

# **1 Genetic architecture of highland adaptation in Zea mays**

## **1.1 Questions**

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

## **1.2 QTL mapping of highland adaptation traits in high x low mapping populations from Mexico and S. America**

- Phenotyping at 4 sites:
  - low Mexico (RS)
  - high Mexico (RS)
  - Missouri (SFG)
  - growth chamber (MBH)
- 960 F2:3 families; 40 checks
- population development (RS, SFG)
- genotyping and mapping (JRI, SFG)
- DNA extraction, genotypes (SFG)
- Sequence parents (JRI)
- Mapping (SFG)

## **1.3 Admixture mapping in mex/parv hybrid zone**

- collection trip (MBH)
- 500 individuals from Ahuacatitlan in Mexico (MBH, RS)
- DNA extractions, genotyping (MBH)
- phenotyping (MBH, RS)
- mapping (MBH/GC)

## 1.4 Phenotypes

- macrohairs (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 Bloom)
- ionomics (Ivan via letter of support)

## 2 Introgression, admixture, and adaptation

### 2.1 Questions

- Are introgressed loci adaptive?
- Does evidence of introgression and 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)
- Introgression and adaptation in additional admix pops (JRI, GC)

### 2.3 Global analysis of highland haplotypes

- Occurrence of highland haplotypes/QTL/SNPs in global pops (MBH)
- 500 worldwide accessions GBS (MBH)
- Case study in Chihuahua (ACJ)

### **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 Toluqueo
  - 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 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