The Genomic Basis of Local Adaptation in Maize

June 20, 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?

    (a) PT x T43 NIL population development

    (b) Fine map pigmentation

    (c) 4 parents + mex + parv RNAseq time series

    (d) Allelic series at some other QTL in T43, B73 and CML457

- 10 parents (4 from F2:3, mexicana, PT, 2 more lowland, 2 more highland)

Outstanding questions

1. Basic timeline?

2. CNIC?