GENOME-WIDE PATTERNS OF CLIMATE ADAPTATION IN TEOSINTE (ZEA MAYS)

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teosinte

Mauricio 2001, Doebley 1997

cultivated maize

Photo by Hugh Ilitis
Maize production

Current distribution of teosinte

(Hufford et al. 2012)
Teosinte as a study system

- Teosintes, *Zea mays* ssp. Wild relatives of maize, same species!
- Large, outcrossing populations
- A lot of genetic, phenotypic and environmental variation among populations
- Genetic tools and resources of maize available

Photo by M.B. Hufford
Two subspecies of *Zea mays*

- **Zea mays ssp. *mexicana***
  - High elevations (1600-2700 m)
  - More common to hybridize with maize

- **Zea mays ssp. *parviglumis***
  - Lower elevations (400-1900 m)
  - Rare crossing with maize
  - Progenitor of maize

*Photo: M. B. Hufford*

Doebley & Ilitis 1980, Fukunaga et al. 2005
Objectives

Detect and describe the genetic basis of local adaptation in teosinte

Investigate the distribution of adaptive variation among subspecies, populations and along the genome
21 sampled populations
12 individuals per population

Environmental data (climate, soil) from public databases

Mean annual temperature
Mean annual precipitation

www.worldclim.org
Genotype Data

• Maize SNP chip (Illumina)
  – Genetic markers (SNPs) developed for maize
  – Targeted in genic regions
  – Average distance between SNPs: 40 kb

• SNPs after quality check: 37 000 SNPs
Population structure

- Strong, complex, hierarchical population structure affected by:
  - Altitude
  - Distance
  - Dispersal
  - Admixture
  - Taxonomy
Patterns of linkage disequilibrium (LD) – chromosome 9

Ting et al. (1964)
Large, polymorphic inversions in teosinte

- Alltogether, four putative large inversions were identified: Inv1n, Inv4m, Inv9e, Inv9d
- They comprise 5% (160 Mbp) of the reference genome
  - Probably more to be found with denser marker sets
Approaches to detect genetic basis of local adaptation

1. $F_{ST}$ outliers under hierarchical model (Excoffier et al. 2009)

2. Population-specific outliers, $F_{FT}$

3. BAYENV, test for correlation between environment and allele frequencies (Coop et al. 2010)

4. PHS, regions of excess haplotype sharing
Correlation with temperature and soil within *mexicana*

33 x enrichment of SNPs associated with temperature range \( (p: <0.001) \)

8 x enrichment of SNPs associated topsoil type \( (p: <0.001) \)
Inversions and local adaptation

• Inversions were 2-fold enriched among environmentally correlated candidate SNPs (p-value < 0.001)

• Inversions are $F_{ST}$ (genetic differentiation) outliers, too
Why local adaptation signal is enriched in inversions?

- Inversions suppress recombination
- And may be adaptive:
  - Dobzhansky: They contain sets of co-adapted alleles
  - Kirkpatrick and Barton (2006): They capture locally adapted alleles
  - Yeaman (2013): genomic rearrangements create clusters of locally adapted loci
Patterns of local adaptation outside inversions

• In *Arabidopsis thaliana* and humans, SNPs correlating with environment are enriched for genic and non-synonymous SNPs (Hancock 2011, 2011)

• In teosinte, we do not find enrichment for genic, non-synonymous, tissue-specific, functional category...
Enrichment for non-coding SNPs in teosinte

Teosinte

Arabidopsis thaliana

Fold Enrichment

F_{ST}  F_{FT}

BAYENV

PC1  PC2  PC3  PC4  PC5  PC6  F_{5}  F_{6}

Environmental correlation

Fold of enrichment for genic SNPs
Synthesis

- Genetic rearrangements and non-coding SNPs seem to play a role in *Zea mays* local adaptation
  - E.g. inversion in chromosome 4 has introgressed from *mexicana* to highland cultivated maize in Mexico (Hufford et al. 2013)
Synthesis

• The complex and large genome of Zea facilitates adaptation through regulatory variation?
  – Genetic changes associated with domestication: apical dominance (*tb1*) and prolificacy (*gt1*) have been mapped to regulatory, non-coding parts of the maize genome (Wills et al. 2013, Studer et al. 2011)
  – Typical to most plants?
Morrell et al. 2012
Thank you!

• Coauthors: Matthew B. Hufford, Sofiane Mezmouk, Jeffrey Ross-Ibarra
• Statistical advice: Joost van Heerwaarden, Andrew Eckert
• Samples: Pesach Lubinsky & Norm Ellstrand, UC Riverside
• Lab: Lauren Sagara

• Funding:

• Publication: Pyhäjärvi et al. (2013) GBE 5:1594:1609