Enhancing Undergraduate Research and Science Communication through Experiential Learning in Plant Breeding

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Keywords: seed germination, RNA extraction, science communication, undergraduate research

Introduction

Poor seed germination in triploid (seedless) watermelon (*Citrullus lanatus*) increases production costs, reduces uniformity, and limits cultivar adoption. Modern multi-omic techniques have characterized traits relevant to germination and can inform breeding strategies for improved seed performance (Wang et al., 2024). Germination is a sensitive process that is physically constrained by seed coats, endogenous hormone balance, and can be exogenously regulated through chemical treatments (Turner et al., 2024).

Research & Extension Experiences for Undergraduates (REEUs) aim to train the next generation of scientists by combining hands-on research with professional science communication. This project aimed to provide an undergraduate researcher with practical training in plant breeding involving experimental design, statistical analysis, laboratory techniques, and scientific communication while contributing to ongoing research on triploid watermelon seed germination and genetic improvement as a part of the Breeding for Controlled Environments (BCE) program.

Methods

The BCE program designed a series of experiments to improve seed germination using five triploid watermelon cultivars inside a growth chamber at the Texas A&M Agrilife Research Center at Dallas. The software JMP was utilized for statistical data analyses and visualizations. Experiments assessed the effects of seed coat alterations and chemical pretreatments designed to relieve physical, hormonal, and physiological constraints on germination.

Scarification treatments compared physical and chemical alterations to the seed coat. Exogenous hormone applications surveyed genotypic plant growth regulator sensitivity. Every treatment was imbibed with either water or H_2O_2, and the treatment with the most improved germination was identified. This culminated with the destructive sampling of a responsive and unresponsive cultivar using optimally treated and untreated seeds throughout germination to extract total RNA. Seed samples were frozen with liquid nitrogen at 12 hours after imbibition, as well as after 54, 102, and 150 hours of incubation. Frozen samples were pulverized with mortars and pestles that were autoclaved for reuse. The RNA was isolated and purified using a Qiagen RNEasy Plant Mini Kit. Broad-Range and IQ Qubit analyses were performed to validate the success of RNA collection.

Preliminary results were synthesized into an abstract with an oral presentation that was rehearsed with peers and improved with mentor direction. The oral paper was delivered to the annual conference of the Southern Region American Society for Horticultural Science.

Results

The paper presentation was recognized with the 1st place award in the J.B. Edmond Undergraduate Paper Competition, and the abstract will be published in the conference proceedings as a supplement to the HortScience journal. RNA extraction success varied between cultivars, treatments, and days of collection. Samples collected immediately after imbibition were consistently scored poorly. The most suitable untreated RNA samples for sequencing were collected on days 4 and 6. The responsive cultivar, when treated, yielded suitable RNA 2, 4, and 6 days after incubation.

Conclusions

This REEU internship successfully achieved its training objectives. The undergraduate developed skills in experimental design, data analysis, lab techniques, and scientific communication. This project generated adequate RNA samples for future transcriptomic studies aimed at characterizing the genetic mechanisms underlying improved seed germination and treatment responsiveness.

References

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