a combined 129 unique genotypes across the three years of this project. This result represents a 258% increase in the genotypes evaluated over what was proposed. The measurement and documentation of condition requirement was successful in each year of the project. However, the total number of genotypes with conditioning requirement evaluations done was less than what we obtained for harvest date. This limitation stems from complexities to ripening fruit. For example, some genotypes were unable to meet the target firmness to be called "conditioned" because they developed storage disorders such as scald and decomposition. In 2022, we documented conditioning requirements for 32 genotypes. In 2023, we documented conditioning requirements for 71 genotypes. In 2024, we documented conditioning requirements for 94 genotypes. Across the three years of this project, 52 genotypes have documented conditioning requirements based on a single season observation and 63 genotypes have documentation for two or three seasons. In total, we documented a combined 115 unique genotypes across the three years of this project. We were able to document condition requirement for 89% for the genotypes we harvested.

For the past three seasons, we have documented harvest date and cold conditioning requirements for >100 unique genotypes. We have documented a strong peak in harvesting dates for pears between 225 and 275 days into the calendar year (August 13th – October 2nd) (**Fig. 1A**). The mean harvest date for pears evaluated in this study was on the 245th day of the year (September 2nd). However, a few varieties were found to be harvesting after October 2nd and represent extremely late ripening genotypes. The cold conditioning requirements for the pears evaluated in this study ranged from as low as 9.5 days to a much as 125 days post harvesting (**Fig. 1B**). A peak in conditioning requirement was observed between 25 and 50 days. The mean requirement for conditioning was ~47 days. Although weakly correlated (Kendall's $\tau = 0.2$), harvest date was significantly associated with the cold conditioning requirement (**Fig. 1C**). We found many genotypes that were exceptions to this

trend - harvested relatively early yet required extensive condition time to reach desirable firmness. These genotypes include varieties such as ‘Talgarskaya Krasavitza’ and ‘Giant Seckel’ and breeding lines NJ Rock R27 T65 and US 84909-184. These genotypes could serve the purpose to breed for conventional harvest dates with long conditioning requirements, resulting in longer marketing window for pear. Alternatively, several genotypes were identified as having short conditioning requirements and represent more ideal material for direct-to-market applications and breeding objectives. These genotypes included varieties such as ‘Bell’, ‘Mac’, ‘Summercrisp’, and breeding lines such as NY 10355 and US 84907-078. Furthermore, varieties such as ‘Passe Crassane’ and ‘Marie Louise’ could be used to target late harvest dates but low conditioning requirements. Testing if harvest date and conditioning requirement is predictively inherited needs to be tested.

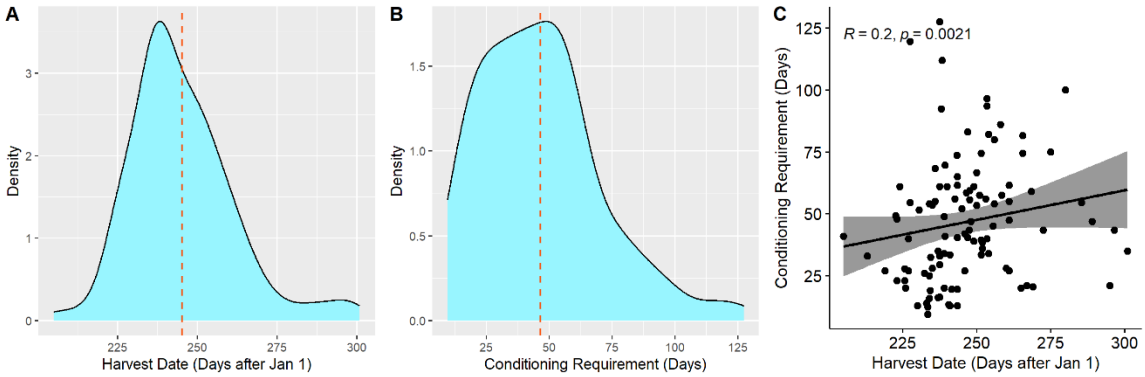

Figure 1. A) Variation in harvest date for pear germplasm. B) Cold conditioning requirements in pear germplasm. C) Correlation plot between harvest and cold conditioning requirement. Red dashed lines indicate the mean. Correlation significance test conducted using Kendall's τ test.

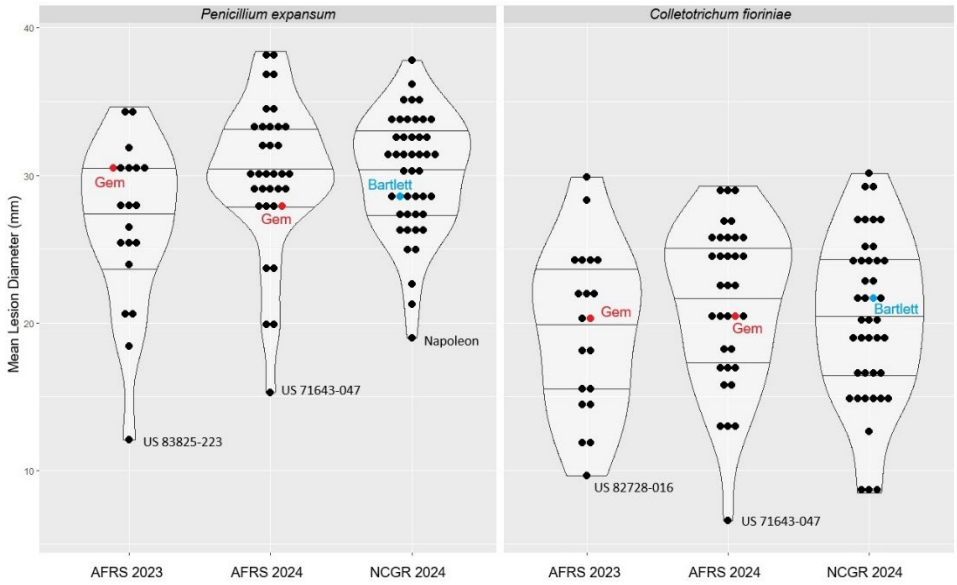

Figure 2. Variation in mean decay lesion diameter in pear germplasm 7 days after inoculation with *Penicillium expansum* or *Colletotrichum fioriniae*. The mean lesion diameter of each pear genotype tested in 2023 and 2024 is represented by a dot. Lines indicate the lower quartile, median, and upper quartile. Control genotypes ‘Gem’ and ‘Bartlett’ are indicated by red and blue dots respectively.

A total of 91 genotypes (45 from NCGR and 46 from AFRS) were directly challenged with *P. expansum* or *C. fioriniae*. Eight genotypes from AFRS were tested in both 2023 and 2024. 'Gem' and 'Bartlett' were included as controls that are highly susceptible to both *P. expansum* and *C. fioriniae*. The mean decay lesion diameter after 7 days ranged from 12.05 mm to 38.40 mm for *P. expansum* and 6.58 mm to 30.11 mm for *C. fioriniae* (**Fig. 2**). Location where pear germplasm was harvested (NCGR or AFRS) and year tested (AFRS 2023 vs. AFRS 2024) did not have a significant effect on mean decay lesion diameters (**Fig. 2**). We found seven genotypes had significantly reduced lesion sizes when challenge with *P. expansum* compared to 'Bartlett' in 2024. These included three from NCGR ('Golden Spice', 'Riehl Best', and 'Napoleon') and four from AFRS (US 71643-047, US 79439-004, US 83825-223, US 99422-202) (**Fig. 3**). All genotypes that were identified as significantly less susceptible to *P. expansum* in 2024 were also significantly less susceptible to *C. fioriniae* except for Napoleon which was not challenged with *C. fioriniae* due to limited fruit. Napoleon has previously been reported to be resistant the pathogen *Monilinia.* Two of the identified genotypes (US 83825-223 and US 79439-004) were also tested the previous year. In 2023, US 83825-223 was also significantly less susceptible to *P. expansum* and *C. fioriniae* compared to 'Gem' and 'Bartlett', while 79439-004 was significantly less susceptible to *C. fioriniae* but not *P. expansum*. We plan to retest genotypes that had significantly less decay in 2023 or 2024 again in 2025 to generate at least 2 years of data for each genotype.

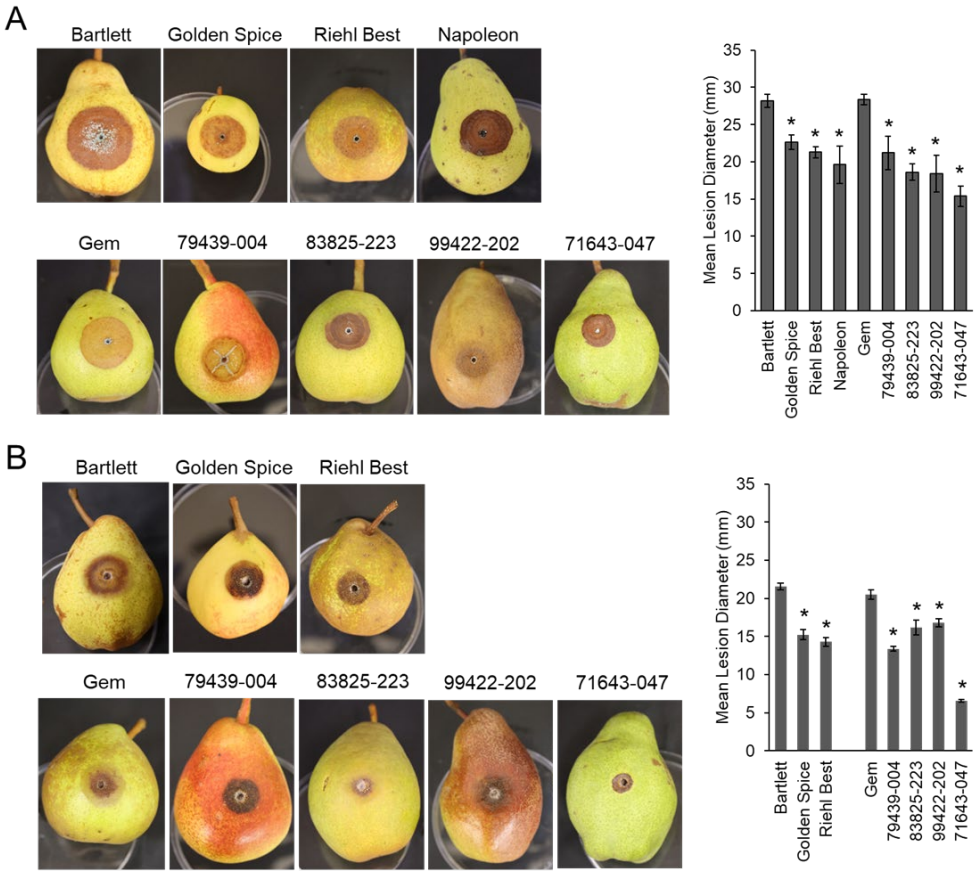

Figure 3. Wound inoculation of pear genotypes with *Penicillium expansum* (A) or *Colletotrichum fioriniae* (B). A representative image of lesion development 7 days post inoculation is shown for selected pear genotypes inoculated in 2024. Bars represent the mean lesion diameter (mm) ± standard error. A * indicates a significant difference of $p < 0.05$ compared to Bartlett using a one-way ANOVA followed by post-hoc Dunnett's test.

Objective 2: We have documented fruit size measurements for all three years of this study. These measurements included length, diameter, and weight. As expected, we observed a correlation between weight and the other two measurements (**Fig 4**). We have successfully selected a wide range of variation in these measurements within the germplasm. The longest genotypes we've identified are breeding lines US 71643-047 and US 67251-045. We also observed that breeding lines with more recent hybridization with Asian species tend to be larger in diameter and weight such as NJ 12, NJ 15, and ILL-2ON-028. Additional breeding lines were identified as being relatively high in weight and more similar in length vs diameter measurements (symmetrical) such as advanced selection US 84907-166. Regarding NCGR genotypes, we observed varieties with desirable measurements that could be used to breeding for size. For example, 'Beurré Clairgeau' and 'Marie Louise' are relatively long, 'Bergamotte Arsene Sannier' is large in diameter and weight. Conversely, varieties such as 'Merricourt' and 'Zelinka' are small and then to be elongated, whereas 'Golden Spice' is small but round (**Fig. 4**).

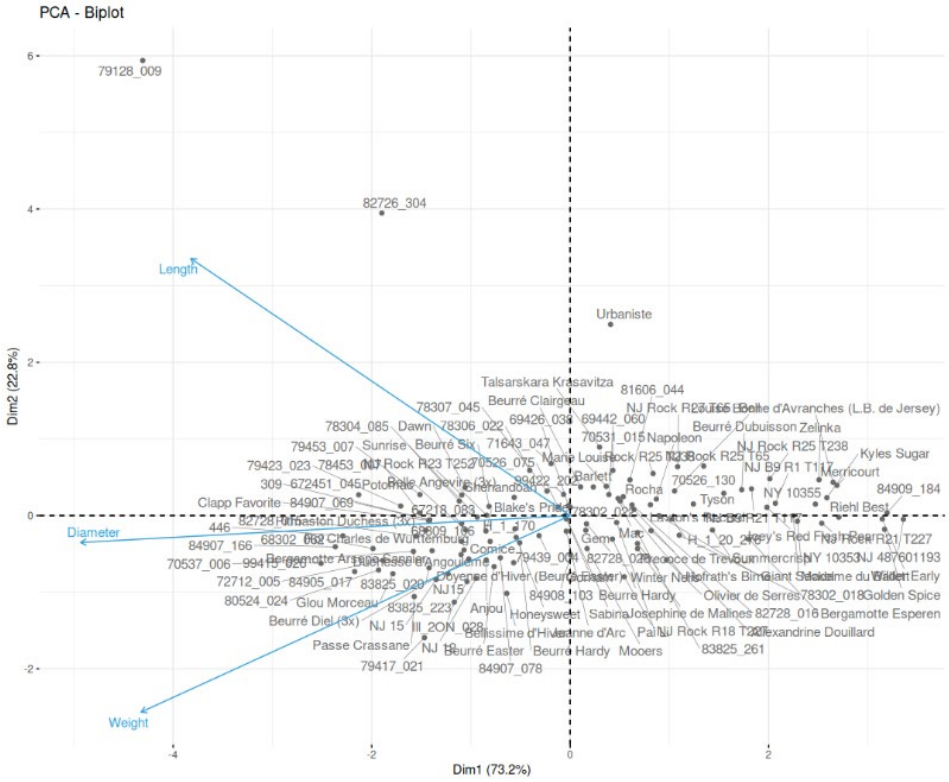

Figure 4. PCA plot of fruit size measurements. Blue arrows represent the direction of the variable as it increases in measurement.

Since 2022, we have analyzed 117 unique genotypes of pear for fruit quality traits. These traits are represented as replicated measurements on a per replicate pear basis for juice yield, total soluble sugar (TSS) content (ºBrix), pH, titratable acidity (TA), and total phenolic content (bitterness). For 67 genotypes, we have documented fruit quality across two or three seasons. The remaining 50 genotypes have only a single season representation. Within this germplasm, we found that the average juice yield was ~89 mL/fruit (**Fig. 5A**). The juiciest varieties were found to be breeding lines including US 99415-026 at 171 mL/fruit. For sweetness, we identified several historic varieties that were nearly two-fold higher than the germplasm's average of ~13 Brix (**Fig. 5B**). These high TSS varieties include 'Louise Bonne d'Avranches' (25.98º Brix), 'Urbaniste' (21º Brix), 'Riehl Best' (20.68º Brix), and 'Olivier de Serres' (19.8 ºBrix). The highest TSS value in the USDA breeding program was US 78302-022 at 14.63º Brix. These historic varieties could serve as new germplasm resources for increasing sweetness in the breeding program. Titratable Acidity (TA) within the germplasm averaged 3.83 g/L **(Fig. 5D**). However, we identified three breeding lines that were three- to four-fold higher than the average (US 70531-015, US 71643-047, and US 82726-304).

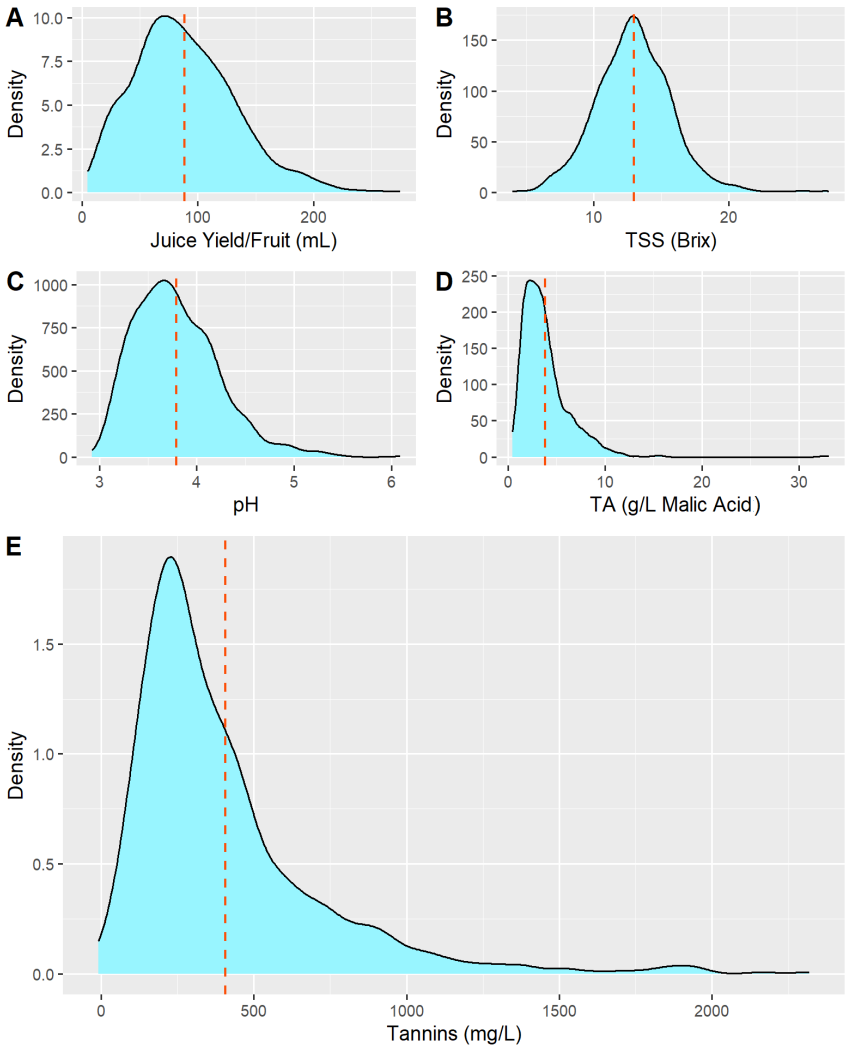

Figure 5. Density plots pear fruit quality metrics A) juice yeild in mL/fruit, B) TSS (Brix), C) pH, D) TA (g/L Malic Acid), and E) Tannins (mg/L).

Higher acidity has been correlated with consumer preference for increased flavor and, thus, represent desirable genetics already present in the USDA breeding program. Lastly, we documented the variation in tannins (i.e. phenolic) content in this germplasm. Tannins contribute to the bitter and astringent flavor profiles and are generally undesirable. We found the average to be ~400 mg/L within the germplasm (**Fig. 5E**). The highest recorded tannin contents belong to historic varieties 'Bellissime d'Hiver' and 'Hofrath's Birne' at >1300 mg/L. A breeding line that is only a generation or two removed from an interspecific hybridization NJ Rock R21 T227 was the second highest at 1326 mg/L and is recognized as the most bitter fruit in the breeding germplasm. Generally, many of the breeding lines were (35 genotypes) were found to have below the average tannin content. This group included the advance testing line US 79439-004 at 197 mg/L. Other industry standard varieties were also identified as containing <400 mg/L of tannins ('Comice', 'Clapp Favorite', 'Gem', and 'Bartlett'). This information on fruit quality is invaluable to aiding in the improvement of pear flavor within the breeding program.

Objective 3: Resilience to physical damage during shipping and handling is a critical trait for pear breeding moving forward. Many of the standard varieties currently produced are highly susceptible to scuffling, punctures, and bruising while they traverse the logistics pipeline. To overcome those limitations, we set out to phenotype germplasm to simulated and actual shipping and handling stress. The simulated stress was conducted using the robot arm programmed to simulate trucking (shaking) and drop forces. Here, we evaluated eight replicated fruits from 38 different genotypes. We evaluated the average damage (bruises/fruit, punctures/fruit, and percent compromised/damage severity) for each genotype (**Fig. 6A**). Over 28 of the evaluated genotypes exhibited some to high susceptibility to damage. However, ten genotypes were found to be resistant with no recorded damage. Of those ten, five were from the same cross/family; US 78302, which is a hybridization of US 56112-146 [US 309 open pollinated] × 'Madame Ernest Baltet'. We fortunately have one of the grand parents in our

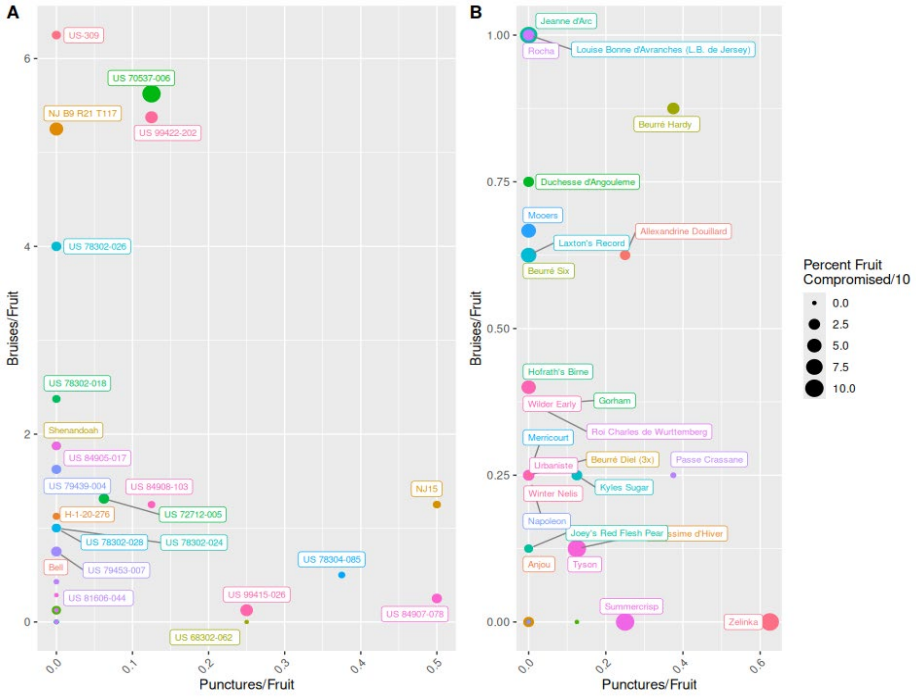

Figure 6. Quantification of buises, punctures, and percent fruit compromised from A) simulated and B) actual shipping stress. Percent fruit compromised is scaled to 10% of acutal values. Fruit with variety names or numbers listed indicate susceptiblity to shipping stress.

germplasm (US 309), which exhibited the highest bruising rate observed (**Fig. 6A**). This result suggests that either the unknown pollen parent of the US 56112-146 or ‘Madame Ernest Baltet’ is providing this resistance, if it’s proven to be genetically controlled/influenced. Further study of this important result is needed. We additionally evaluated 34 of the varieties shipped from USDA NCGR for real-world shipping damage (**Fig. 6B**). Of the 34, only six were found to be free of damage. These included ‘Burre Dubuisson’, ‘Buerré Easter’, ‘Clapp Favorite’, ‘Josphine de Malines’, ‘Marie Louise’, and NY 10353. These varieties represent germplasm material that should be further evaluated for genetic potential in providing shipping and handling resiliency.

Objective 4: Publication and dissemination of these results are forthcoming. We anticipate preparing two or three publications that summarize the results of objectives 1 and 2 in the Fall of 2025. One publication will solely focus on the results obtained related to the disease resistant screening. The other one or two publications will focus on the harvest date, conditioning requirements, and fruit quality metrics. All works will be published in open-access journals and notification of publication will be shared with the respective funding associations and committees. Preliminary results from the natural disease incidence and plant pathogen inoculation testing in Objective 1 were presented at the American Phytopathological Society Annual Plant Health Meeting in July 2024, the American Society for Horticultural Science Annual Conference in September 2024, and at the Cumberland-Shenandoah Fruit Workers Conference in December 2024.

Executive Summary

Project title: Germplasm evaluation for fruit quality and post-harvest traits

Key words: pears, germplasm characterization, breeding, disease resistance, supply chain resiliency

Abstract: The USDA pear breeding program has spent 100-plus years breeding for increased disease resistance often to the detriment of fruit quality. Having established strong disease resistance in the breeding program, new breeding directions for the program are to improve fruit quality, post-harvest disease resistance, and resiliency to the supply chain. However, information is lacking on these traits in the breeding program and at the USDA pear collection in Corvallis, OR. To fill this gap in knowledge, we set out to evaluate 50 high potential germplasm lines for harvest date, cold conditioning requirement, post-harvest disease resistance, fruit size and quality, and supply chain resiliency. We surpassed our goals and identified harvest date and conditioning requirements for over 100 historic varieties and breeding lines, resulting in the identification of desirable late harvesting and cold conditioning genotypes. We additionally screen over 50 of those genotypes for susceptibility to *Penicillium expansum* and *Colletotrichum fioriniae.* Seven genotypes were found to be significantly resistant compared to commercial varieties ‘Bartlett’ and ‘Gem’. We have also evaluated over 100 genotypes of pear for fruit size and fruit quality. We identified several varieties of pear with sugar content nearly two-fold higher than the average in the germplasm (~20 or more °Brix). Furthermore, we found the USDA breeding program contains several breeding lines with extremely high acid content, a desirable trait for more flavorful eating experience. Lastly, we evaluated over 50 genotypes for supply chain resiliency. We found a family of breeding lines that were all highly resistant to damage in simulated shipping conditions. The pedigree of that family suggests a historic variety - ‘Madame Ernest Baltet’ - could be a source for that resiliency. These results, ultimately, will guide the breeding program in determining desirable crosses for improving fruit quality and postharvest traits.