

2024 Orders

- Nyam, Clement, University of Wyoming-Sheridan R&E Center
 - Mountain Big Sagebrush and Wyoming Big Sagebrush (119 accessions)
 - Genetic diversity, restoration and reclamation purposes
- Bush, Kyla, University of Wyoming (21 accessions)
 - Conducting research on the germination of a variety of weed species in different light conditions. In some crop fields, certain species will still germinate in densely populated fields with a low R:FR ratio. Will be investigating the relationship between seed longevity and germination of these species under far-red light.
- Ahmad, Ilyas, University of Wyoming - Sheridan R&E Center
 - Chickpea (504 accessions - core collection)
 - Winter survival/hardiness and potentially further drought tolerance work
- Harris, Donna, University of Wyoming
 - Alfalfa (4 accessions)
 - Weevil resistance
 - Forage Field Pea (1 accession)
 - Forager - joint release back in the 90's between UW and UN
 - Sugar beet (8 accessions)
 - high-throughput phenotyping on sugar beets using drone technology



Screening Alfalfa Genotypes for Alfalfa Weevil Resistance and Quality Traits

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Introduction

Alfalfa (*Medicago sativa* L.) is a vital crop for the agricultural economy in the Western United States. However, the emergence of alfalfa weevil (*Hypera postica*) insecticide resistance, particularly to type II pyrethroids, poses a significant threat to alfalfa production. Therefore, it is impotent to identify a naturally resistant genotype to combat this issue.

Research Objectives

- A. To develop a screening strategy through a no-choice detached leaf feeding bioassay to mitigate alfalfa weevil resistance.
- B. To evaluate the nutritive content and identify high quality genotypes through Near-Infrared Spectroscopy (NIR).

Materials and Methods

No-Choice Detached Leaf Feeding Bioassay

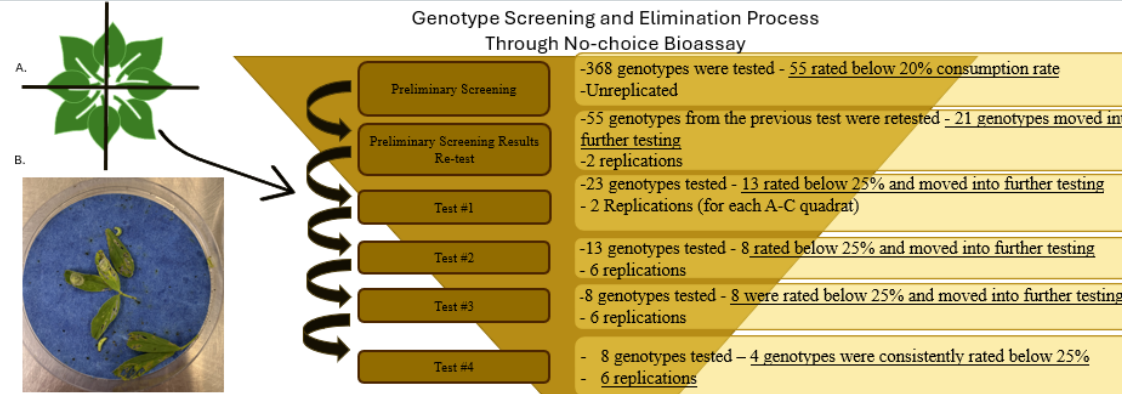
- **Establishment** - 2023, 368 genotypes (including susceptible cultivars) from the USDA germplasm collection were planted in an irrigated randomized complete block hill plot experiment, with three replications, at the Sheridan Research and Extension Center (ShREC)
- **Collection** - 2024, two trifoliate were harvested from each alfalfa genotype's hill plot and placed into petri dishes. Alfalfa weevil larvae (J1, J2, J3) were collected from a single location at the ShREC facility.
- **No-Choice Assay** - Five weevils were placed onto each petri dish containing two trifoliate and incubated in a growth chamber set to 27°C with a 14-hour photoperiod for a duration of 4-5 days.
- **Consumption Rating** - Percent consumption was rated on a scale from 0 to 100, where 0 indicated no consumption and 100 indicated complete skeletonization of the trifoliate.

NIR Analysis

- **Collection** - The upper 6-8 inches of biomass was collected, consisting of upper stems, leaf tissue, and flower parts. Subsequently, the samples were subjected to further drying in ovens for 48 hours to ensure complete desiccation.
- **Grinding** - Using a Thomas-Wiley Laboratory Mill Model 4 and a Retsch SM 200 Mill, dried biomass was ground to 1mm partial size.
- **NIR** - To conduct alfalfa forage quality testing, we utilized 25 Legume Hay, NIRS Forage and Feed Consortium, Berea, KY.

Results

Genotype Screening and Elimination Process Through No-choice Bioassay



➤ Four genotypes (genotypes (PI 478542, PI 478549, PI 315477, and PI 369534) consistently exhibited a consumption rate below or equal to 25% across the six tests performed and demonstrated tolerance to alfalfa weevil (*Hypera postica*) pest damage and consumption (Figure 3).

Figure 1. Screening process and elimination of alfalfa accessions through a no-choice detached leaf feeding bioassay.

A. Quadrates plots were split into during test 1.
 B. Petri dish assay

➤ An analysis of variance (ANOVA) for crude protein revealed significant difference (p-value = 0.001) among accessions. Figure 2, shows the top 10 accessions for crude protein content. The orange shows the four genotypes of interest.

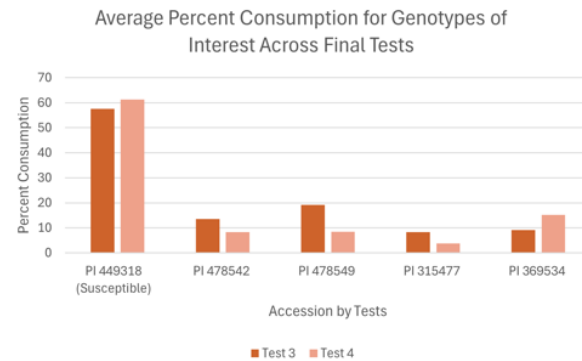


Figure 3. Average percent consumption for genotypes (PI 478542, PI 478549, PI 315477, PI 369534, and susceptible PI 449318) across test 3 and 4.

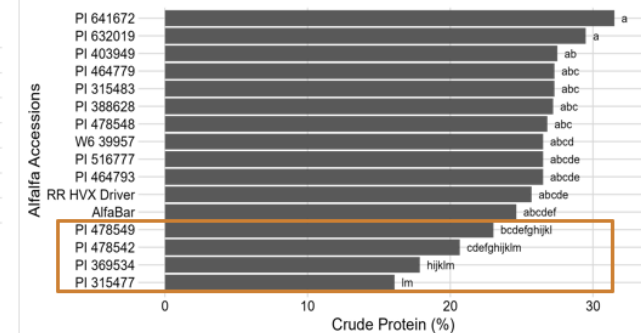


Figure 2. Examination of crude protein content across the top ten accessions, two susceptible checks (RR HVX Driver and AlfaBar), and the four genotypes of interest (PI 478542, PI 478549, PI 315477, PI 369534).

Discussion

- Four genotypes were found using the no-choice assay that had a consistent consumption rate below or equal to 25%. However, these genotypes of interest were not among the top 10 genotypes (figure 3) for crude protein content.
- In 2025, we will rescreen the top 55 genotypes and evaluate the germplasm using both the no-choice assay and additional screening methods.

References

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- Walker, D. R., Narvel, J. M., Boerman, R. H., Ali, J. N., & Parrott, W. A. (2004). A QTL that enhances and broadens Bt insect resistance in soybean. *Theor Appl Genet*, 109(1051-1057), 1051-1057.

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Drone-mounted Ground Penetrating Radar (GPR) Predicts Sugar Beet (*Beta vulgaris* L.) Root Yield

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Introduction

- Sugar beet root biomass is critical for yield and breeding decisions (Rui, Z., Zhang, Z., & Chen, T. (2024))
- Traditional biomass assessment is destructive and time-consuming
- Drones with optical sensors are unable to penetrate below the ground
- Drone-mounted GPR offers a direct, non-invasive method to estimate root biomass by sensing underground structures

Objectives

- Evaluate the use of drone-mounted GPR to predict sugar beet root biomass
- Identify and extract spectral features from GPR signals to enable accurate biomass prediction

Hypothesis

- GPR-extracted features are predictive of root biomass and can support non-destructive yield prediction

Data Acquisition

- Five commercial sugar beet varieties were tested in a RCBD with six replications at Lingle, WY (2023)
- A GPR System with 600–1300 MHz bandwidth, 1000 MHz central frequency was mounted on DJI M300 RTK drone

Material & Methods

- **Signal processing:**
 - 2D Fourier Transform on B-scans
 - Multi-Scale Feature Extractor (MSFE)
- **Statistical Analysis:** Multiple linear regression (MLR)
- **Evaluation:** 10- fold cross validation



Figure 1: Data Collection using drone-mounted GPR before (right) and after beets were topped (left)

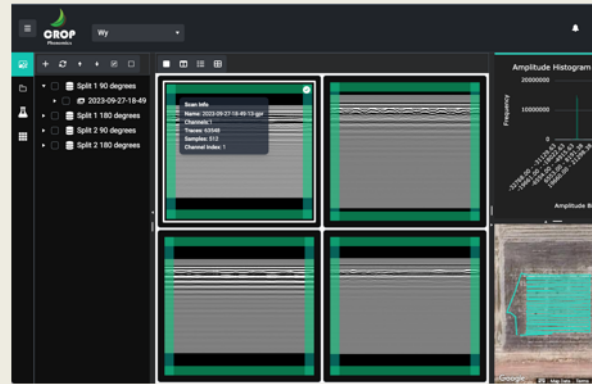


Figure 2: Processing and Frequency domain analysis performed using GPR Studio Cloud (Crop Phenomics LLC)

Results

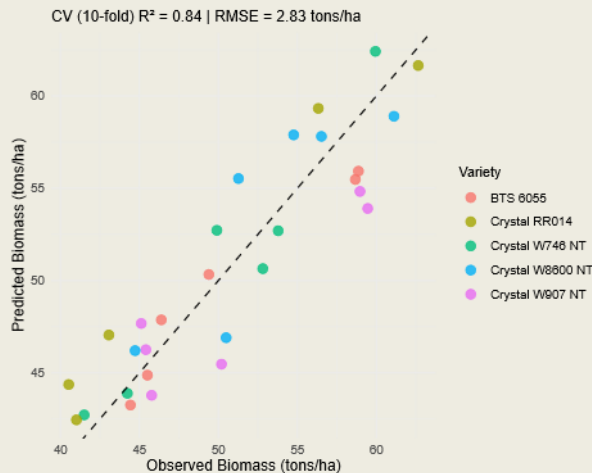


Figure 3: MLR Actual vs Predicted Biomass

Table 1: Coefficient table on GPR features

Term	Estimate	Std. Error	t value	p value	95% CI Lower	95% CI Upper
(Intercept)	27.694	2.113	13.1	5.82×10^{-13}	23.35	32.04
features.4.2	17.692	5.403	3.275	0.002992	6.587	28.8
features.4.17	17.642	5.201	3.392	0.002229	6.951	28.33

Discussion

- The MLR model using GPR two features was predictive of root biomass ($p < 0.01$)
- Cross-validated RMSE suggest acceptable predictive error (2.83 tons/ha)
- The model explained 84% of the variance in biomass ($R^2 = 0.84$)
- Practical utility of drone-mounted GPR makes it suitable for field deployment and in breeding programs

Conclusion

Drone-mounted GPR provides a promising non-invasive high-throughput solution for root phenotyping in precision agriculture.

Future Work

- Test more varieties and multiple locations
- Optimize feature extraction methods

Acknowledgments

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Reference

Rui, Z., Zhang, Z., & Chen, T. (2024). A Review of Field Plant Phenotyping Platform, Sensing and Navigation Technology. Transforming Technologies in Smart Agriculture: New Applications During the Past Decade, 1-46