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.

### 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.

### 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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