Improving Sweet Sorghum for the Southeast

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Introduction

The sugary juice of sweet sorghum (*Sorghum bicolor* (L.) Moench) is traditionally used to make edible syrup, but it can also be used to produce ethanol or other bio-based chemicals. The bagasse can be burned for energy or used for cellulosic ethanol, and the grain and leaf portions for livestock feed. Sorghum is more drought tolerant than corn (*Zea mays* L.), and also requires less nitrogen, making it an attractive alternative biofuel source, particularly in the Southeast, which has a long warm growing season. However, few hybrid cultivars are available, and various insects and diseases can be problematic in this region. Development of hybrids and improvement of insect and disease resistance are the major goals of our breeding program.

Hybrid development

Most current sweet sorghum cultivars are pure lines or open-pollinated varieties. Because they are tall plants that often lodge, mechanical seed harvest is difficult, and this is a major limitation to expanding acreage of this crop for biofuel production. Hybrid seed can be produced using short-statured male-sterile seed parents, facilitating mechanical seed harvesting, and potentially taking advantage of heterosis. However, only a few sweet sorghum seed parents are currently available, and they have not been tested in the Southeast.

Materials and Methods: A randomized complete block experiment was conducted at Tifton, GA in 2012 and 2014 (two replications/yr) to compare three female lines, 19 male lines, and 57 hybrids (Design II) for various yield components. The three females were N109, N110, and N111; the males are listed on the *x*-axis in Fig. 1. At harvest, a sample of three stalks was taken from each plot and separated into leaves, stems, and panicles, and the juice was extracted from the stems with a roller mill. All components were weighed both fresh and dried. The yield of each component was estimated based on its proportion of the total biomass yield. Juice brix was measured using a hand-held digital refractometer. Sugar yield was estimated by multiplying [(Brix – 3)/100] by the juice weight. Plant height, lodging percentage, and days to anthesis were also recorded (not shown).

Results: Most hybrids produced similar sugar yields as their inbred male parents, while grain yields (panicles) were often greater in hybrids than inbreds.

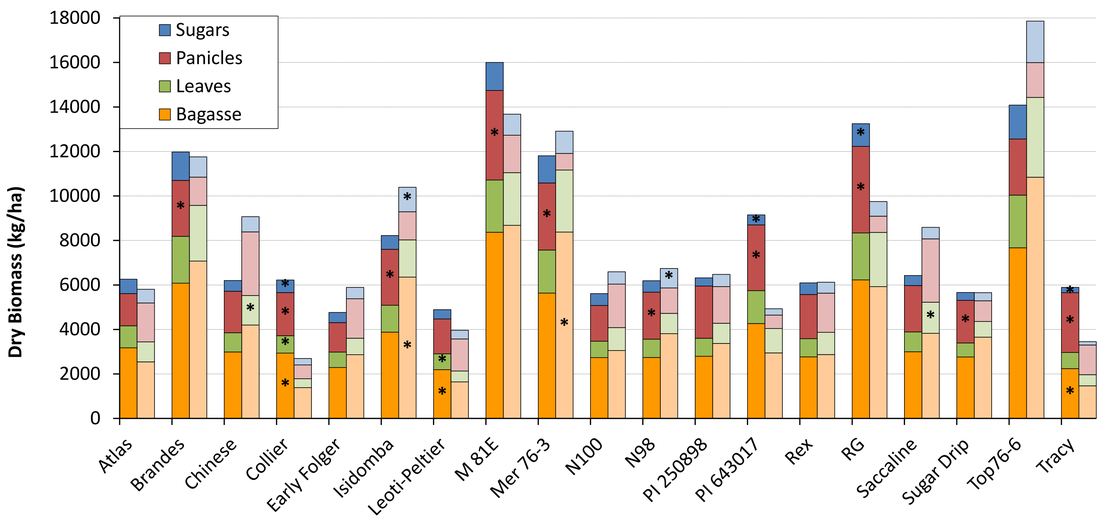

Fig. 1. Hybrid means (dark bars) of 19 male parent lines (*x*-axis), each crossed with three female testers, versus male inbred means (light bars) for four yield components (legend). Where there is a significant difference between the hybrid and inbred mean, the greater component is marked with a *.

Root knot nematode resistance QTL

Root knot nematodes parasitize the roots of numerous crop species, causing significant damage to crops such as cotton, sugar beet, and vegetables. Root knot nematodes are also known to parasitize sorghum, but they do not seem to cause significant damage to the crop. However, planting susceptible sorghum varieties may increase the nematode population, endangering subsequent rotational crops. Incorporation of nematode resistance into sweet sorghum should help to make it more attractive for rotation with susceptible crops. A previous greenhouse-based screening of over 100 sweet sorghum entries identified wide variation in nematode reproduction ability on the different entries.

Materials and Methods: A highly resistant line, Honey Drip, was crossed with susceptible line Collier. The parents, F_1 and 130 F_2 plants were grown in the greenhouse and infected at 28 d with 4000 juvenile stage 2 (J2) nematodes/pot. Eggs were collected and counted 56 d after inoculation. DNA from the highest and lowest 46 plants was subjected to Genotyping by Sequencing and quantitative trait locus (QTL) analysis.

Results: A major QTL was identified on Chromosome 3, which explained 57% of the phenotypic variance for number of eggs (log-transformed), and 70% for eggs/g root (also log-transformed). Simple sequence repeat (SSR) markers were developed from flanking sequences to facilitate introgression of this gene into other lines (Fig. 2.)

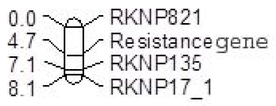

Fig. 2. Resistance gene QTL region with mapped SSR markers on Chromosome 3. Distances on the left are in cM.

Planting date effects on hybrids

This study was conducted in order to evaluate genotype by environment interaction among sweet sorghum inbred lines and their hybrids, and to determine optimal planting dates for these lines and hybrids in southern Georgia.

Materials and Methods: Three female lines, five male lines, (Atlas, Chinese, Dale, Isidomba, and N98) and their 15 hybrids were planted in a randomized complete split plot design with three replications in 2013 and again in 2015 at Tifton, GA. Planting dates (April, May, and June) were the main plots and the 23 entries were the subplots. Harvested components were measured as in the Hybrid Development study (this poster).

Results: In 2013, later planting resulted in greater lodging, while the opposite trend was observed in 2015. A strong genotype by planting interaction occurred for lodging percentage. Hybrids of N109 tended to have less lodging than hybrids of N110 and N111. Later planting resulted in faster maturity, but the effect was greater in 2013. Hybrids flowered consistently earlier than their male parents. In 2013, later planting resulted in reduced sugar yields, likely due to excessive rain, while in 2015 the late planting tended to yield more sugar than the earlier plantings.

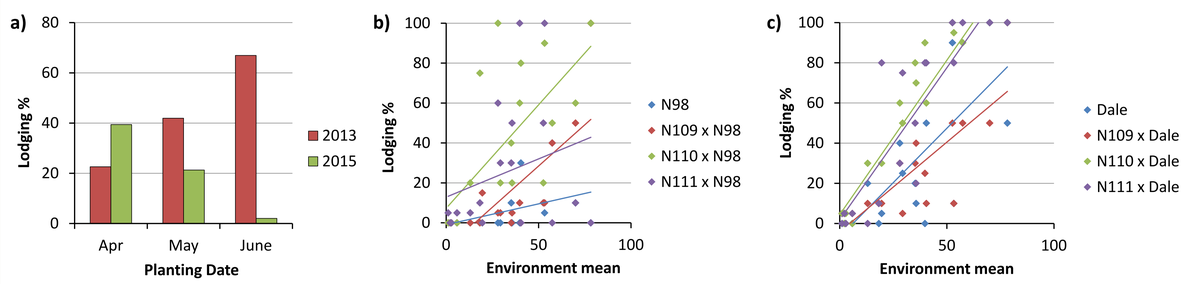

Fig. 3. a) Mean lodging percentage by planting. **b)** Genotype by environment interaction (individual performance vs. environmental mean) for lodging percentage in N98 and its hybrids, and **c)** Dale and its hybrids, as examples.

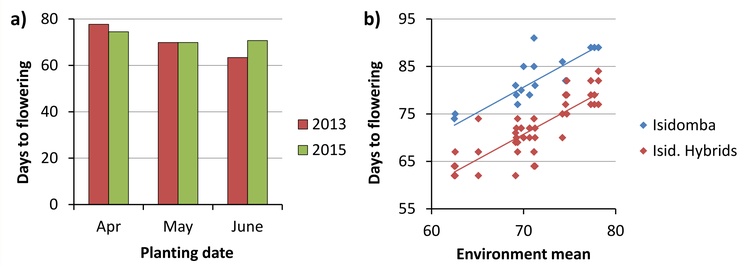

Fig. 4. a) Mean days to flowering by planting. **b)** Genotype by environment interaction (or lack thereof) for days to flowering in Isidomba and its hybrids, as an example.

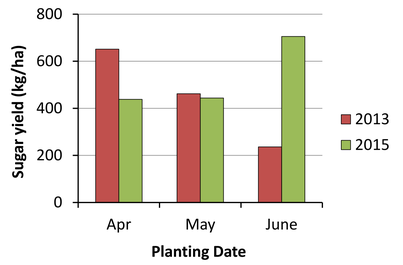

Fig. 5. Mean sugar yields by planting.

Sugarcane aphid resistance

Sugarcane aphid (*Melanaphis sacchari* (Zehntner)) (Hemiptera: Aphididae), has recently become a serious pest on sorghum in the Southern U.S. Sugarcane aphids colonize the lower leaves first, and then gradually move upward on plants as the population builds. Colonies can build up quickly to large numbers on the undersides of infested leaves. Aphids ingest phloem sap from the leaves, thus reducing plant growth and yields. Both aphids and the large amount of honeydew that accumulates on the leaf surfaces can interfere with mechanical grain harvesting. Secondary sooty mold grows on the honeydew, and is an easily visible indicator of infestation. Leaf discoloration or chlorosis often occurs in response to aphid feeding, followed by delayed flowering or failure of panicle development in susceptible genotypes. Some insecticides are available to control this pest, but genetic resistance is being pursued as a viable control strategy.

Fig. 6. Sugarcane aphids on Johnsongrass (alternate host) in Tifton, GA, April, 2015.

Fig. 7. Resistant and susceptible entries in the sweet sorghum breeding nursery, Tifton, GA, 2015. Note the sooty mold on the ground beneath the susceptible entry.

Materials and Methods: In 2014, an F_2 mapping population (AN109 x Entry 22) was planted in the field at Tifton, GA for mapping disease resistance. This was the first year that sugarcane aphid was found on sorghum in Georgia. Some individual plants appeared to have less honeydew and sooty mold, suggesting aphid resistance. Plants were assessed for aphid damage by rating leaf discoloration (1 = healthy green leaf to 6 = dead, dried out leaf) and sooty mold (1 = no sooty mold to 9 = 100% leaf area covered, and plant is dead). DNA has been collected for Genotyping by Sequencing analysis to map the location of resistance genes. Other accessions are also being screened in the field for potential resistance (Fig. 7).

Results: F_1 plants of the cross AN109 (susc.) x Entry 22 (res.) are susceptible, suggesting a recessive resistance gene. The distribution of the sooty mold ratings in the F_2 also supports this, but also suggests that other genes are involved.

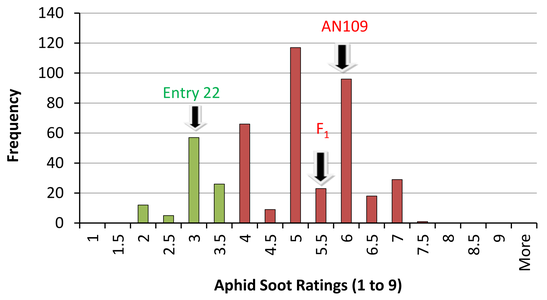

Fig. 8. Frequency distribution of sooty mold ratings in the F_2 population (n=480). Ratings ≤ 3.5 are considered resistant (green bars), and ratings ≥ 4 are considered susceptible (red bars). Mean ratings for the parents and F_1 are indicated.