Using Recombinant Inbred Lines of Sorghum for Studying Genetic Control of Inter-specific Hybridization Between *Sorghum bicolor* and *S. halepense*

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Introduction

- Cultivated sorghum (*Sorghum bicolor*) and its weedy relative johnsongrass (*S. halepense*) have the potential to cross-pollinate and produce viable hybrids due to genetic similarities **(Ohadi et al. 2017)**.
- In previous research, the majority of hybrids were found to be tetraploids, likely due to the production of 2n female gametes in sorghum **(Hodnett et al. 2019)**.
- It was also found that the level of outcrossing highly varied across sorghum lines **(Sias 2020)**, but little is understood on the genetic control of this trait.
- The Recombinant Inbred Lines (RILs) can serve as a powerful tool for genetic mapping of traits of interest and can be used to decipher the chromosomal regions that influence outcrossing between these two species.

Objective

- To understand the genetic control of gametic factors affecting interspecific hybridization.

Materials and Methods

- Location: Texas A&M University Research Farm, College Station.
- Duration: April 2020 to August 2020.
- Design: Completely Randomized Design, 3 replications.
- RIL sorghum lines (female): 200 lines developed from crosses between sorghum inbreds with high (Tx623) and low (Tx378) outcrossing potential with johnsongrass, based on **Sias (2020)**.
- Plot size: single row of 6 m
- RIL lines (female) were allowed to cross with naturally occurring johnsongrass (male) under field conditions **(Figure 1)**.
- The male gametocide agent trifluoromethanesulfonamide (TFMSA) was applied to the RIL lines to make them male sterile and prevent selfing (concentration: 20mg/ml in an aqueous solution containing 5% glycerol and 0.25% tween 2013) **(Figure 2a)**.
- During flowering, any fertility revertants were identified and removed periodically.
- At seed maturity, 15 random panicles were harvested individually from within each plot for characterizing percent seedset and outcrossing.
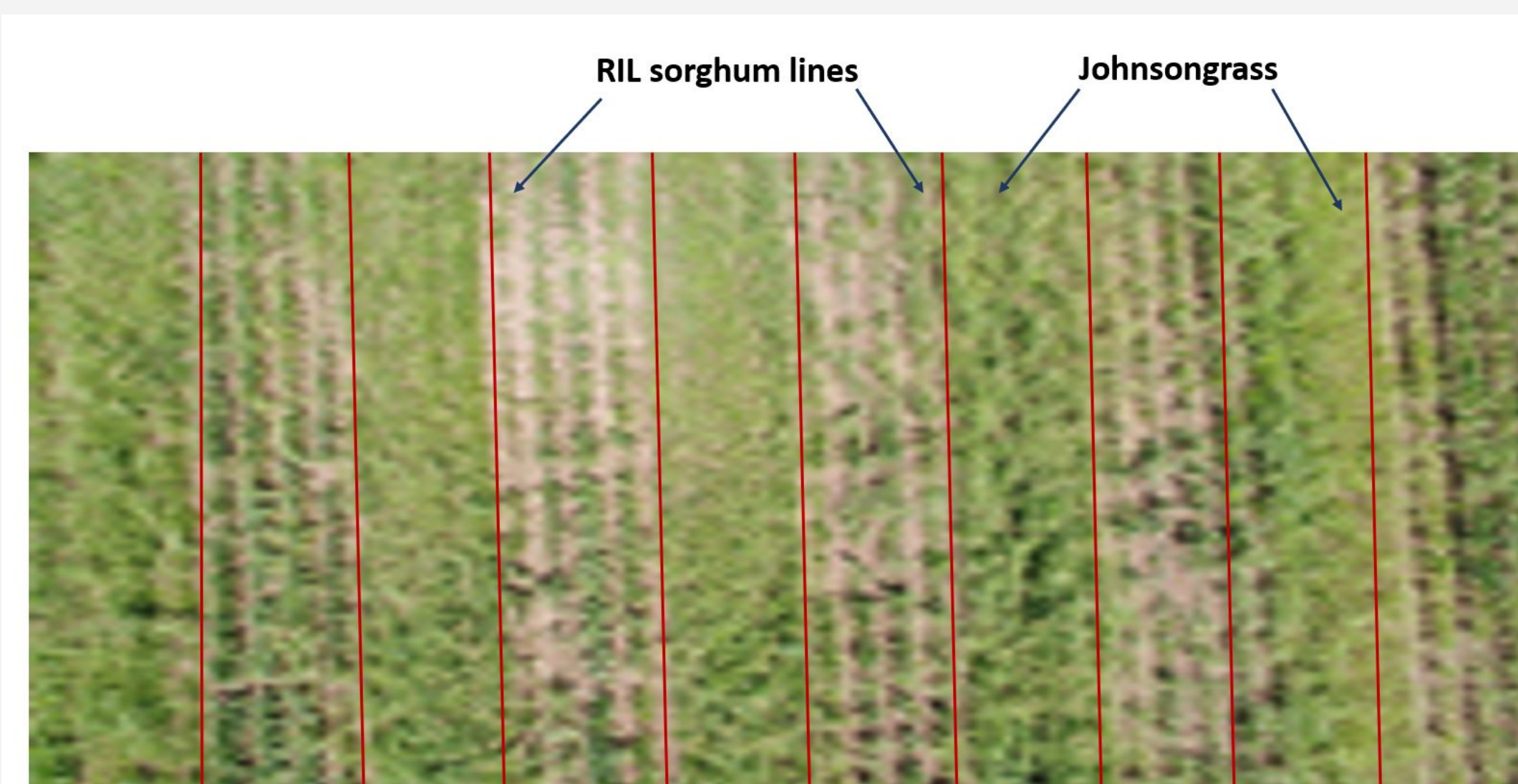

Figure 1. Aerial view of the field showing the RIL lines and johnsongrass

Results

- Preliminary results show the presence of high variability in outcrossing potential across the different RIL lines investigated.
- The mean and range values for outcrossing among all RIL lines studied were 0.23% and 0 to 2.8%, respectively **(Figure 2b)**.
- The RIL-129 and the parent B.Tx623 had the highest seed set at 2.8 and 1.2%, respectively.
- The top three RIL lines with the most outcrossing potential with johnsongrass were RIL-129, RIL-102, and RIL-066.

Figure 2. a) Images showing the RIL lines established in a field infested with johnsongrass, and application of the male gametocide TFMSA on the RIL lines; b) Panicles from different RIL lines, illustrating the variability in outcrossing potential as shown by seed set differences.

Discussion and Conclusions

- Preliminary results showed substantial variation in seed set among the 200 RIL lines evaluated here.
- The genetic make-up of the RIL lines with the highest seed set potential (RIL-129, RIL-102, and RIL-066) is currently being investigated using the Genotyping By Sequencing (GBS) approach.
- Results are expected to provide novel insights on the genetic control of outcrossing between sorghum and johnsongrass.

Future Research

- Sequencing data analysis and genetic mapping.
- Comparison of the phenotype with genotype.

References

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- Ohadi S, Hodnett G, Rooney W, Bagavathiannan M (2017) Gene flow and its consequences in Sorghum spp. Critic Rev Pl Sci 36:367-385.
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