

Genomic Architecture of Highland Adaptation in Maize

April 21, 2014

1 Genetic architecture of highland adaptation

1.1 Questions

- What is the genetic basis of highland adaptation?
- How much is shared between Mexico and South America?
- Between maize and teosinte?

1.2 QTL of high x low in Mexico and S. America

- Map at 3 sites: low Mexico (RS), high Mexico (RS), Missouri (SFG)
- 960 F2:3 families; 40 checks
- population development (SFG)
- genotyping and mapping (JRI, SFG)
- DNA extraction, genotypes (SFG)
- Sequence parents (JRI)
- Mapping (SFG)

1.3 Admixture mapping in *mex/parv* hybrid zone

- 500 individuals (plant extra) from Ahuacatitlan (MBH, RS)
- DNA extractions (ACJ)
- collection trip (MBH)
- genotype calling (MBH, ACJ)
- mapping (GC)

1.4 Phenotypes

- macro hairs (SFG, RS, MBH)
- flowering time (SFG, RS, MBH)
- tassel morphology (SFG, RS, MBH)
- plant height every 2 weeks & at flowering (SFG, RS, MBH)
- biomass (SFG, RS, MBH)
- # ears (mz), 50k weight (mz/teo), total seed weight (mz) (SFG, RS, MBH)
- stem/plant color (SFG, RS, MBH)
- germination depth, temp in greenhouse (F2:3 only; MBH)
- roots (inquire with Topp, Bloom)

2 Adaptation and introgression

2.1 Questions

- Are introgressed loci adaptive?
- Does evidence of natural selection correspond to QTL?
- Are highland QTL/loci widespread in highland climes?

2.2 Introgression and Admixture

- GBS of 30 inds x 10 pops x 2 subspecies (mex & maize) (JRI)
 - Popgen on maize/mexicana introgression (JRI, GC)
- GBS Additional 5 admixed parv/mex populations (50 inds. each) (JRI)
 - Popgen on additional admix pops (JRI, GC)

2.3 Global analysis of highland haplotypes

- Occurance of highland haplotypes/QTL/SNPs in global pops (MBH, ACJ)
 - 500 worldwide accessions GBS (MBH)
- Case study in Chihuahua (ACJ)
- BAYENV2 selection on altitude in SEEDs data (RS, ACJ, GC/JRI)

3 Functional characterization of QTL

3.1 Questions

- What do QTL/selected loci/introgressed loci) do?

3.2 Fine map pigmentation

- PT x T43 NIL population (RS)
- GBS genotyping (MBH)

3.3 Allelic series for QTL of interest

- 10 parents:
 - 4 parents F2:3
 - mexicana TIL18
 - Palomero Toluqueño
 - 2 lowland landraces
 - 2 highland landraces
- Cross into 3 parents for phenotyping
 - B73 (SFG)
 - T43 (MBH)
 - CML457 (RS)

3.4 RNAseq

- Time series analysis of plants in field (ACJ)
- 15 Lines
 - 4 F2:3 parents
 - 1 NIL chr4,
 - 1 each mex & parv TIL
 - B73, CML457, T43, PT
 - highland/lowland landraces used in allelic series (MBH to inbreed)
- 12 plants per line per environment (2 pools of 6)
- 4 stages/tissues per plant
- 2 environments (high/low fields)

4 Broader Impacts

4.1 Exchange Program

- 2 students per year
- 3-6 month stint in other lab
- Training: next-gen analysis, crossing & phenotyping, mapping

4.2 Phenotyping workshop

- Yearly workshop at UM
- Participants pay to purchase handheld
- 2 day workshop provides software, training on phenotyping in maize

4.3 Software

- R code for novel analysis for admixed populations
- Software & pipelines on github

4.4 Germplasm resources

- NIL population & F2:3 submitted to stock center