

# Genomic Architecture of Highland Adaptation in Maize

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## 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
- 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 Phenotyping workshop**

### **4.2 Software**

### **4.3 Germplasm resources**