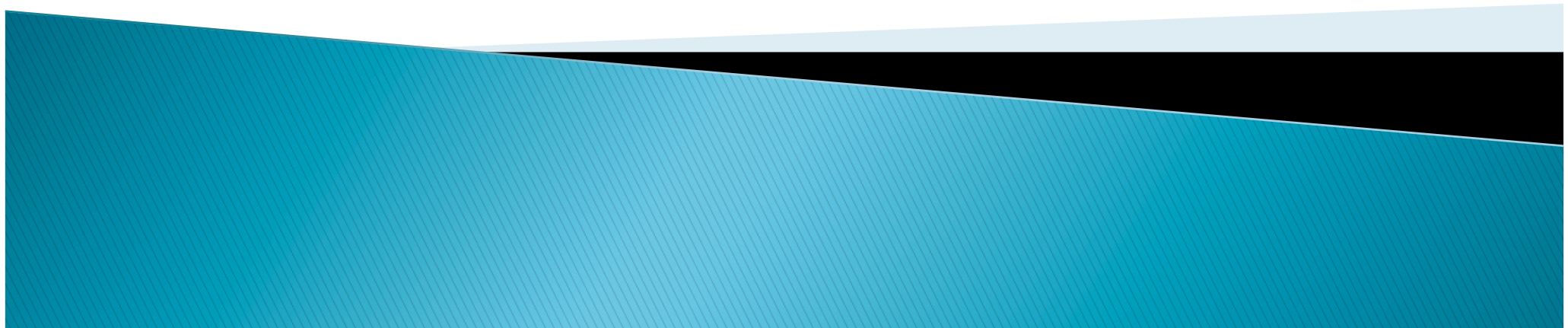


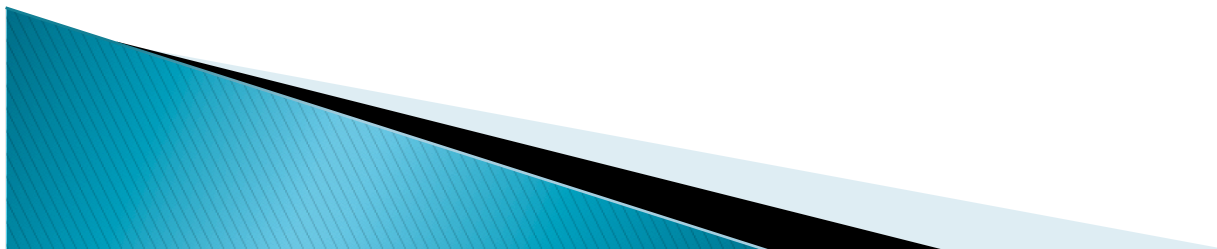
# Sweet Sorghum

Maya Mileck



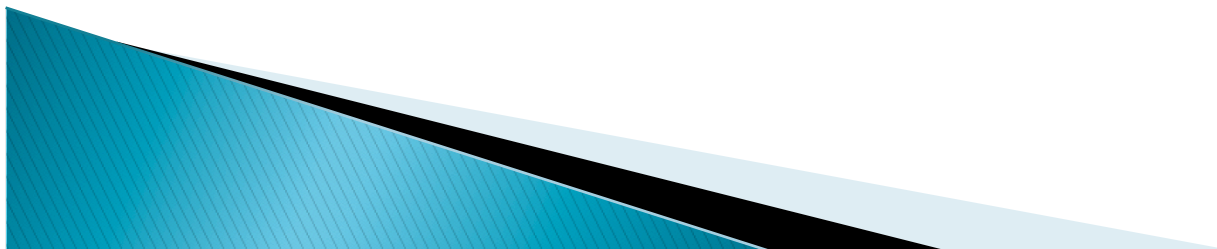
# Overview

- ▶ What is sweet sorghum
- ▶ Potential as a biofuel
- ▶ Transformation with bombardment
- ▶ My project



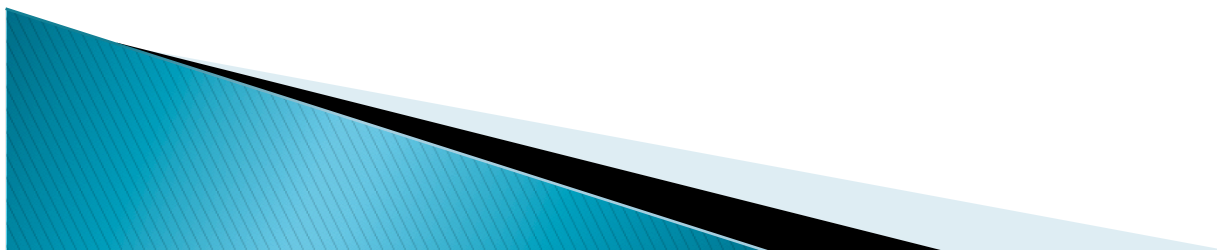
# Sweet Sorghum

- ▶ Accumulates high levels of sugar, mostly sucrose, in stalk
- ▶ Closely related to sugarcane
- ▶ Differs from grain and forage but still produces grain and high biomass



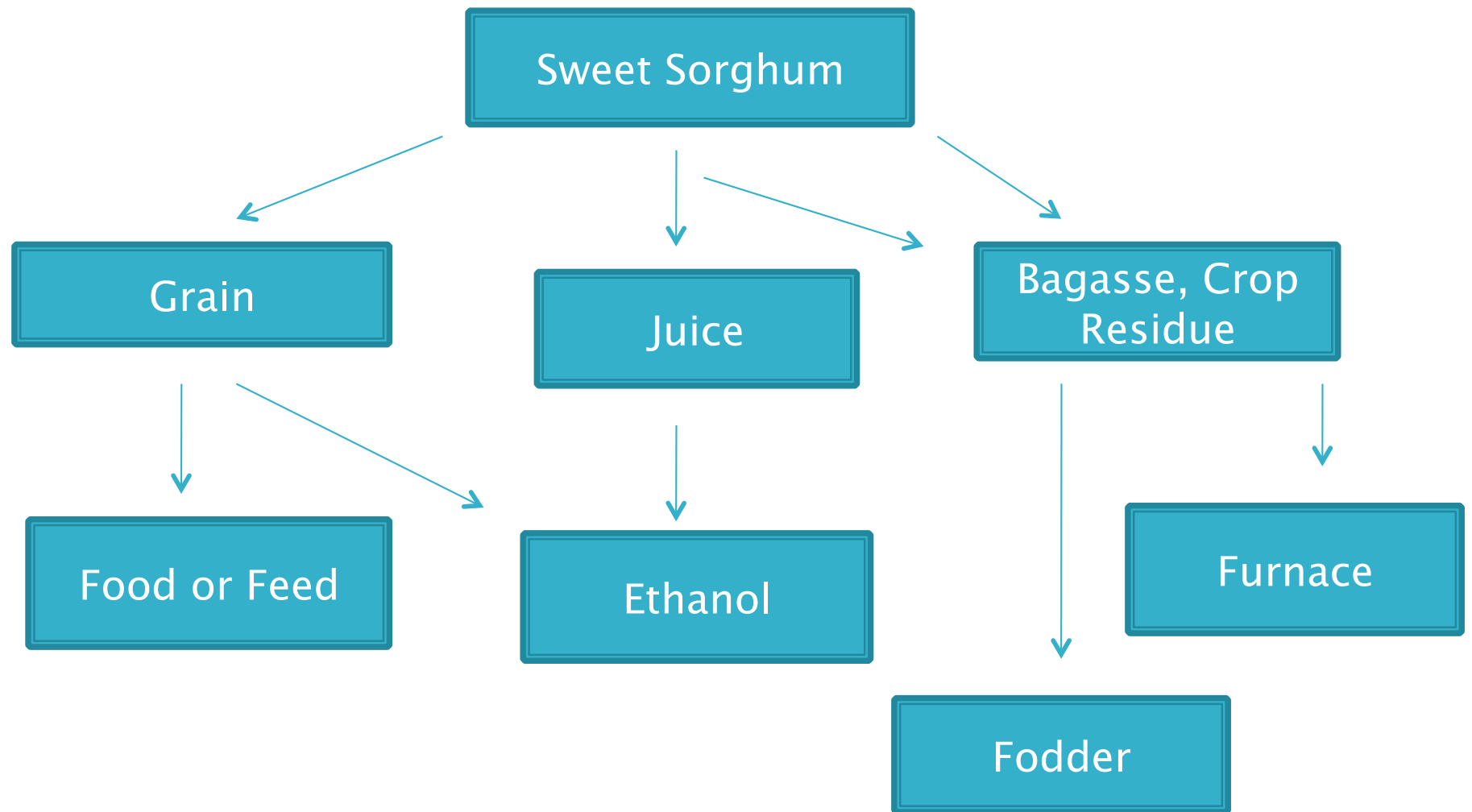
# Potential as a Biofuel

- ▶ Has the appropriate composition and yield for a potential biofuel
- ▶ Juice, grain, fodder and bagasse
- ▶ Sugar and starch: easiest ways to produce ethanol
- ▶ Grain: feed or ethanol production
- ▶ Leftover stalk and bagasse: fodder or burned



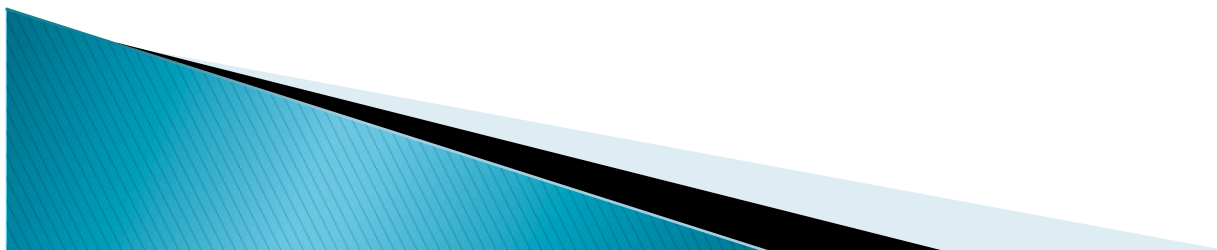


# Sorghum Processing



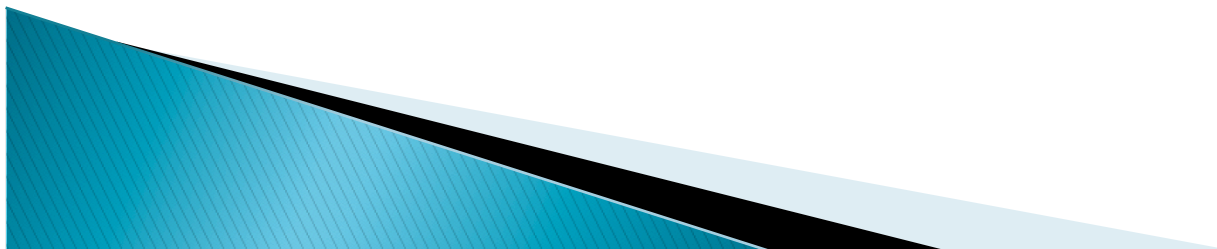
# Stress Tolerant and Efficient

- ▶ Ability to grow on marginal land
- ▶ No food–fuel issues
- ▶ Drought tolerance
- ▶ Low nutrient inputs
- ▶ Short duration (4 mo.)
- ▶ Efficient (low cost; high output)
- ▶ Annual, responsive to supply and demand changes



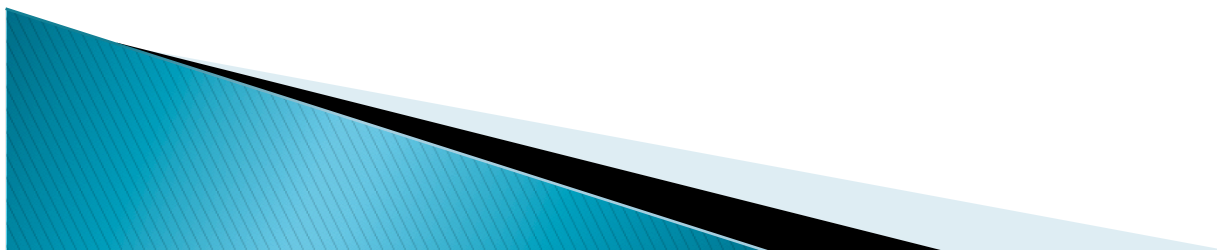
# Diverse

- ▶ Widely adaptable/flexible
  - Land races/cultivars
  - Biomass production (sugar, grain, biomass)
- ▶ Relatively well studied genome
- ▶ Existing genetic variation



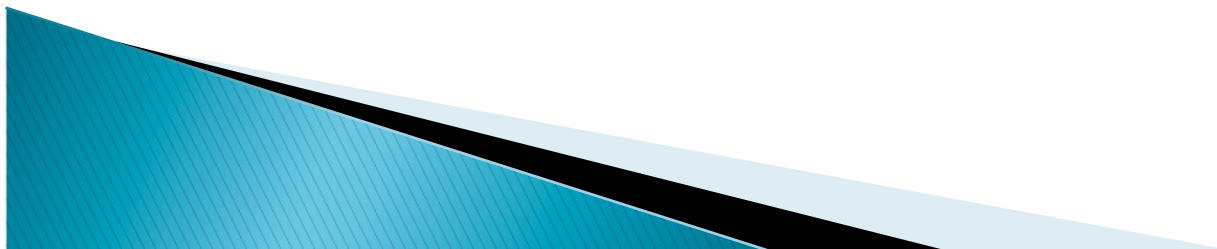
# Existing Genetic Variation

- ▶ Diversity of cultivars
- ▶ Brown midrib mutants (*bmr*)
  - Reduced lignin
  - Greater digestibility
  - Mutations in genes for enzymes of the lignin biosynthesis pathway
- ▶ Waxy mutation (*wx*)
  - Low amylose, high amylopectin
  - Improved ethanol conversion
- ▶ Photoperiod-sensitive
  - Longer growing season—maximize biomass



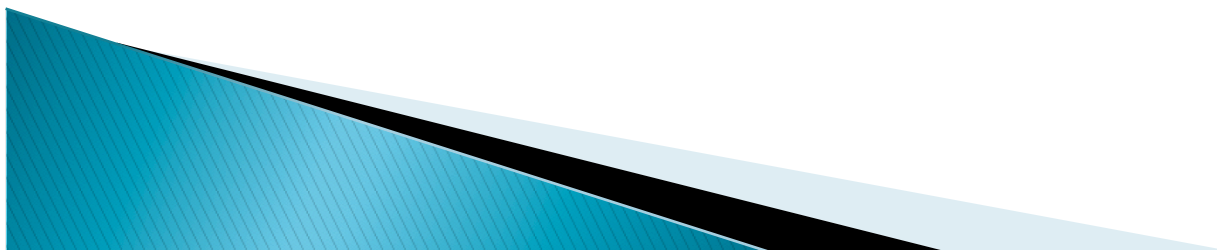
# Model system

- ▶ Smaller genome
- ▶ Sequenced
- ▶ Grain and sweet exist
  - ▶ Can look for potential changes that lead to sugar storage
- ▶ Good genetic and physiological model for sugarcane



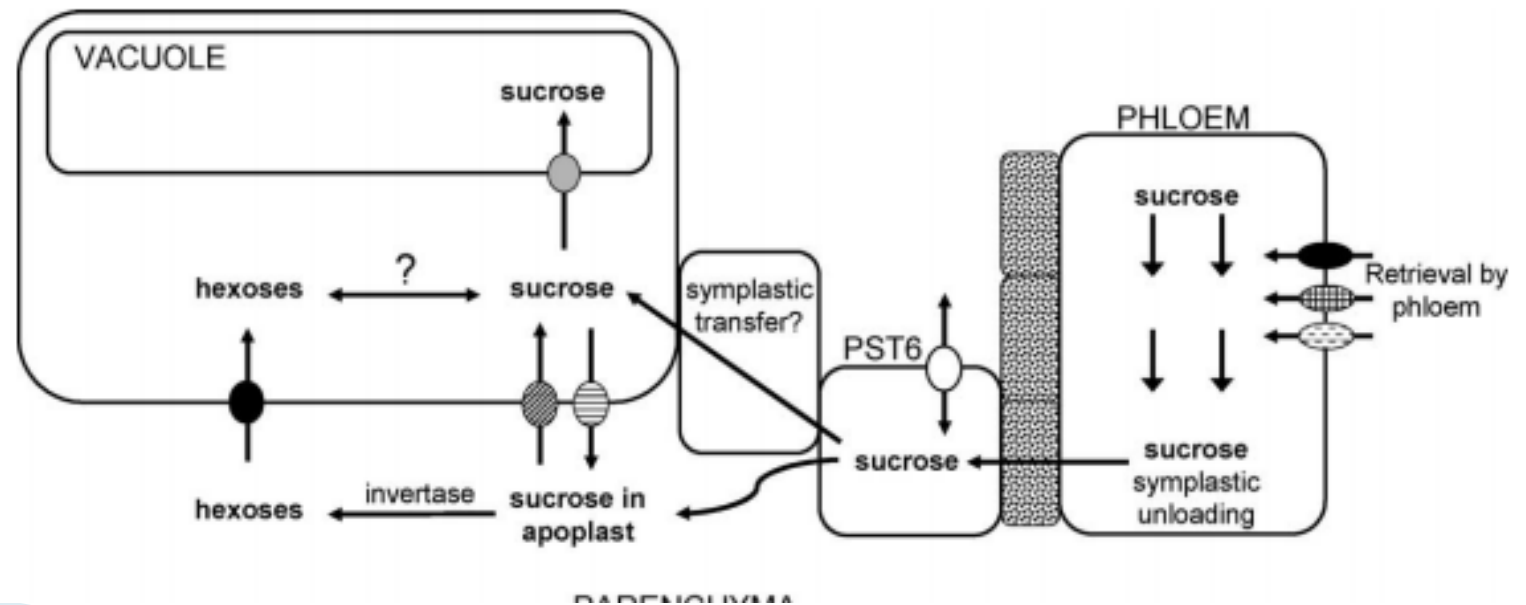
# Genes linked to higher sugar content

- ▶ Microarray analysis of sweet vs. grain sorghum
- ▶ Same species so it is much easier to do this
- ▶ 103 down-regulated
  - Cellulose and lignocellulose related genes
  - Cell wall formation genes
- ▶ 51 up-regulated
  - Starch degradation
  - Heat shock proteins
  - Abiotic stress proteins
- ▶ Application
  - Better understand sorghum
  - Improve other biofuel crops
  - “sweet sorghum-like transgenic corn”



# Sugar accumulation

- ▶ Sucrose transport not fully understood
- ▶ Sugarcane and sorghum similar
- ▶ Apoplastic vs. symplastic movement
- ▶ Intermediate hexoses



# Comparison to other potential crops

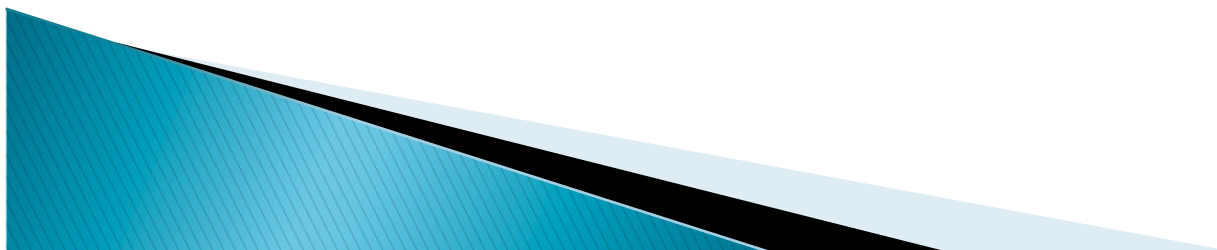
- ▶ Efficient (low cost; high output)
- ▶ 2/3 ethanol production compared to sugarcane
- ▶ Higher quality sugar
- ▶ Stalks can be used as bioenergy or to feed animals
- ▶ Grain can instead be used as food or fodder
- ▶ Cheaper to produce (\$75/L) than sugarcane (\$112/L) and corn (\$89/L)
- ▶ No fuel–food competition





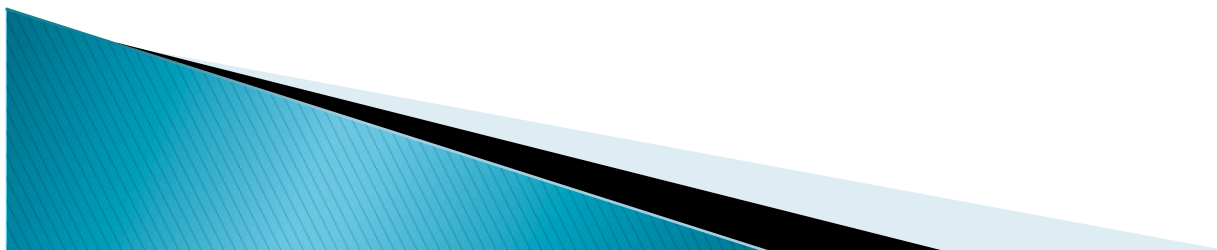
# Barriers to Biofuels

- ▶ Second generation biofuels, more costly, but necessary
- ▶ Difficult to break down secondary cell wall
- ▶ Lignin composition
  - Inhibits degradation, fermentation
  - Reduces conversion efficiency
- ▶ Cellulose, difficult and costly to break down



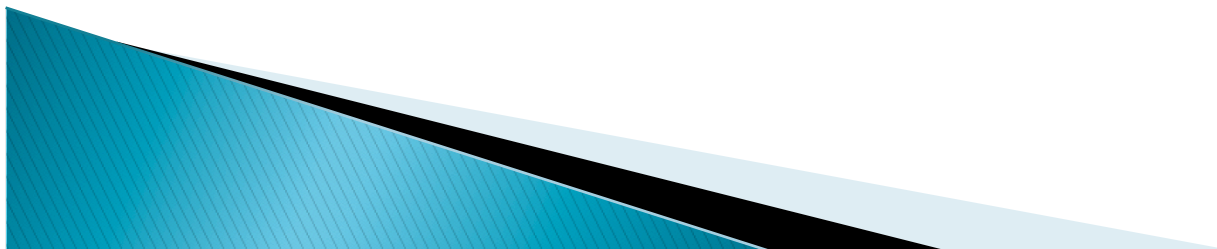
# Possible Improvements for Sorghum

- ▶ Traditional breeding with available germplasm
- ▶ Hybrids
- ▶ High-energy sorghum (grain+sweet)
- ▶ Transformants!
  - Pest and disease resistance
  - Cellulase producing
  - Altered lignin composition
  - Altered cell-wall composition
  - Improved sugar storage



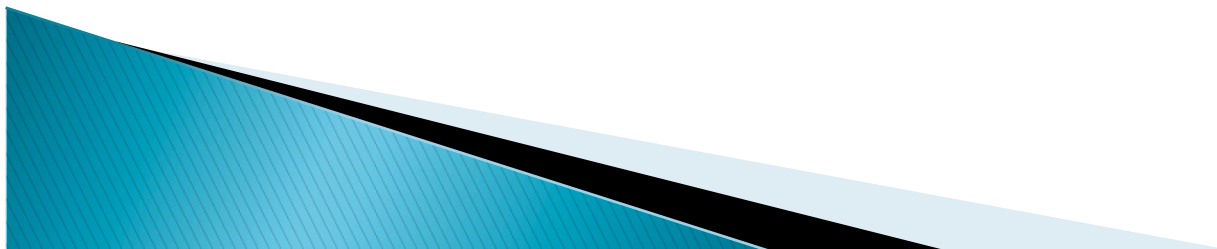
# Genetic Transformation of Sweet Sorghum

- ▶ Anshu Raghuwanshi, Robert Birch
- ▶ Motivation: sorghum as a biofuel!
- ▶ Sweet sorghum has never before been successfully transformed



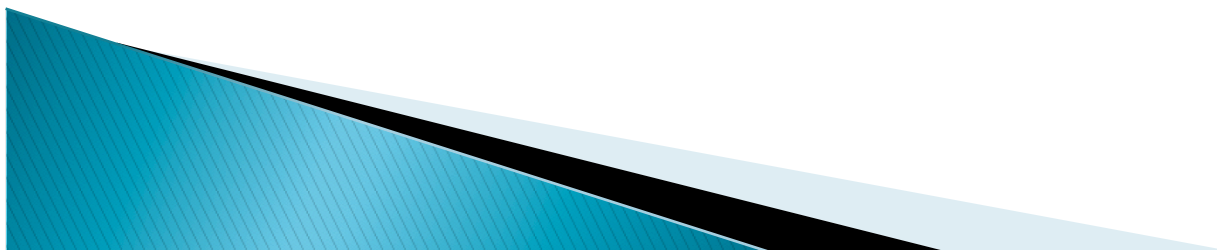
# Overview

- ▶ Screened for varieties amenable to tissue culture
- ▶ Optimized tissue culture and regeneration conditions
- ▶ Established transformation and selection protocol



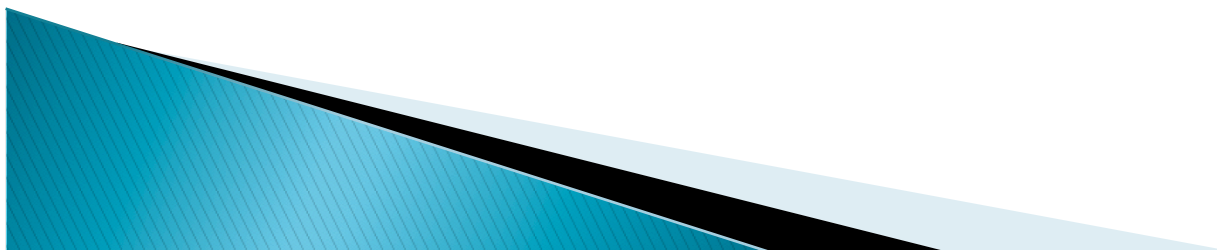
# Initial Screening

- ▶ Screened 32 Sweet sorghum varieties
  - Callus initiation (3–4 months in dark)
- ▶ 5 different media
- ▶ Results:
  - R19188, Ramada, Wray
  - Modified M11 (mM11)



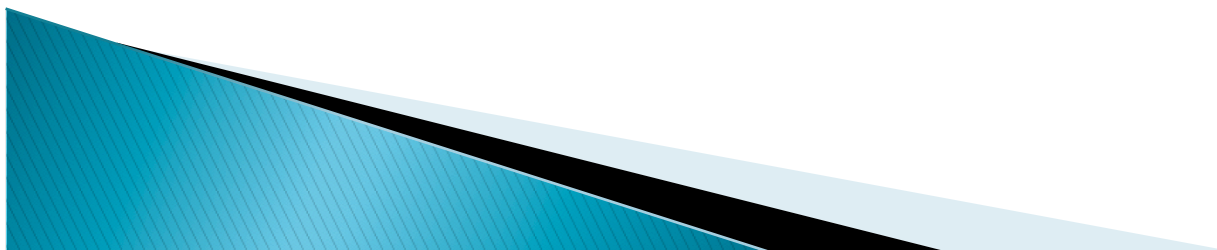
# Regeneration and Hormones

- ▶ Ramada showed the highest regenerability after tissue culture (greater than 85%)
- ▶ Hormones were optimized for Ramada: vary through callus induction, selection, and multistep regeneration



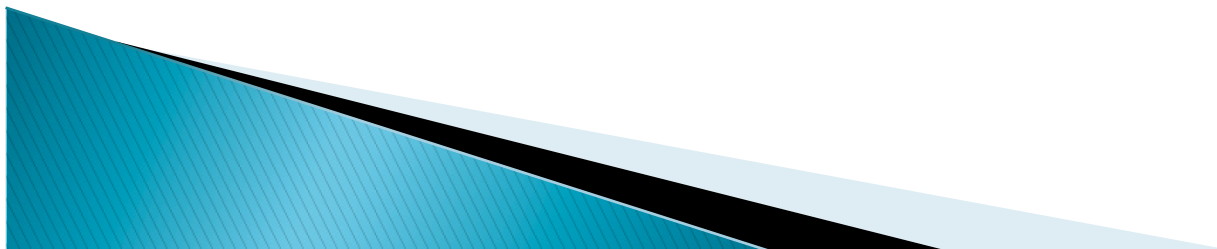
# Protocol

- ▶ Callus Induction
  - 4 days on mM11
- ▶ Selection
  - 3 weeks on selection media
    - mM11 + 40mg/L hygromycin
  - 8–12 weeks on callus proliferation media
    - mM11 + 0.5mg/L kinetin + 40mg/L hygromycin
- ▶ Regeneration w 40mg/L hygromycin
  - 2 weeks on regeneration medium
    - mM11 – 2,4-D, + 3mg/L BAP + 1mg/L TDZ
  - 2–3 weeks on shoot elongation medium
    - MS salts, sucrose, casein hydrolysate, CuSO<sub>4</sub>, 2mg/L BAP, NAA, phytigel
- ▶ Rooting
  - 5–8 weeks on rooting media
    - MS salts, sucrose, casein hydrolysate, NAA, phytigel



# Transformation, Selection, Regeneration

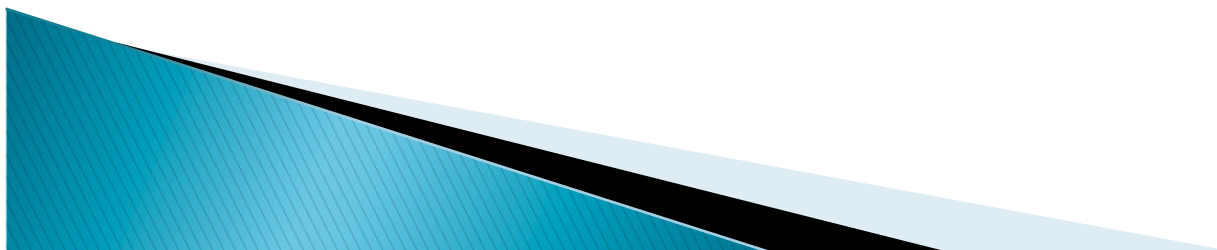
- ▶ Bombardment
- ▶ Co-transformation
  - Hygromycin phosphotransferase
  - Luciferase
- ▶ Selection
  - Hygromycin
- ▶ Regeneration
  - 0.09% efficiency
  - 16 lines
  - 2 albino, 1 only roots
  - 9 planted in greenhouse, 3 stunted and sterile
  - 17,000 embryos!!





# My Project

- ▶ Transform Ramada using the protocol from this paper
- ▶ Use Agrobacterium rather than bombardment
- ▶ Use PMI-GFP rather than hpt
- ▶ Gentler transformation and selection
- ▶ Super cool because no one has done it before!!



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# mM1 1

- ▶ 0.004  $\mu$ M BAP
- ▶ No micronutrients
- ▶ MES buffer
- ▶ Copper Sulfate
- ▶ Pyridoxal-5-phospate (not HCl)
- ▶ Agar
- ▶ pH 5.8

