Sorghum Conversion and Introgression Programs

Two strategies for exploiting unadapted germplasm for crop improvement

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TAES—USDA Sorghum Conversion Program

- 1963-1999
- 1,596 unadapted sorghum accessions entered into Conversion program
- ~ 30-50 converted lines critical to sorghum production worldwide

- SC23
- SC33
- SC35
- SC56
- SC103
- SC108
- SC110
- SC120
- SC155
- SC175
- SC170
- SC599
- SC748
- B35
- SC414
- SC265
- SC326
- SC265
- SC372
- SC650
- SC1079

Figure 1. Procedure used in converting exotic varieties to short early types.
Reliance on Key Conversion Lines

Why few impactful lines?
- Exotic, but elite
- Exotic, but not elite

Often, lines were partially converted
Reinstated Sorghum Conversion (RSC) Program

- 2009-2015
- 136 unadapted sorghum accessions “partially” converted
- Released early generation material (F₃ & BC₁F₃)
- ~20 RSC partially converted lines of potential value to sorghum production (forage and grain)

- RSC17
- RSC35
- RSC62
- RSC66
- RSC68
- RSC94
- RSC111
- RSC112
- RSC104
- RSC116
- RSC119
- RSC130
- RSC132
- RSC133
- RSC135
- RSC87
- RSC124
- RSC87
- RSC105
- RSC93
- RSC74
- RSC53
- RSC77
- RSC40

Figure 1. Procedure used in converting exotic varieties to short early types.
RSC Marker-assisted Breeding Scheme

**Cross**

- DONOR PARENT: Tx406 {ma_1, Ma_2, ma_3, 4-dwarf}
- UNADAPTED PARENT (50 each cycle)

**F_1**

- Self Pollinate

**F_2 population**

{~1,800 - 2,000 plants each population}

**Phenotype F_2 plants**

{select ~20 early flowering, dwarf plants each population}

**Genotype-by-Sequence F_2 Selections**

{~20 F_3 per population : 1,000 F_2 each cycle}

**Identify “Best” F_3 lines based on Genotype**

{Highest % recovery of unadapted parent genome}

{5 selections per each population}

**Backcross**

**Release F_3 or BC_1F_3 RSC lines**

{5 F_3’s & BC_1F_3’s per each population}
RSC Marker-assisted Breeding Scheme

- Introgress recessive $dw$ & $ma$ alleles from Tx406 into unadapted parental genome
  - Significant linkage drag of Tx406 genome flanking introgressed recessive $dw$ & $ma$ alleles (Chromosomes 9, 6, & 7)

- Genotype (GBS) to reduce linkage drag
  - ~40 Mbp flanking $ma_6$, $ma_1$, $dw_2$ on chromosome 6

Graphical Genotype: Chromosome 6

- Introgression of $ma_6$, $ma_1$, $dw_2$
- Marker-assisted recovery of exotic genome
Genome Analysis of RSC Germplasm:

Recovery of recurrent parent genome hindered by introgression of recessive temperate-zone “adaptive” alleles

- **F₃ RSC germplasm** (based on GBS marker data)
  - 23% ± 8% donor parent (Tx406) genome
  - 43% ± 7% heterozygous
  - 34% ± 8% unadapted parent genome

- **BC₁F₃ RSC germplasm** (based on GBS marker data)
  - 13% ± 4% donor parent (Tx406) genome
  - 17% ± 6% heterozygous
  - 70% ± 6% unadapted parent genome
RSC Lines Breeding Value

RSC Lines Selections: Potential for International Distribution

- Evaluated 375 RSC (F₃ & BC₁F₃) lines in 2016
  - Breeding value estimated by Dr. Fred R. Miller
- RSC lines (33) advanced based on estimated breeding value
- Testcross hybrid trial evaluation 2018
  - Multi-location yield trial
  - Two testers
    - TxARG-1, Tx2928
    - David Horne, Dr. Nikhil Patil
Future of Sorghum Conversion Programs

- Conversion should be limited to accessions with unique traits
  - Traits may be lost during conversion if targeted genes are linked to \( dw \) or \( ma \) loci (chromosome 6, 7, 9)

- “….It is increasingly rare that first-cycle crosses involving converted or partially-converted sorghum lines will produce parents of commercial grain hybrids…” (D. Jordan 2011)

- “….the genetic diversity residing in unadapted sorghum germplasm can be exploited in a manner that addresses the needs of the hybrid seed industry…” (Klein et al. 2017)
Germplasm Utilization & Enhancement of Sorghum Strategy (GUESS)

**Objective:** The improvement of sorghum hybrids by introgressing desirable traits from exotic and unadapted germplasm into elite sorghum inbreds

**Approach:** Incorporates methods used by the Germplasm Enhancement of Maize (GEM) program and the Australian Sorghum Diversity Enhancement Program

**Experimental Design:** Utilize two elite public inbreds (B & R) as the recurrent parents, traits from exotic sorghum germplasm will be introgressed via backcrossing.....
GUESS Program Germplasm Diversity

- Unadapted germplasm selected based on:
  - genetic diversity
  - traits of interest
  - recommendations from sorghum community

- Unadapted germplasm
- Elite R inbred
- Elite B inbred

Relationship tree of germplasm selected for GUESS program vs. elite public inbreds
Program: Development of BC$_1$F$_2$ Populations
GUESS Program:
- Line development, hybrid trials, & NAM populations

2018 summer
- BC₁F₂ Populations

2019 summer
- BC₁F₃ Populations

2020 summer
- BC₁F₄ Populations

winter 2020
- Generate BC₁F₄ Testcross Hybrids

2021 summer
- Preliminary Hybrid Trials
  - Identify individual populations and lines with superior performance

2022 summer
- Multi-location Hybrid Trials
  - Multi-location testcross hybrid trials
    - TAMU AgriLife nurseries
    - seed company nurseries
  - Phenotype BC₁F₂ lines for traits of interest
  - Distributed BC₁F₄ lines to companies for proprietary testcross evaluation

2022 summer
- BC₁NAM Resource Development
  - Genotype by sequencing of BC₁F₄ lines
  - Initiate accuracy & analyses of phenotypic data
  - Initiate trait mapping
    - JICIM
    - GWAS
Collaborators & Funding

- Dr. Fred R. Miller MMR Genetics LLC (retired)
- Richardson Seed LLC
  - Dr. Jody Gilchrest
  - Dr. Gabriel Krishnamoorthy
  - Larry Richardson
- Texas A&M University
  - Professor Patricia E. Klein
  - Dr. Leo Hoffmann (GUESS Project Director)
  - Dr. Nikhil Patil
  - Texas AgriLife Sorghum Breeding Team