

Calculation of Heritability and Genetic Correlations Between Yield Traits of Sugarcane (*Saccharum* Spp.) in Early Selection Breeding Populations in Louisiana

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Introduction

Sugarcane ratooning or regrowth is an important trait to farmers that saves them money for replanting. Sugarcane breeding requires the development of many genotypes with many years of evaluation to identify the best yielding variety. Approximately 70,000 commercial genotypes are planted in Louisiana and during the breeding process with seven evaluations with roughly 10% selection for the first three stages and roughly 50% selection for the remainder. Because of the large number of genotypes full evaluation of all genotypes' ratooning ability is not possible. The majority of the diversity is in non-replicated single row plots. Measuring the diversity using traditional methods is not possible. The Animal Model, which is used by animal breeders to measure diversity, is a possible solution to this problem. This model requires large populations and pedigrees, but does not need replicated plots to calculate statistics such as narrow sense heritability. In this study we will evaluate the yield and ratooning ability of second line trials from two crops in Louisiana to determine heritability and genetic correlations.



Table 1 Narrow sense heritabilities and genetic correlations calculated using Animal Model

	Stalk Population		Stalk Weight		Cane Yield		Sucrose Yield		Sucrose Content	
	h ²	SE	h ²	SE	h ²	SE	h ²	SE	h ²	SE
1R	0.05	0.04	0.00	0.00	0.02	0.03	0.01	0.02	0.01	0.01
Corr	0.73	0.24	0.98	0.18	1.00	0.74	1.00	failed	0.60	0.59
2R	0.15	0.07	0.12	0.07	0.11	0.06	0.07	0.05	0.06	0.03
Ratooning	0.16	0.07	0.00	0.04	0.06	0.06	0.01	0.04	0.02	0.02

Table 2 Genetic correlations between stalk weight and number

Stalk	Weight 1R	SE	Weight 2R	SE
Number 1R	-0.83	0.24	-0.57	0.34
Number 2R	0.10	0.41	-0.16	0.37

Materials and Methods

Second line trials at the USDA-ARS Sugarcane Research Station in Houma Louisiana are non-replicated single plot rows evaluated in three crops (plant cane, first and second ratoon). Measurements were taken for stalk population (stalks ha⁻¹), mean stalk weight (kg), sugar content (g kg⁻¹), cane yield (Mg ha⁻¹), and sugar yield (Mg ha⁻¹). Heritability estimates and genetic correlations were estimated by a restricted maximum likelihood model utilizing WOMBAT software where genotype, year and location are treated as random effects with seventeen years of first and second ratoon data from plants assigned from second line.

Results and Discussion

Narrow sense heritability values were low for all traits but for stalk number, stalk weight and cane yield had higher heritability in the second ratoon ≤ 0.2 compared to the first ≤ 0.1 (Table 1). The increase in heritability of most traits from the first ratoon to the second indicates that selection for ratooning ability would be better in the second ratoon. Sugar traits such as sucrose yield (Mg ha⁻¹) and content had very low heritability with the second ratoon slightly higher than the first. This is unexpected because sugar traits are well known for being highly heritable. One possible cause of this low heritability could be that the population tested was selected previously for high sucrose leaving less diversity to be analyzed. Having high stalk number and stalk weight in ratoon is important for yield. Stalk number and stalk weight had high genetic correlations between the ratoon crops. Stalk population and stalk weight had negative genetic correlations, but these were higher in first ratoon than second (Table 2). Generally stalk population and stalk weight are negatively correlated and in this study the genetic correlations are also negative but the trend decreases in the second ratoon. Also first ratoon stalk number negatively correlates with second ratoon stalk weight. This indicates that selection for high stalk number in first ratoon may select for lower stalk weight but less so in second ratoon.