Combining diversity within the cultivated Sorghum gene pool for decoding heterosis

Eyal Fridman

The RH Smith for Plant Sciences and Genetics
Faculty of Agriculture, Food, and Environment
The Hebrew University
Rehovot, Israel

Adaptation, and sources of variation

Genotype → Environment → Phenotype

Hybridization → G2P → G2H

Which of the models is more prevalent?

Dominance
- Bruce 1910
- Jones 1917
- Cokerham and Zheng 1996

Overdominance
- Crow 1948
- Stuber et al. 1992
- Lu et al. 2003
- Semel et al. 2006

Epistasis
- Powers 1944
- Melchinger et al. 2007
- Tang et al. 2010

Heterotic trait loci (HTL) mapping

Biparental populations:
- Test-crossing of introgression, recombinant inbred or mutant lines:
  - Semel et al. 2006. Tomato ILs
  - Meyer et al. 2010. Arabidopsis RILs and ILs.
  - Frascaroli et al. 2007, 2012. Maize RILs, NILs.
- Immortalized F2 populations:
  - Hua et al. 2003. Rice
  - Tang et al. 2010. Maize

Multi-allelic populations:

Heterosis Mapping in Plants

Birchler et al. (2006) PNAS

ODH - Overdominant heterosis

DDH: Overdominant heterosis
**Sorghum bicolor**

**Agriculture:**
- Sorghum ranks 5th in cereals for global production.
- It is used as human food, animal feed and ethanol production.

**Genetics:**
- Fully sequenced (Paterson et al. 2009)
- The 730 megabase genome is app. 1/3 of the maize genome.
- LD levels are in between maize and arabidopsis.
- About 80% of genetic variations in the wild species are represented within land races and cultivated varieties.

---

**Working flow- Sorghum diallel**

**Crops**
- 126 genotypes X 7
- 54 reciprocal (Minimal phenotype)
- 157 genotypes X 4
- 18 reciprocal
- 142 genotypes X 4

**Field phenotype**

**Dpw4.1 grain yield heterotic trait locus (HTL)**

**Whole-plant phenotype**

**Reproductive traits:**
- Dry Panicle Weight (DPW)
- Grain Dry Weight (GDW)
- Grain Number (GN)
- Panicle architecture traits –
  - Rachis length (RL)
  - No. of whorls (WN)
  - No. of primary branches (PBN)
  - Length of primary branches (PBL)
  - No. of secondary branches (SBN)
  - No. of secondary branches with tertiary branches (TBN)
- Days to Flowering (DTF)

**Vegetative traits**
- Height (PH)
- Stem diameter (D)
- Vegetative weight (VGW)

**Grain quality:**
- Grain nitrogen concentration (GNC)
- Grain Nitrogen (GRN)
- Grain Carbon (GCC)

---

**Heterosis distribution**

1. **Vegetative**
2. **Reproductive**
3. **Quality**

Ben-Israel et al., 2012

Ben-Israel et al., Submitted
Interplant relationship under heterosis

Direct phenotype: Trait values

Derived phenotype: Heterosis values

Genotype By Seq.

- Genomic DNAs were digested individually with ApeKI (recognition site: G|CWCG), and GBS libraries were constructed.

- DNA sequencing was performed on the Illumina Genome Analyzer.

- Has been sequenced with the larger Sorghum collection (Morris et al. 2013,PNAS) – reliable SNP calling

**Results:**
- 28,231 SNPs -- data for all FLs
- 2 SNPs – informative SNPs, in which rare allele is represented by 3 or more FLs.

Mapping HTLs - SNPs

- Four models were used to test for association between each SNP and heterosis values: Overdominant, Dominant, recessive and additive (following correction for pop structure).

\[ Y_{ij} = \mu + \alpha_i + \beta_j + e_{ijk} \]

- The model showing minimum AIC (Akaike information criterion) value was considered as the best fitted model.

HTL map- Grain nitrogen traits

All genetic model

Diallel vs F2
**HTL map - Yield traits**

- **Overdominance**
- **Complementation**

**Grain number regulator 10.1 (SbGnr10.1)**

**Yeast heterozygosity~nonadditivity landscape**

**Co-localization of Yield HTLs**

- HTL identified in both years (P<0.001)
- All genetic models

**Gnr10.1-- F2 analysis**

**Implementing Efficient Allele Mining Approach**

*ComSeq*, for Compressed Sequencing, combines NGST with computational tools based on the mathematical field of Compressed Sensing.

- 5,000 DNAs
- Of M2 families

**Genome scan**

- 10.17918291

**Reciprocal hemi assay (hybrid bcknd)**

**Introgression assay (homozygous bckgnd)**

**ComSeq** based reconstruction of rare allele carrier

+ Yaniv Erlich [MIT], Zhanguo Xin [USDA]

**Shental et al. (2010) Nucl Acid Res**
Summary and prospect:

• Heterosis in sorghum is predominantly driven by dominance complementation
• Tradeoff release under heterosis between GDW and GN (canalization on GDW)
• Genome scan in diallel identify known and unknown causal variation underlying agronomic traits
• Fine mapping and gene targeting for genes of grain yield heterosis should consider whole-genome hybrid background
• Next wave of investigating of molecular mechanisms underlying would benefit from investment and advancements in allele editing

Comparative association

Phenotypic Analysis

Grain nitrogen content 7.1 (Gnc7.1)

Finer mapping of HTL

ortholog. The wheat GRAIN PROTEIN CONTENT B1 (GPC-B1)

Liu et al. (2006) Science

Imri Ben-Israel
Habte Nida
Dhruv Srivastava
Ilana Glikaite
Silvia Shaked
Rachel Shapira
Lior David

Support:
Nofar (MOST)
Yissum-HUJI

Jianming Yu
Yuye Wu
Sahron Mitchell (Cornell)
Noam Shental
Yaniv Erlich
Dina Zielinski

Andreas Graner
Nils Stein
Benjamin Kilian

Asaf Distelfeld
Raz Avni

Morris et al. (2013) PNAS

Ben-Israel et al. In prep


Finer mapping of HTL