

The Genomic Basis of Local Adaptation in Maize

June 12, 2013

Catalyzing New International Collaborations (NSF)

Due Date: Rolling acceptance.

1. Need to submit request for support to NSF Plant Genome prior to submitting grant.
2. Funds two meetings to discuss grants/preliminary data, two seasons of line development, sequencing of mapping population parents and/or GBS of populations.

Plant Genome Research Program (NSF)

Due Date: March 2014.

Components

1. Genetic architecture of highland adaptation

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

 - (a) QTL of high x low in Mexico and S. America (SF-G (& RS?))
SF-G on S. America and Mexico?
Grow both high and low? Who does which?
 - (b) *parviglumis* x *mexicana* cross
Doebley has seed of TC1: (*mex* x *parv*) x A158 (who?)
 - (c) Admixture mapping in *mex/parv* hybrid zone (GC & MBH)
GC on analysis, new theory (better precision mapping?)
MBH on phenotyping and genotyping
2. Adaptation and introgression

Questions: Are introgressed loci adaptive? Does evidence of natural selection correspond to QTL? Are highland haplotypes that are widespread in maize adapted to highland climes?

- (a) Increased depth/precision relative to Hufford *et al.* 2013 (JR-I)
- (b) Global analysis of highland haplotypes and/or F_{ST} in low/high pops (Oaxaca, Ethiopia, Guatemala, etc.) (MBH & ACJ)
- 3. Functional characterization of QTL
 - Questions:** What do the QTL (or selected/introgressed loci) do?
 - Something here about RS's NILs or other introgression pops. (RS)

Outstanding questions

1. Where will growouts take place? Puerto Rico (SF-G), Mexico, Hawaii?
2. Do we include highland and lowland sites for all phenotyping?
3. What will South American cross include?
4. What needs to be sequence/GBSed for CNIC and Plant Genome grant?
 - (a) Outbred highland landraces X lowland Doebley inbred (SF-G will set this up summer 2013)?
 - (b) DH highland landrace X lowland Doebley inbred (MBH growth chamber w/ seed from SF-G)?
 - (c) Highland Murray inbred X lowland Doebley inbred
5. Do we try to drill down on a small set of genes?
6. Should we include Southwest US material (there are both highland and lowland accessions)?
7. Do we include *parviglumis* x *mexicana* cross and if so who does it?
8. What are broader impacts/outreach? Continue US-Mexico student exchange program currently implemented in Maize Centromere NSF-Plant Genome Grant?
9. Monthly and annual meetings?
10. Students/pdocs/shared field work?
11. Do we measure other (harder) phenotypes?
 - (a) Root chilling
 - (b) UV sensitivity
 - (c) Germination
12. Can we leverage SEED data being generated by CIMMYT (GBS of many, many landraces)?
13. Basic budget (personnel, sequencing, field facilities)?
14. Basic timeline?