

## Impact of Repeated Weed Exposure on the Competitive Ability of Wheat

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## INTRODUCTION

- Plants are subjected to numerous biotic and abiotic stress and thus, have evolved mechanisms to cope with these stress conditions.
- It has been shown plants can store and recollect memories of past stress (plant memory response) <sup>[1]</sup>.
- This memory response could either be advantageous or maladaptive to the plant <sup>[2]</sup>.
- Genetic, biochemical and epigenetic factors may contribute to plant stress memory <sup>[3]</sup>.



## **RESULTS AND DISCUSSION**



### **OBJECTIVE**

 Understand how multigenerational weed exposure affects spring wheat growth and yield.

### **HYPOTHESIS**

• Transgenerational priming has the potential to influence the competitive ability of spring wheat.

## **MATERIALS AND METHODS**

Experiments were conducted at the Kimberly Research and Extension Center from April 2021 to December 2022. **Experimental design:** 4 treatments, completely randomized with 15 replications.

#### **Treatments:**

- 1. Wheat only: one wheat plant per pot.
- 2. Wheat-Italian ryegrass: one wheat surrounded by 8 ryegrass.



# Seed Weight Wheat-ryegrass Nheat-wheat Wheat only p < 0.001 p < 0.001 p < 0.001

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Figure 2: Shoot biomass (A), number of seed heads (B), number of seeds per plant (C), and seed weight (D) as influenced competition treatments in 5 generations. Letters represent the treatment groupings. Within each generation, bars with same letters depict no significant difference according to Tukey's HSD at the 0.05 probability level.

- Wheat grown in the absence of weed competition showed a significant increase in shoot biomass, number of seed heads, seed number, and seed weight in the 2<sup>nd</sup>, 3<sup>rd</sup>, 4<sup>th</sup> and 5<sup>th</sup> generations (Figure 2A, 2B, 2C and 2D).
- Thus, plant stress memory may have a beneficial impact on wheat grown alone without any competition in subsequent generations.

3. Wheat-Kochia: one wheat surrounded by 8 kochia plants. 4. Wheat-Wheat: one wheat surrounded by 8 wheat plants.



**Figure 1**: Graphical representation of the four treatments.

#### Management, Data Collection and Analyses:

- Surrounding plants were planted on the same day.
- No fertilizer was applied in order to maximize competition.
- Overhead irrigated 2 times a day.
- Central plants covered with pollination bags to prevent crosspollination.
- Wheat was harvested at maturity.

#### **Relative Yield**



**Figure 3:** Yield relative to wheat only control in all 5 generations.

## Results show a Generation \* Treatment interaction

#### where:

- The weeds caused a significant reduction in wheat growth and yield parameters in the 2nd generation of stress treatments compared to the 1st generation.
- However, the severity of wheat yield loss reduced after two generations of weed stress.
- This suggests that the maladaptive impact of weed transgenerational memory was strongest in the second generation of stress treatments.
- Generally, the strength of this maladaptive impact decreased in the third generation and reduced further in the fourth and fifth generations of stress treatments.



#### For the repeated generations of stress treatments:

Seeds from 1<sup>st</sup> generation used to plant 2<sup>nd</sup> generation, Seeds from 2<sup>nd</sup> generation used to plant 3<sup>rd</sup> generation, Seeds from 3<sup>rd</sup> generation used to plant 4<sup>th</sup> generation, Seeds from 4<sup>th</sup> generation used to plant 5<sup>th</sup> generation.

Data collected on central wheat plants at harvest include shoot biomass, number of seeds per plant, and seed weight (yield). Data were analyzed using linear mixed-effects ANOVA in R statistical language.

Means separated using Tukey's HSD ( $\alpha = 0.05$ )

### FUTURE RESEARCH

#### **Common garden experiments:**

The original seed and seeds from the five generations would be grown in the greenhouse at the same time.

Yield data and additional data on chlorophyll content, and photosynthetic rate would be collected.

#### **Transcriptomic and Epigenetic phase:**

RNA-Seq for Differential Expression of genes.

DNA Methylation, and ChIP-Sequencing of histones.

### REFERENCES

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